

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72  
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71  
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein; 6.70  
 445363; NM\_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70  
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63  
 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59  
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57  
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57  
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55  
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete; 6.55  
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55  
 422785; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51  
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49  
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A; 6.44  
 427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42  
 430280; AA361258; Hs.237868; interleukin 7 receptor; interleukin 7 receptor; 6.42  
 432938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42  
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40  
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3\_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3\_HUMAN TUBBY; 6.40  
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39  
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39  
 441384; AA447849; Hs.288650; retinoic acid induced 3; retinoic acid induced 3; 6.38  
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34  
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34  
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypept; 6.31  
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright; 6.31  
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mis5, S. pombe) 6; minichromosome maintenance deficient (mi; 6.31  
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30  
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30  
 415829; AW450198; Hs.163742; ESTs; ESTs; 6.28  
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26  
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25  
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25  
 428918; AL036967; Hs.2324; protamine 2; protamine 2; 6.24  
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19  
 424415; NM\_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19  
 407245; X90568; Hs.172004; titin; titin; 6.18  
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18  
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16  
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13  
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12  
 430521; NM\_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10  
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10  
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino; 6.09  
 402260; ; NM\_001436; Homo sapiens fibrillarin (FBL), mRNA, transcript (F8A), mRNA; NM\_001436; Homo sapiens fibrillarin (FBL); 6.09  
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05  
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); interferon, alpha-inducible protein (clo; 6.04  
 402678; ; Target Exon; Target Exon; 6.03  
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01  
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01  
 420596; NM\_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01  
 420676; AI434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00  
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99  
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98  
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98  
 413313; NM\_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95  
 417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94  
 449569; AI656634; Hs.195389; ESTs; ESTs; 5.92  
 436576; AI458213; Hs.77542; ESTs; ESTs; 5.90  
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89  
 420005; AW271106; Hs.133294; ESTs; ESTs; 5.89  
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88  
 403171; ; C2001472; gij5809678[gij5809678]AAB41848.2 (U64675) sperm membrane protein BS-63 [Homo sapiens]; C2001472; gij5809678[gij5809678]AAB41848.2 (U64; 5.87  
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87  
 406137; ; NM\_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA, VERSION NM\_000178.1 GI; NM\_000179; Homo sapiens mutS (E. coli) h; 5.85  
 423787; AI295745; Hs.236204; nuclear pore complex protein; nuclear pore complex protein; 5.85  
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84  
 452796; AB011100; Hs.30656; KIAA0528 gene product; KIAA0528 gene product; 5.84  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80  
 447359; NM\_012093; Hs.18268; adenylate kinase 5; adenylate kinase 5; 5.79  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78  
 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1\_HUMAN ALU S; 5.75  
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5\_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5\_HUMAN LEUKE; 5.74  
 436251; BE515055; Hs.296585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73  
 421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71  
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69  
 425159; NM\_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspartate; 5.69  
 401704; ; NM\_021195; Homo sapiens claudin 6 (CLDN6), mRNA. VERSION NM\_020982.1 GI; NM\_021195; Homo sapiens claudin 6 (CLDN6); 5.66  
 425358; AL079658; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin assoc; 5.65  
 402677; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.64  
 409264; NM\_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63  
 432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63  
 409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63  
 430252; AI638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61  
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61  
 452816; AA131789; Hs.61509; ESTs; ESTs; 5.60  
 402679; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.59  
 414291; AI289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58  
 453028; AB006532; Hs.31442; RecQ protein-like 4; RecQ protein-like 4; 5.58  
 453905; NM\_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56  
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-associ; 5.55  
 419660; BE280337; Hs.194653; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino ; 5.55  
 446979; AI654443; Hs.197683; ESTs; ESTs; 5.54  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kin; 5.53  
 418962; AA714835; Hs.271863; ESTs; ESTs; 5.53  
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 5.52  
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); integrin, alpha L (antigen CD11A (p180); 5.52  
 449322; AI638616; Hs.196566; ESTs; ESTs; 5.51  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51  
 415141; AA189099; Hs.26817; ESTs, Weakly similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7\_HUMAN ALU S; 5.48  
 454048; H05626; Hs.6921; ESTs; ESTs; 5.46  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45  
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 fis, clone HE; 5.44  
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44  
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisi; 5.44  
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class ; 5.44  
 427668; AA289760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43  
 449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22802 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 5.41  
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40  
 450746; D82673; Hs.278589; general transcription factor II, i; general transcription factor II, i; 5.40  
 425966; NM\_001761; Hs.1973; cyclin F; cyclin F; 5.39  
 418134; AA397769; Hs.86617; ESTs; ESTs; 5.38  
 432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37  
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, m; 5.36  
 428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.; 5.35  
 406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 5.34  
 415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII); 5.33  
 448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor; 5.32  
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 5.32  
 429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32  
 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A; 5.30  
 414907; X0725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30  
 422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29  
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosop; 5.28  
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26  
 416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer anti; 5.21  
 450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20  
 409670; AJ368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20  
 429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20  
 409808; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19  
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 doma; 5.19  
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 5.16  
 437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-asso; 5.15  
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15  
 436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor t; 5.14  
 426752; X69490; Hs.172004; titin; titin; 5.13  
 415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2; 5.13  
 400263; ; Hs.75309; Eos Control; Eos Control; 5.13  
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin a; 5.12  
 427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10  
 407347; AA829847; ; gb:od40d07.s1 NCL\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Ahu repetitive element, mRNA sequence.; gb:od40d07.s1 NCL\_CGAP\_GCB1 Homo sapiens; 5.10  
 458933; AI638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10  
 450431; AW136797; Hs.266041; ESTs; ESTs; 5.09  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08  
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-recept; 5.08  
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05



- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03  
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03  
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02  
 433592; NM\_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog); 5.02  
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha 2 (RAG cohort 1, importin alpha 1); 5.00  
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00  
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99  
 402145; ; Target Exon; Target Exon; 4.99  
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99  
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, cont; 4.98  
 419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97  
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97  
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96  
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96  
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94  
 426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91  
 440129; AA865818; Hs.369523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-like; 4.91  
 453922; AF053306; Hs.35708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1; 4.90  
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88  
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88  
 437162; AW005505; Hs.5454; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87  
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG51) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIG; 4.87  
 421350; AF0301608; Hs.278188; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene; 4.87  
 409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86  
 424304; NM\_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86  
 437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase tra; 4.84  
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83  
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82  
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82  
 424081; NM\_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81  
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81  
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor (gly; 4.81  
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80  
 409101; NM\_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79  
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79  
 447250; AI879099; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79  
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78  
 448950; AF288687; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78  
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C; 4.78  
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76  
 420261; AW205093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 4.76  
 421905; AI660247; Hs.32699; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H; 4.75  
 413880; AI660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74  
 418355; L42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; ATPase, H7 transporting, nongastric, alp; 4.74  
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74  
 428024; Z29057; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74  
 421845; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72  
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72  
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70  
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bamacan); chondroitin sulfate proteoglycan 6 (bama; 4.70  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69  
 449475; AI348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69  
 420062; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69  
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIIB (25-hy; 4.69  
 436856; AI469355; Hs.127310; ESTs; ESTs; 4.68  
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67  
 411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67  
 426726; AA488915; Hs.171955; trophinin associated protein (tastin); trophinin associated protein (tastin); 4.67  
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67  
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66  
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65  
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, ; 4.65  
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64  
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64  
 415724; NM\_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63  
 435045; BE297155; Hs.143898; ESTs; ESTs; 4.62  
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62  
 414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62  
 436685; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62  
 449515; AI653378; Hs.302012; ESTs; ESTs; 4.61  
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61  
 420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61  
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61  
 413441; A1929374; Hs.75367; Src-like-adaptor; Src-like-adaptor; 4.60  
 456847; AI360456; Hs.86088; ESTs; ESTs; 4.58  
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57  
 426935; NM\_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57  
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56  
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L ORF; 4.55

- 443068; A1188710; Hs.374480; ESTs; ESTs; 4.55  
 441607; NM\_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54  
 453227; AW135862; Hs.243991; ESTs; ESTs; 4.52  
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51  
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascin homolog like); singed (Drosophila)-like (sea urchin fas; 4.51  
 453613; F06838; Hs.374476; ESTs; ESTs; 4.50  
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H; 4.50  
 412507; L36645; Hs.73964; EphA4; EphA4; 4.50  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49  
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo; 4.49  
 406547; ; Target Exon; Target Exon; 4.49  
 443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48  
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47  
 448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47  
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46  
 446236; NM\_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46  
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46  
 420340; NM\_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 complex); CD32 antigen, zeta polypeptide (TIT3 com; 4.46  
 413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt; 4.44  
 421819; NM\_013403; Hs.108665; zinedin; zinedin; 4.44  
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44  
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, Dr; 4.43  
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; ESTs, Highly similar to A35661 DNA excis; 4.43  
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42  
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42  
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42  
 413186; AJ077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic; 4.42  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40  
 424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39  
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37  
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35  
 400440; X83957; Hs.83870; nebulin; nebulin; 4.35  
 437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34  
 430478; NM\_014349; Hs.241535; apolipoprotein L, 3; apolipoprotein L, 3; 4.34  
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33  
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33  
 415995; NM\_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33  
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30  
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfam; 4.29  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29  
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled recepto; 4.28  
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28  
 426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28  
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component; 4.27  
 437908; A1082424; Hs.351043; ESTs; ESTs; 4.27  
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27  
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26  
 439334; A1148976; Hs.112062; ESTs; ESTs; 4.26  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25  
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24  
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24  
 447528; A1612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22  
 449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22  
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22  
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22  
 425356; BE244879; Hs.155939; inositol polyphosphate 5-phosphatase, 145kD; inositol polyphosphate 5-phosphatase, 14; 4.22  
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21  
 444535; AF011466; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21  
 417088; M54915; Hs.81170; pim-1 oncogene; pim-1 oncogene; 4.20  
 421707; NM\_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20  
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20  
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18  
 418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18  
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17  
 413686; A1469213; Hs.71404; ESTs; ESTs; 4.17  
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus; 4.16  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16  
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15  
 409421; AA199883; Hs.67624; ESTs; ESTs; 4.15  
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14  
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14  
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to M; 4.13  
 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbonate; 4.13  
 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitochondrion; 4.13  
 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 95; 4.12  
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12  
 400205; Hs.81848; NM\_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM\_006265; Homo sapiens RAD21 (S. pombe); 4.12  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11  
 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10  
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans [C.elegans]; 4.10  
 432512; NM\_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to protamine replacement); 4.10  
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09  
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription factor 3, gamma (48kD); 4.09  
 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09  
 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G protein) alpha 12; 4.09  
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; 4.08  
 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08  
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-receptor type 12; 4.08  
 452069; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08  
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker-related subfamily, beta member 2; 4.07  
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic acid transporters), member 3; 4.07  
 424517; A1539444; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12169 fis, clone MA; 4.07  
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe combined immunodeficiency); 4.06  
 446791; AJ632278; Hs.195922; ESTs; ESTs; 4.06  
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), catalytic subunit; 4.06  
 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta 3 subunit; 4.06  
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); 4.06  
 425923; NM\_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, delta polypeptide; 4.05  
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04  
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrate 1; 4.04  
 439176; AJ446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; 4.04  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule 1); 4.04  
 410068; A1633888; Hs.58435; FYN-binding protein (FYN-120/130); FYN-binding protein (FYN-120/130); 4.03  
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03  
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03  
 451050; AW937420; Hs.351869; ESTs; ESTs; 4.02  
 449667; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02  
 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01  
 437527; AJ241019; Hs.145644; ESTs; ESTs; 4.01  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase; 4.00  
 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF1210; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00  
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor 1 gamma; 4.00  
 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99  
 433577; AW007080; Hs.284192; ESTs; ESTs; 3.99  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); 3.99  
 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99  
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98  
 402398; ; C19000263.gi|3108023|gb|AAC15755.1| (AC004659) BC62940.2 [Homo sapiens] [56335; C19000263.gi|3108023|gb|AAC15755.1| (AC004659) BC62940.2 [Homo sapiens] [56335; 3.97  
 408414; A114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; 3.97  
 415012; NM\_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97  
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kinase); 3.95  
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; 3.95  
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine protease; 3.95  
 430770; AA765694; Hs.123296; ESTs; ESTs; 3.94  
 442994; A1026718; Hs.16954; ESTs; ESTs; 3.94  
 420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor, NK-p46); lymphocyte antigen 94 (mouse) homolog (activating NK-receptor, NK-p46); 3.94  
 438456; AA913381; Hs.279763; ESTs; ESTs; 3.94  
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A) expressed in; 3.93  
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93  
 424829; NM\_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR superfamily, member 16); 3.93  
 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93  
 425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93  
 421910; NM\_014568; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associated kinase; 3.92  
 413761; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenase 1; 3.92  
 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92  
 400262; ; Hs.75309; Eos Control; Eos Control; 3.90  
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90  
 435206; AJ432364; Hs.160594; ESTs; ESTs; 3.90  
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90  
 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90  
 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89  
 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89  
 407013; U53637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89  
 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88  
 400261; ; Hs.1802; Eos Control; Eos Control; 3.88  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88  
 422933; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); 3.87  
 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87  
 417767; BE242241; Hs.82542; acylxyacyl hydrolase (neutrophil); acylxyacyl hydrolase (neutrophil); 3.87  
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor, beta polypeptide; 3.87

- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86  
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86  
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86  
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86  
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86  
 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85  
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85  
 418978; T85295; Hs.268606; ESTs; ESTs; 3.84  
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84  
 442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84  
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84  
 434689; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83  
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83  
 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83  
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82  
 449433; AJ672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82  
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81  
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80  
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80  
 422753; A928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 poly; 3.79  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79  
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79  
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79  
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79  
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 6; frizzled (Drosophila) homolog 6; 3.79  
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78  
 425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78  
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78  
 429687; AI675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77  
 414177; AI351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77  
 445817; NM\_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77  
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76  
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repai; 3.76  
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76  
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76  
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor, alpha polypeptide); integrin, alpha 5 (fibronectin receptor,; 3.75  
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75  
 405484; ; C3002124\*gi12737280[ref]XP\_006682.2|keratin 18 [Homo sapiens]]6633; C3002124\*gi12737280[ref]XP\_006682.2|k; 3.75  
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75  
 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75  
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74  
 431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 to ALU8\_HUMAN ALU S; 3.74  
 453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74  
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74  
 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74  
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73  
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypotheti; 3.73  
 451295; AJ557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73  
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73  
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpo; 3.71  
 423523; AW299828; Hs.193580; ESTs; ESTs; 3.71  
 413407; AJ356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71  
 448336; R53848; Hs.44976; ESTs; ESTs; 3.70  
 422083; NM\_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70  
 416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70  
 442200; AW590572; Hs.235768; ESTs; ESTs; 3.70  
 414280; BE410769; Hs.75873; zyxin; zyxin; 3.69  
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69  
 415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69  
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69  
 446522; NM\_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69  
 422785; AIB24114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68  
 401083; ; NM\_016582\*Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM\_016579.1 GI; NM\_016582\*Homo sapiens peptide transpo; 3.68  
 413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68  
 452690; AJ536070; Hs.15085; ESTs; ESTs; 3.68  
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2\_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 to ALU2\_HUMAN ALU S; 3.68  
 415010; NM\_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68  
 428579; NM\_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68  
 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66  
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG Islands. Contains the NIFS gene for  
 cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65  
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;  
 3.65  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65  
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C; 3.65  
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN20), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

- 451558; NM\_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65  
 450295; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyros; 3.64  
 437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA667999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64  
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep; 3.64  
 444386; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64  
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63  
 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63  
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63  
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc; 3.62  
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62  
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62  
 411165; NM\_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62  
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62  
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61  
 438795; AA825792; Hs.377119; gb:od84b11.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCI\_CGAP\_Ov2 Homo sapiens ; 3.61  
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61  
 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60  
 423217; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60  
 444985; AI677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60  
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM\_023929); zinc finger protein RINZF (NM\_023929); 3.59  
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59  
 415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel  
 glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59  
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57  
 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57  
 423576; NM\_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57  
 440270; NM\_015986; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57  
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57  
 404976; ; NM\_014323; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM\_014323; Homo sapiens zinc finger prot; 3.57  
 449656; AA002008; Hs.188633; ESTs; ESTs; 3.56  
 413795; AL040178; Hs.142003; ESTs; ESTs; 3.56  
 406859; AI581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56  
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56  
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; 3.56  
 424263; MT77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)  
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high affi; 3.55  
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible ikappaB kinase; IKK-related kinase epsilon; inducible ik; 3.55  
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotate; 3.55  
 450931; N25158; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55  
 425836; AW955696; Hs.90960; ESTs; ESTs; 3.54  
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54  
 440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54  
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53  
 421652; NM\_014141; Hs.105552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53  
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); transformer-2 alpha (htra-2 alpha); 3.53  
 424870; T15545; Hs.244624; ESTs; ESTs; 3.52  
 442794; AJ744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51  
 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.1 - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51  
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51  
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51  
 421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50  
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50  
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50  
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50  
 429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49  
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211\_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211\_HUMAN ZINC; 3.47  
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44  
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07  
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77  
 430439; AL133561; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76  
 435897; AF269223; Hs.128322; t-complex 11 (a murine tcp homolog); t-complex 11 (a murine tcp homolog); 2.53  
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46  
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35  
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33  
 426627; AF012359; Hs.195685; ESTs; ESTs; 2.12  
 438983; AF085884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precursor; 2.07  
 425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99  
 433724; AI827749; Hs.144924; serine/threonine protein kinase SSKT; serine/threonine protein kinase SSKT; 1.68  
 420710; NM\_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
5		AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279
		BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 B1861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
		AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 A1075321 L13823 AA216700 BF771864 AW861859
		BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
		AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
434414	35978_1	AF134164 BF809407 AA218567 BF842863 A1267168 BF876178 BG999253 AW861851 AW858362 A1817548 BF771300 AA113928 AA223422
10		AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
		AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 A1694265 AA045564 BG950256 A1829309 BG987850 BE093175
		BF854337
427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
427521	513212_1	AW973352 BF222929 AW016853 BF059130 A1651829 BE551767 AA558414 A1339359 BF059601 A1961162 A1341422 A1206248 A1206165
15		AA548736 AA768578 A1539081 AW025957 AA736837 N79575 AW594357 AA480892
407347	810943_1	T23514 A1655785
430439	6750_2	AL133561 AL117481 AL122069 AW439292 A1968826 ALO41090

TABLE 57C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
25	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
30	402199	8576116	Minus	84187-84744
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	402678	8113438	Plus	37395-37514,37866-37981
	403171	9838164	Minus	74502-74703
	406137	9166422	Minus	30487-31058
35	401704	3097841	Plus	24712-25374
	402677	8113438	Plus	22135-22309,23063-23238
	402679	8113438	Plus	132079-132216
	402145	8018280	Plus	113086-114800
40	406547	7711513	Minus	172780-174358
	402398	4092817	Minus	24019-24973
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	401083	3424744	Plus	33192-33360
	404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

55	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
	Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
60	UniGene Title:	UniGene gene title
	R1	90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

65	430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; 35.25
	422282; AF019225; Hs.114309; apolipoprotein L; MoLA_ExcB; TM=Y; SS=M; 33.25
	414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phospho; TM=M; SS=Y; 31.68
	415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3 ; aldo_ket_red; TM=M; 31.04
	417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none, none; 28.50
70	439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 27.43
	417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 25.98
	413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT; none; 25.38
	418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT; none; 25.28
	425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisomIV, HATPase_c; SS=M; 23.58
75	421733; AL119571; Hs.1420; fibroblast growth factor receptor 3 (ach; ig, pkinase; TM=Y; SS=M; 21.24
	424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1; TM=Y; SS=M; 20.45
	447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 19.78
	408243; Y00787; Hs.624; interleukin 8; HLH_PAS; IL8; TM=M; 18.90
	427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; 18.75
80	410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; SS=M; 18.63
	444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothet; Collagen; TM=M; SS=M; 18.60
	452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig_Rhbd_glycop; TM=Y; SS=M; 18.55
	415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4; LM; TM=M; 18.25

- 413132; NM\_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic); PKI; SS=M; 17.73  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig; TM=Y; SS=M; 17.68  
 450746; D82673; Hs.278589; general transcription factor II, i; none; SH3, PX; 17.12  
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase; PLAT; TM=M; 16.88  
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone\_rec; zf-C4; TM=M; 16.78  
 439941; AI392640; Hs.18272; amino acid transporter system A1; Aa\_trans; TM=Y; 16.75  
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 16.56  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys; ig; FAD\_Synth; ldh; ldh\_C; pkinase; SS=M; 16.43  
 414883; AA926960; CDC28 protein kinase 1; CKS; 16.20  
 438091; AW373062; nuclear receptor subfamily 1, group I, m; hormone\_rec; zf-C4; none; 15.80  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH; lb; Lipase; GDSL; TM=M; 15.70  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1; pkinase; TM=M; 15.63  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz; Frizzled; 7tm\_2; TM=Y; SS=M; 15.45  
 434293; NM\_004445; Hs.3798; EphB6; EPH; lbd; fn3; pkinase; SAM; TM=Y; SS=M; 15.43  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF; lectin\_c; sushi; TM=M; SS=M; 15.28  
 443991; NM\_002250; Hs.10082; potassium intermediate/small conductance; CaMBD; SK\_channel; ion\_trans; TM=Y; SS=M; 15.10  
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig; TM=Y; SS=M; 14.90  
 423306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib); CBM\_21; TM=M; 14.80  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; 14.73  
 429345; R11141; Hs.199695; hypothetical protein; K\_tetra; SAM; 14.58  
 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig; lsodh; Ribosomal\_L6; F-box; TM=Y; SS=M; 14.55  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; PAAD\_DAPIN; HIN; TM=M; 14.53  
 446008; NM\_004403; Hs.13530; deafness, autosomal dominant 5; none; TM=M; SS=M; 14.35  
 429556; AW139399; Hs.98988; ESTs; none; TM=M; 14.18  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand; SS=M; 14.13  
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y\_phosphatase; Band\_41; PDZ; SS=M; 13.90  
 426657; NM\_015865; Hs.171731; solute carrier family 14 (urea transport); UT; TM=Y; 13.83  
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase; hexokinase2; none; 13.80  
 400843; ; NM\_003105; Homo sapiens sortilin-related; EGF; fn3; ldl\_recept\_a; ldl\_recept\_b; granulin; BNR; TM=Y; SS=M; 13.78  
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA; ABC\_tran; CoaE; TM=M; 13.38  
 432314; AA533447; Hs.312989; ESTs; Xlink; none; 13.25  
 413109; AW389845; Hs.110855; ESTs; PHO4; none; 13.15  
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank; pkinase; TM=M; 13.13  
 426490; NM\_001621; Hs.170087; aryl hydrocarbon receptor; PAC; PAS; TM=M; 12.93  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like; pkinase; Recep\_L\_domain; Furin-like; pkinase; Recep\_L\_domain; Peptidase\_M24; 12.43  
 440249; A1246590; Hs.249175; ESTs; TatD\_DNase; pkinase; death; none; 12.38  
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; SS=M; 12.38  
 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36; TM=Y; SS=M; 12.03  
 439569; AW602166; Hs.222399; CEGP1 protein; EGF; TNFR\_c6; granulin; CUB; Keratin\_B2; TIL; TM=M; SS=M; 11.93  
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 f1s, clone NT; Aa\_trans; none; 11.88  
 408000; L11690; Hs.198689; bulous pemphigoid antigen 1 (230/240kD); efhand; spectrin; GAS2; SH3; Plectin; RA; Xylose\_isom; Flid; bZIP; Tropomyosin; Myc-LZ; M; ldh\_C; CH; AIP3; TM=M; 11.88  
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; rrm; hormone\_rec; zf-C4; sugar\_tr; 11.85  
 433470; AW960564; ; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 11.80  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb\_DNA-binding; THF; DHG\_C; YH; THF; DHG\_C; CAP; GLY; AAA; LON; Peptidase\_C9; bZIP; M; xan\_ur\_permease; HCO3\_cotransp; TM=M; 11.69  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus); 7tm\_1; 7tm\_2; TM=Y; SS=M; 11.50  
 426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp58612022 (f; none; TM=Y; SS=M; 11.48  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C; IMPDH\_N; CBS; integrin\_B; Ricin\_B; lectin; 11.38  
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none; TM=Y; SS=M; 11.23  
 436729; BE621807; ; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 11.18  
 409960; BE261944; Hs.339673; hexokinase 1; none; none; 11.02  
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3; PDZ; Guanylate\_kin; TM=M; 10.78  
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin\_ADF; SS=M; 10.63  
 427654; AA410183; Hs.137475; ESTs; ion\_trans; vwc; IGFBP; lsp\_1; 10.58  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh; TM=M; SS=M; 10.53  
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor ( ; SH3; PH; RhoGEF; TM=M; 10.53  
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone K; none; none; 10.52  
 436856; A1489355; Hs.127310; ESTs; pkinase; rrm; TM=M; 10.48  
 451035; AU076785; Hs.430; plasmin 1 (I isoform); efhand; CH; Adaptin\_N; SS=M; 10.38  
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; integrin\_B; EGF; PSI; TM=Y; SS=M; 10.35  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa; Integrin\_A; FG-GAP; TM=Y; SS=M; 10.34  
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA; NB-ARC; PAAD\_DAPIN; NA; NA; 10.25  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5; TM=Y; SS=M; 10.18  
 437852; BE001836; Hs.256897; ESTs; Weakly similar to dJ365012.1 [H.s.a; GPS; 7tm\_2; TM=Y; 10.13  
 400752; ; NM\_003105; Homo sapiens sortilin-related; EGF; fn3; ldl\_recept\_a; ldl\_recept\_b; granulin; BNR; TM=Y; SS=M; 10.08  
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese; DSPc; TM=M; 10.05  
 426728; NM\_007118; Hs.171957; triple functional domain (PTPRF interact; SH3; ig; pkinase; PH; spectrin; RhoGEF; TM=M; 10.05  
 400496; ; ENSP00000224716; GTP-binding protein SAR; none; TM=Y; 10.01  
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3; PDZ; Guanylate\_kin; TM=M; 10.00  
 404568; ; NM\_022071; Homo sapiens hypothetical pro; SH2; TM=M; 10.00  
 444823; BE262989; Hs.12045; putative protein; Mra1; MBOAT; TM=M; SS=Y; 9.93  
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand; kazal; art; ras; 7tm\_1; TM=M; 9.90  
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2; SH3; TM=M; 9.90  
 424954; NM\_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53; WD40; IRK; TM=M; 9.88  
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase; TM=M; 9.85  
 439223; AW238299; Hs.250818; UL16 binding protein 2; ldl\_recept\_a; PKD; MHC\_1; TM=M; SS=Y; 9.83  
 429238; NM\_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y\_phosphatase; TM=Y; SS=M; 9.80  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese; DSPc; Y\_phosphatase; TM=M; 9.73  
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none; none; 9.73  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y\_phosphatase; DSPc; TM=M; 9.72  
 403912; ; C5000394; g112737280[rel]XP\_006682.2] k; none; TM=M; 9.70  
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none; spectrin; SH3; PH; CH; 9.70



- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase;TM=M; 9.68  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinasin,fn3,Y\_phosphatase;TM=M; 9.63  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M; 9.63  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3\_PI4\_kinase,FAT,FATC;TM=M; 9.55  
 430259; BE550182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 9.50  
 428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none;TM=M; 9.50  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M; 9.50  
 448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST\_C,Ets,SAM\_PNT,ABC2\_membrane,myosin\_head,IQ,Myosin\_N,bZIP,zf-  
 C2H2,PHD,BTB,TFIS,AT\_hook,SAM;TM=M; 9.50  
 414911; NM\_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40,homeobox,LM;TM=M; 9.48  
 451295; AJ557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase,DAG\_PE-bind,pkinase\_C,OPR;none; 9.45  
 402328; ; Target Exon; pkinase;TM=M; 9.44  
 443710; AJ928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha;none; 9.42  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 9.42  
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS\_kinase,ATP-sulfurylase,PRK,Thymidylate\_kin;SS=M; 9.40  
 418827; BE327311; Hs.47166; HT021; none;TM=M; 9.40  
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1\_HUMAN CALCI; pkinase;none; 9.35  
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE\_p10,ICE\_p20;SS=M; 9.28  
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR\_c6;TM=Y;SS=M; 9.25  
 430024; AJ808780; Hs.227730; integrin, alpha 6; integrin\_A\_FG-GAP;TM=Y;SS=M; 9.23  
 452696; AI826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate\_kin,PDZ,SH3; 9.13  
 434263; N34895; Hs.44648; ESTs; ig;none; 9.13  
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal\_S14,ank,pkinase,death;none; 9.10  
 429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase,metallothio;TM=M;SS=M; 9.08  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,Jamlinin\_Nterm,integrin\_B;SS=M; 9.08  
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22,Claudin;none; 9.07  
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoeE; 8.98  
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M; 8.93  
 438000; AI825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M; 8.90  
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.90  
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.88  
 437056; AI147061; ; gb:ok33a11.s1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S; none,spectrin,SH3,PH,CH; 8.78  
 445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGap;TM=M; 8.78  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 8.70  
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.68  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 8.65  
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept\_Y\_phosphatase;SS=M; 8.65  
 430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3\_cotransp;TM=Y; 8.64  
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M; 8.60  
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal\_S14; 8.60  
 429109; ALD08637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M; 8.60  
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8\_HUMAN ALU S; none,7tm\_1; 8.55  
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG\_PE-bind,RBD; 8.43  
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none;none; 8.40  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 8.39  
 448209; AW160489; Hs.20709; tetraspan 5; transmembrane4;TM=Y;SS=M; 8.33  
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 8.33  
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase\_2;TM=M; 8.31  
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm\_1;TM=Y;SS=M; 8.30  
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK;none; 8.28  
 446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA,SKI;TM=M; 8.23  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none;none; 8.20  
 427274; NM\_005211; Hs.174142; colony stimulating factor 1 receptor, for; ig,pkinase;TM=Y;SS=M; 8.18  
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none;none; 8.15  
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 8.15  
 417386; AL037228; Hs.82043; D123 gene product; NUDIX,secY,E1\_dehydrog,transket\_pyr;TM=Y;SS=M; 8.13  
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 8.10  
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 8.09  
 425424; NM\_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M; 8.08  
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin\_A;none; 8.05  
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo\_seg;TM=M;SS=M; 8.03  
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 8.03  
 404891; ; Target Exon; none;none; 7.95  
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none;none; 7.93  
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 7.93  
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 7.91  
 438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase,ABC1;none; 7.90  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR\_c6,Acyl-CoA\_hydro; 7.90  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan\_ur\_permase,RA; 7.88  
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2.; Furin-like,pkinase,Recep\_L\_domain,YLP;TM=Y;SS=M; 7.86  
 405036; ; NM\_021628; Homo sapiens arachidonate lip; lipoxygenase,complex1\_49kd,PLAT;TM=M; 7.83  
 418529; AW005695; Hs.250897; TRK-fused gene; Band\_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 7.83  
 431912; AI660552; Hs.76549; ESTs, Weakly similar to A56154 Abl subst; none,Acyl-CoA\_dh,Acyl-CoA\_dh\_M,Acyl-CoA\_dh\_N; 7.80  
 432981; NM\_002733; Hs.3135; protein kinase, AMP-activated, gamma 1 n; CBS,Aa\_trans;TM=M; 7.78  
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo; Sec7,PH,ANF\_receptor,lig\_chan,WD40,IRK; 7.78  
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH,DAG\_PE-bind,PH,Involucrin,M;TM=M; 7.78  
 431183; NM\_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER\_lumen\_recept;TM=M;SS=M; 7.78  
 400845; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 7.73  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran,SMC\_N,SMC\_C,DUF164;none; 7.73  
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ\_con,Y\_phosphatase,SH2; 7.70  
 403212; ; NM\_019595; Homo sapiens intersectin 2 (IT; SH3,ethand,C2,PH,RhoGEF;TM=M; 7.70  
 441190; H09073; Hs.25046; ESTs; E1-E2\_ATPase,C,Calcium\_ATPase\_N,Hydrolase;none; 7.68

- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm\_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,ve,zf-B\_box;TM=Y;SS=M; 7.68
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,kinase;SS=M; 7.65
- 447898; AW969638; Hs.112318; 6.2 kd protein; none;none; 7.65
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN,HIN;SS=M; 7.63
- 5 401927; ; C17000914; gi8394367[refNP\_058549.1] s; none;; 7.60
- 407347; AA829847; ; gb:cd40407.s1 NCI\_CGAP\_GCB1 Homo sapiens; RhoGAP,SH2,kinase,POLO\_box,none; 7.58
- 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3,none; 7.57
- 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin\_A,PHO4,kinase,ubiquitin; 7.55
- 10 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase; ty; none;none; 7.55
- 421489; AJ922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
- 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
- 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylylkinase,SRP54;TM=M; 7.50
- 430570; AJ417881; Hs.292464; ESTs; 7tm\_2,Fz,Frizzled,none; 7.50
- 15 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
- 420676; AJ434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG\_PE-bind,none; 7.48
- 444252; R21135; Hs.54985; ESTs; none;none; 7.47
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3,PI4\_kinase;TM=M; 7.47
- 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
- 20 418546; AA224827; ; gb:nc32g04.s1 NCI\_CGAP\_Pr2 Homo sapiens ; vwa,Integrin\_A,FG-GAP,none; 7.45
- 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43
- 452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypothet; none,kinase; 7.40
- 432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 neuronal pr; DEAD,helicase\_C,rrm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp\_1,Ribosomal\_S21,rvp;TM=M; 7.40
- 25 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,kinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 7.40
- 421429; NM\_014922; Hs.104305; death effector filament-forming Ced-4-l; LRR,PAAD\_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
- 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone\_rec,zf-C4;SS=M; 7.38
- 430016; NM\_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
- 422813; AV656571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
- 30 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFp761G18121 ( ; none,spectrin,SH3,PH,CH; 7.25
- 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,kinase;TM=M; 7.24
- 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
- 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 7.19
- 407591; NM\_000910; Hs.37125; neuropeptide Y receptor Y2; 7tm\_1;TM=Y; 7.18
- 35 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
- 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
- 403344; ; NM\_000341;Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
- 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage\_CLC;TM=Y; 7.14
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar\_lr;TM=Y;SS=M; 7.14
- 40 404875; ; NM\_022819;Homo sapiens phospholipase A2; phoslip;SS=M; 7.11
- 433618; AA602539; Hs.345494; ESTs; G-alpha\_A\_deaminase; 7.10
- 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate\_transp,STAS,HMG\_box; 7.08
- 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPSS;TM=M,SS=M; 7.05
- 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05
- 45 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm\_2,HRM,CSD;TM=Y;SS=M; 7.03
- 400211; ; NM\_003899;Homo sapiens PAK-interacting ; SH3,PH,RhoGEF,Terpene\_synth;TM=M; 7.03
- 438150; AA037534; Hs.342874; transforming growth factor, beta receptor; zona\_pellucida,none; 6.93
- 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, ; proteasome;TM=M; 6.93
- 405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys\_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
- 50 415392; Z44057; Hs.10957; ESTs; PIP5K,none; 6.89
- 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo\_seg,none; 6.88
- 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic ; C2,PLA2\_B;TM=M; 6.85
- 427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2\_N,helicase\_C,Armadiillo\_seg,HEAT;TM=M; 6.83
- 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20,DED;TM=M; 6.80
- 55 400158; ; ENSP00000244302; cDNA FLJ11591 fis, clone; Sm;SS=M; 6.78
- 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT\_bind,STAT\_prot,ion\_trans,PAC,PAS,none; 6.78
- 400844; ; NM\_003105;Homo sapiens sortilin-related; EGF,fn3,Idl\_recept\_a,Idl\_recept\_b,granulin,BNR;TM=Y;SS=M; 6.73
- 457238; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase;; 6.73
- 404440; ; NM\_021048;Homo sapiens melanoma antigen, ; MAGE;TM=M; 6.73
- 60 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kin; Els,SAM\_PNT;TM=M; 6.70
- 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase;TM=M; 6.70
- 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
- 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate\_kin;SS=M; 6.64
- 408638; AW451353; Hs.173328; ESTs; B56,none; 6.63
- 65 408058; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
- 401057; BE563196; ; eukaryotic translation elongation factor; ion\_trans,IQ;TM=Y; 6.60
- 446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none;none; 6.60
- 400528; ; NM\_020975;Homo sapiens ret proto-oncoge; cadherin,kinase;TM=Y;SS=M; 6.58
- 418562; R60669; Hs.124831; CGI-57 protein; none,Skp1,AAA; 6.57
- 70 453826; AL138129; ; gb:DKFp547F152\_r1 547 (synonym: htrf1) ; PK,PK\_C,none; 6.55
- 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFp547C136 (fr, ABC\_tran,GTP\_EFTU,ABC\_membrane,none; 6.54
- 415088; AJ077288; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 6.50
- 453489; AA300067; Hs.33032; hypothetical protein DKFp434N185; F5\_F8\_type\_C,kinase,Els,F5\_F8\_type\_C,kinase,Els; 6.47
- 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46
- 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46
- 75 441712; AW391927; Hs.7946; KIAA1288 protein; AIP3;TM=M; 6.44
- 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7tm\_1; 6.43
- 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY\_C;TM=M; 6.43
- 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M,SS=M; 6.40
- 438941; AF075047; Hs.31864; ESTs; Ca\_channel\_B,SH3,arf,none; 6.40
- 80 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB,none; 6.33
- 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothet; lipoxigenase,PLAT,none; 6.33
- 433255; AJ274270; Hs.96840; KIAA1527 protein; MHCK\_EF2\_kinase;TM=M;SS=M; 6.33
- 427801; AW979155; Hs.298275; amino acid transporter 2; Aa\_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin,BAG,Tropomyosin;; 6.30  
 438464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none,none; 6.30  
 453977; AA886006; Hs.250427; ESTs; pkinase,P2X\_receptor,E1-E2\_ATPase,Hydrolase; 6.30  
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras,ar1,PP2C;TM=M; 6.30  
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180KD); DNA\_gyraseB,DNA\_topoisolv,HATPase\_c,DNA\_gyraseB,DNA\_topoisolv,HATPase\_c; 6.29  
 404342; ; C7002192:gij7299207[gjb]AAF54404.1] (AE0; none;TM=M; 6.27  
 409274; NM\_003930; Hs.52644; SKAP55 homologue; SH3,PH;SS=M; 6.25  
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 6.23  
 405429; ; Target Exon; Y\_phosphatase,none; 6.23  
 404975; AL042279; ; uncharacterized hypothalamus protein HT0; kringle;TM=Y;SS=M; 6.20  
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin,EGF,ig,Neuregulin,EGF,ig; 6.18  
 446883; AW452756; Hs.16354; hypothetical protein FLJ10955; DEAD,helicase\_C,rm,Ndr,Cys\_kno1,TIL,vwa,vwc,vwd,IQ,Rla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp\_1,Ribosomal\_S21,rvp;TM=M; 6.18  
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M; 6.15  
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y; 6.15  
 421836; AF109129; Hs.108787; phosphatidylinositol glycan, class N; none,none; 6.14  
 447727; AI421079; ; tumor necrosis factor receptor superfamily; none,synaplobrevin; 6.13  
 401536; ; NM\_002530; Homo sapiens neurotrophic tyr; ig,pkinase,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.11  
 444317; AI140566; Hs.143436; ESTs; Weakly similar to PLHU plasmin [H; PAN,kringle,trypsin,PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN; 6.10  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR\_LY6,ET,PLA2\_inh;SS=M; 6.08  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M; 6.08  
 450107; AI873287; Hs.257812; ESTs; ICE\_p20,DED;TM=M; 6.05  
 418175; AW967054; Hs.206312; ESTs; Weakly similar to I38022 hypotheli; zf-C2H2,BTB,K\_tetra,Syntaxin,none; 6.05  
 408983; NM\_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC\_tran,ABC\_membrane,PRK,Bac\_export\_3;TM=Y; 6.05  
 439738; BE245502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema,PSI,integrin\_B;TM=Y; 6.03  
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none,none; 6.03  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.03  
 446650; AB016625; Hs.15813; solute carrier family 22 (organic cation; sugar\_tr;TM=Y;SS=M; 6.03  
 405102; ; C15001220:gij4469558[gjb]AAD21311.1] (AF; DAG\_PE-bind,PH,RhoGEF,DC1;SS=M; 6.03  
 400121; ; Eos Control; SH3,PH,RhoGEF,Terpene\_synth;TM=M; 6.03  
 415327; H22769; ; gbyrn54c02.r1 Soares infant brain 1N1B H; SH3,PDZ,Guanylate\_kin;SS=M; 6.03  
 404148; ; NM\_002944; Homo sapiens v-ros avian UR2 ; fn3,pkinase,DUF139;TM=Y;SS=M; 6.03  
 405531; ; Target Exon; PDZ,CARD,Guanylate\_kin;TM=M; 6.00  
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B) ; NDK,none; 6.00  
 427270; H47921; Hs.174139; chloride channel 3; voltage\_CLC,CBS,none; 5.99  
 423774; L39064; Hs.1702; interleukin 9 receptor; none;TM=M;SS=M; 5.98  
 424124; AA335609; Hs.7589; ESTs; Weakly similar to A46010 X-linked ; pkinase,TBC; 5.98  
 411040; AF007393; Hs.177574; protein-kinase, interferon-inducible dou; HLH;TM=M; 5.95  
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer,7tm\_1,none; 5.88  
 453902; BE502341; Hs.3402; ESTs; none,none; 5.88  
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa\_trans;TM=Y; 5.86  
 436154; AA764950; Hs.119898; ESTs; ethanol,DAG\_PE-bind,DAGKa,PHD,DAGKc,PSI,none; 5.85  
 455358; AW902641; ; gb:OV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase,Somatomedin\_B,Phosphodiester,none; 5.83  
 414108; AI267582; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol\_BP,pkinase;TM=M; 5.82  
 452547; AA335295; Hs.74120; adipose specific 2; LEA;TM=M; 5.82  
 415204; T27434; ; gb:hbc2294 Human pancreatic islet Homo s; Na\_Ca\_Ex,Calc-beta,none; 5.80  
 435563; F210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y; 5.78  
 456097; C15702; Hs.288028; ESTs; Moderately similar to I54374 gene ; dsrm,FKBP; 5.78  
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle.; E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase;TM=Y; 5.77  
 436246; AW450963; Hs.119991; ESTs; none,DNA\_gyraseB,DNA\_topoisolv,HATPase\_c; 5.75  
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC\_tran,PRK;TM=Y;SS=M; 5.75  
 425854; AA749190; ; ESTs; RhoGAP,SH2,pkinase,POLo\_box,none; 5.74  
 424160; T74062; ; gbyrc1f01.r1 Soares infant brain 1N1B H; ROK,none; 5.70  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN,MK;TM=M;SS=Y; 5.69  
 437613; R19892; Hs.10267; MLL1 protein; none,none; 5.68  
 410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4 ; TBC;SS=M; 5.68  
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M; 5.66  
 426500; NM\_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M; 5.63  
 406930; U04691; ; gb:Human olfactory receptor (OR17-219) g; none;TM=Y;SS=M; 5.60  
 401044; ; Target Exon; none,ICE\_p20,ICE\_p10,CARD,Peptidase\_M1; 5.56  
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 5.55  
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RR; aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_PI4\_kinase,FAT,FATC,BolA,RUN;TM=M; 5.53  
 426248; T18988; Hs.293658; ESTs; pkinase,none; 5.50  
 418426; NM\_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase,death;TM=M; 5.43  
 417086; AA194446; ; ESTs; Weakly similar to S55024 nebulin ; ank,death,ZUS,EGF,kringle,trypsin,Nebulin,LM;SS=M; 5.43  
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupl; 7tm\_1,SH2;TM=Y;SS=M; 5.40  
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF;SS=M; 5.40  
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, com; pkinase,TBC,Rhodanese;TM=M; 5.38  
 419355; AA428520; Hs.90061; progesterone binding protein; hema\_1;TM=Y;SS=M; 5.35  
 411188; BE161168; ; gb:PMO-HT0425-170100-002-a10 HT0425 Homo; adenylatekinase,none; 5.35  
 422461; NM\_003417; Hs.117077; zinc finger protein 264; zf-C2H2,KRAB,TFIIS;TM=M; 5.28  
 426348; BE465686; Hs.17433; hypothetical protein FLJ20967; none,none; 5.25  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y\_phosphatase,Ribosomal\_S3\_N;TM=M; 5.23  
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin,Exo\_endo\_phos,IQ;TM=M; 5.22  
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER\_lumen\_recept,Ribosomal\_L11,Ribosomal\_L11\_N;TM=Y;SS=M; 5.21  
 434368; AW519020; Hs.73893; dopamine receptor D2; pkinase,SH3,none; 5.15  
 405586; ; NM\_000299; Homo sapiens plakophilin 1 (ec; Armadillo\_seg;TM=M; 5.13  
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase,none; 5.12  
 407443; AF227138; ; gb:Homo sapiens candidate taste receptor; none;TM=Y;SS=M; 5.11  
 416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep\_L\_domain,fn3,none; 5.10  
 401886; ; NM\_021783; Homo sapiens XEDAR (XEDAR); mR; TNFR\_c6;TM=M;SS=M; 5.08  
 410314; AW860708; Hs.18851; hypothetical protein FLJ10875; myb\_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M; 5.08

- 401579; AL031447; ; Homo sapiens, clone IMAGE:4053044, mRNA; Neur\_chan\_LBD, Neur\_chan\_memb, none; 5.05  
 445873; AA205970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-; PABP, rrm, pkinase, 14-3-3; 5.05  
 417529; AA203634; ; gb:zx58b09.r1 Soares\_fetal\_liver\_spleen\_1; pkinase, UBA, KA1, none; 5.03  
 417527; AA203524; ; gb:zx56e10.r1 Soares\_fetal\_liver\_spleen\_1; SH3; SS=M; 4.98  
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptkB; TM=M; 4.96  
 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid\_phosphat, none; 4.93  
 404298; ; C6001238; gij121715|sp|P26697|GTA3\_CHICK; none; GST\_C, GST\_N, pkinase; 4.85  
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; none; TM=M; 4.82  
 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC, tran, ABC, membrane; TM=Y; 4.73  
 422366; T83882; Hs.97927; ESTs; pkinase, none; 4.64  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; 4.48  
 426925; NM\_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone H; Esterase, enolase, Peptidase\_S9; TM=M; 4.45  
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm\_1; TM=Y; SS=M; 4.40  
 400749; ; NM\_003105; Homo sapiens sortilin-related; EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 4.38  
 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4; TM=Y; SS=M; 4.33  
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ktl\_recept\_a, PKD, MHC\_1; TM=M; SS=Y; 4.31  
 400751; ; NM\_003105; Homo sapiens sortilin-related; EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 4.18  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; SS=M; 3.90  
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none, none; 3.88  
 458760; AA98631; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3, cotransp, SH3, RhoGAP, xan\_ur\_permease, FCH; SS=M; 3.85  
 441218; BE327561; Hs.202345; ESTs; none; WD40, E1-E2, ATPase, Cation\_ATPase\_C, Cation\_ATPase\_N, Hydrolase; 3.78  
 419073; AW972170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; SS=M; 3.76  
 451385; AA017656; ; gb:ze39h01.r1 Soares retina N2b4HR Homo; Atrophin-1, enolase, Atrophin-1\_Y\_phosphatase, SH2, fibrinogen\_C, TIM; 3.60  
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase, DAG, PE-bind, pkinase\_C, OPR; TM=M; 3.30  
 409582; R27430; Hs.271565; ESTs; none; Neur\_chan\_LBD, Neur\_chan\_memb; 3.28  
 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1\_LC3; SS=M; 3.23  
 436740; AW975133; ; gb:EST387239 MAGE resequences, MAGN Homo; none, EPH, lbd, fn3, pkinase, SAM; 3.20  
 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked; none, IRK; 3.20  
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none; NA; NA; 3.13  
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit; none, none; 3.10  
 400846; ; ; sortilin-related receptor, L(DLR class); EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 3.09  
 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (f; none, Na\_H\_Exchange; 3.03  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar\_tr; TM=Y; SS=M; 3.02  
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothetel; IRK, none; 2.98  
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member, death, TNFR\_c6; TM=Y; SS=M; 2.93  
 401279; ; C13000351; gij2494033|sp|Q64398|KGDG\_MES; none, none; 2.88  
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema, pkinase, TIG, PSI, none; 2.83  
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK; TM=Y; 2.80  
 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase; TM=M; 2.75  
 441699; AW511126; Hs.127572; ESTs; none, Aa\_trans; 2.73  
 458781; A444821; Hs.63085; ESTs, Weakly similar to MPP3\_HUMAN MAGUK; SH3, PDZ, Guanylate\_kin, L27; TM=M; 2.73  
 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4; TM=Y; SS=M; 2.70  
 453487; R31770; Hs.56562; ESTs; 7tm\_1, none; 2.68  
 421279; AW664878; Hs.106645; ESTs; pkinase, none; 2.68  
 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none, none; 2.65  
 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc; TM=M; 2.63  
 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF; TM=Y; 2.62  
 425212; AW962253; Hs.171618; ESTs; pkinase, none; 2.60  
 427344; NM\_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur\_chan\_LBD, Neur\_chan\_memb; TM=Y; SS=M; 2.58  
 423629; AW021173; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage\_CLC, CBS, none; 2.55  
 456737; BE247203; Hs.124831; CGI-57 protein; abhydrolase\_2; TM=M; SS=M; 2.53  
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm\_1; TM=Y; SS=M; 2.53  
 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y7; none, none; 2.50  
 448324; A1571356; Hs.34174; ESTs, Moderately similar to ALU8\_HUMAN A; ICE\_p20, CARD, ICE\_p10, none; 2.50  
 402256; ; Target Exon; pkinase, UBA, none; 2.43  
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI, 7tm\_1, none; 2.40  
 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothetel; none, spectrin, SH3, PH, CH, 2.40  
 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP\_binding, ion\_trans; TM=Y; 2.35  
 419630; W57756; ; gb:zd20g10.r1 Soares\_fetal\_heart\_NbHH19W; z-C3HC4, none; 2.35  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm\_1; TM=Y; SS=M; 2.35  
 400704; ; Target Exon; lig\_chan, SBP\_bac\_3, ANF\_receptor; TM=Y; SS=M; 2.33  
 400149; ; Eos Control; acid\_phosphat; TM=Y; SS=M; 2.30  
 459327; AW149706; Hs.7859; gb:xf41d02.x1 NCL\_CGAP\_Bm50 Homo sapien; PHD, PWWP, SET, pkinase, ig; 2.30  
 452220; BE158006; Hs.212296; ESTs; Integrin\_A, FG-GAP, none; 2.25  
 416690; H84078; Hs.108551; ESTs; pkinase, none; 2.23  
 408354; A1382803; Hs.159235; ESTs; none, none; 2.23  
 452203; X57522; transporter 1, ATP-binding cassette, sub; ABC, tran, ABC, membrane, SRP54, Thymidylate\_kin; TM=Y; SS=M; 2.21  
 405093; ; C12001101; gij7522643|pi|T32733 AMPA g; none, none; 2.20  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; 2.20  
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 2.18  
 417185; NM\_002484; Hs.81459; nucleotide binding protein 1 (E.coli Min; ParA, fer4\_NiH, ArsA\_ATPase; TM=M; 2.18  
 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 2.18  
 413627; BE182082; Hs.246973; ESTs; Armadillo\_seg, IBB; TM=M; 2.18  
 407415; AF073328; ; gb:Homo sapiens tetracycline transporter-; none, none; 2.15  
 450592; A1701555; Hs.202562; ESTs; pkinase, none; 2.15  
 428767; A421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1; none, pkinase, ig; 2.15  
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 2.15  
 419122; A1401360; Hs.44410; ESTs; ABC, tran, ABC, membrane, none; 2.10  
 446420; AW015693; Hs.135614; ESTs; ion\_trans, none; 2.05  
 420076; AA827860; Hs.293717; ESTs; DUF59, pkinase; 2.05  
 409416; AW388359; Hs.10667; ESTs; transmembrane4; TM=Y; SS=M; 2.03  
 428766; AA477989; Hs.98800; ESTs; TPR, 7tm\_1; 2.03  
 427001; NM\_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; TM=M; 2.03

453709; AL119133; ; protein kinase C substrate BOK-H; none,histone; 2.03  
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00  
 456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88  
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7Im\_1; 1.65  
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00  
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 588

Pkey: Unique Eos probeset Identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI368880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537892 AI203723 AI857576 AA584410 AW371667 BM172363
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T55222 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF99056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW080570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08083 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AI547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262390 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL50751 AL547978 AL545286 AL540643 AU118627 AL601379 BI085912 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790435 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW080570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08083 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AI547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262390 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL50751 AL547978 AL545286 AL540643 AU118627 AL601379 BI085912 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790435 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895

			AW651691 BMD48974 BMD43805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528531 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316958 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
5	437056 422940 409745	428504_3 58443_1 MH1944_5	AW976398 AI147061 AA765223 AA743380 AI803927 BC012771 BG397153 BF366196 AA337277 AA319285 AW843252 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI0029864 BI006277 BI007627 BI006266 BI006991 BI006590 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
10	407347 418546 432407	810943_1 242836_1 MH1429_12	T23514 AI655785 T59708 AA224827 T59843 BE156903 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA507122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
15	423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM125292 BM128665 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 L16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI753932 BI910138 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA771194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 I16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
20	400211	3532_1	BC000486 BC001930 UI5008 NM_004597 BG326561 AV761269 BF212132 BG113313 BI838038 BG944198 BG255198 BG164334 BM013507 AV682717 BF028761 BG755489 BG030141 BG105499 BE440103 BF727449 BM454228 BG912181 BM015197 BG395995 AI126579 AW248204 BI857394 BI857319 BG944205 BG323958 BI092930 AV756576 AA280958 BF033078 BE539360 AW247174 BG107836 BE796975 BG170920 AI148142 AI092009 AI336349 AV713409 BF685591 BE516029 AV713166 BE909458 BE743868 BM018218 AI340153 BE206806 AI159916 AI184271 BE208585 BI862286 C18760 BG219364 AI122677 BE207297 BF754798 AA314384 BE873951 BG207294 AI148198 AI336189 AI141094 AI308985 BF220098 AI143289 BE856397 AA644001 BE675402 AJ346708 AI052809 AI140082 BF081542 AI342428 AI479625 AA278456 AI750163 BE707501 BG944510 AA314616 AA315774 BF360721 BF738404 AA814194 AA477195 AA932107 F36858 AA363159 BE865458 AA354147 AW904224 AI055855 AA380365 F28474 D59140 AA341946 AA993339 AA323350 F24344 AA374436 BG942061 AA636015 AA852919 T31486 F36334 BG943190 T30319 BG943153 BG941836 T32659 T31160 AA311749 BE710086 BE709911 W23826 BG941639 BF769034 AA026407 AA229555 AV756340 AV714380 AL138129 BG003205 AL138179 BI021773 BE064231
25	453826 447727 400121	366136_1 10123_14 3532_1	AL520734 BI666852 BF870571 BF945361 BF945354 AI770086 BI861138 AI241079 AL043200 BG683612 AW946255 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA771194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 I16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
30	415327	9792_2	BM048470 BG983877 N92089 Z43545 F05783 R35182 H22769 H71928 H63921 R94394 AW195830 AA630220 F02030 R60760 R08204 H71929 BE464731 R62568 H63520 H77840 AL515501 F01971 T71768 N55275 AA883505 AW606824 AA704682 N74193 W57593 AW753776 H60439 AI076352 R31485 BE160931 AW130730 BE160869 AW580256 AW902073 BE702158 AW382079 N76884 BF431013 H38156 AV648937 H80573 AW902569 AW902557 AW902654 AW902641 AW902650 AW902741 AW902644 Z25288 R50577 F00323 D82802 T27434 BF184345 AA364846 BI494468 AA775693 BF195801 AA749190 AI480223 BE327332 AI470017 AW628345 AI917472 AI972264 AI375571 AI652583 AI656167 AI983110 BE550378 AW015085 BE552318 AI631475 AI433447 AA534540 AI865480 AI468119 BF110875 AW512059 W58721 AA827482 R59357
35	455358 415204 425854	1160035_1 1865508_1 2638_3	AW370493 AA923304 AI660828 AA502611 BI017370 AA039704 W65393 BE938514 W65295 BF919626 BI759440 BI838879 AA336207 F12441 BF171187 BE185031 T74062 AW904410 AA260078 BF919629 AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176555 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361 AI193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 AI620346 BG986374 BE706521 C02691 AI596834 F31902 F26078 AA670099 BF475555 F30818 F37524 AJ346558 F28050 F19333 F31637 C03413 AI092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546 AW821260 BE162466 BE161168
40	411188 417529 417527 451385 436740 419630 400149	1072487_1 3302462_1 2431831_1 85022_1 1239008_1 37310_5 16458_1	AA203634 AA203524 W88451 AA019761 AA017656 AA017374 AW975133 AA805813 AA729943 BF232647 AA204668 AA256086 BF574707 W57756 AA249070 BI906494 AA248011 BC003160 NM_001610 X12548 BG386865 BI760866 BI559619 BG323829 AU135543 BI834101 AU142120 AU124511 AU124889 AI558171 AU117286 BI824000 BG386610 BI753285 BI223475 AU134828 BM126369 BE206493 BF751498 AL544274 AY007137 BI828921 BE870130 BF771242 BI835451 BI765655 BI220955 BI223344 BG015924 BI759894 AL527413 BF310568 N31870 N23974 BE514914 I48863 AW860257 BF334625 AA883860 AU141668 AA442562 AU159491 AU148353 AA564123 AU148667 AI377256 AW664004 AI871712 AI141486 AI323351 AI339094 BE206109 AW519033 AI817729 AI332490 AI149455 AI857411 AI763154 AI751608 AI377222 AI081956 AW664229 AI275872 AW168546 AA975270 AI367408 AI687729 AI269164 AW105344 BM193081 BE550930 AI082116 AA854691 AI056249 AI221062 AI290113 D51818 AA732409 BG055125 N85878 AU156121

BF093671 AA053070 T28548 AL570460 BI006862 BI007207 AA373520 W95069 AA629136 AA708164 AI014886 AW168697 D51623 AA577168  
 AI094208 AA028946 AA975078 R16815 BG151132 AI276297 D51676  
 BC014081 NM\_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL555882 AL541576 AL550654 BI823519  
 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470  
 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429  
 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404  
 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220  
 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184  
 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619  
 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256  
 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601  
 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586  
 AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239  
 AA074615 AI291059 AI681053 AA702355 BF439899 AW055166 AI096957 BF223853 AL119659 AI692209 BM312961 AI869297 BE466252 AI292024  
 AA402764 AI214620 AA765312 BF380770 AA442682 AL519746 AW295039 AI037878 AW473433 AI499437 AI401618 AI130831 AA427406 AI042138  
 BG272488 AI828769 AI828764 AI189390 W84635 AA398496 AA761672 AA699520 AI200406 N68093 AI143913 AA993133 AA613306 AI050971  
 AA661905 AA722687 AI749977 AA829345 BG057324 BF001339 AA910169 AA765133 AI360722 AI701849 AI365083 H95974 AI830377 AI312866  
 AI370491 BE858907 N62185 AA705746 BE379632 W93803 AI440333 AW367670 AW367640 N77131 BF993216 AI858263 W52329 N68106 R83113  
 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851  
 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 AI073567 AA004957 AI539585 N95093 H99798 H95072 H96853 AA215712  
 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 AI693577 BE181027  
 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734  
 R58506

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36461
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84974-85125
405036	7543748	Minus	121957-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420923	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
418854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	AI093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microseminoprotein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	54.6
428398	AI249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7



5	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
10	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
15	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
	416585	XS4162	Hs.79386	leiomodulin 1 (smooth muscle)	39.0
	447726	AL137638	Hs.19368	matrilin 2	38.6
20	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
25	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415539	AI733881	Hs.72472	BMP-R1B	34.9
30	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
35	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AI918950	Hs.123642	EphA3	32.7
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	32.4
40	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
	408380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytostatin)	31.4
45	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H7777 transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
50	442993	BE018682	Hs.166196	ATPase, Class I, type BB, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	29.2
55	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023630	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
60	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
65	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442670	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
	403047			NM_005656":Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
70	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AI267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens prostelin mRNA, complete cds	26.4
75	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
	400292	AA250737	Hs.72472	BMP-R1B	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
80	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59822	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448106	AI800470	Hs.171941	ESTs	25.5
	415992	CO5837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW967646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothe	24.5
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
5	418396	AI765805	Hs.26691	ESTs	24.1
	412088	AI689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abl-interacting protein ArgBP2	24.0
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
10	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypothe	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	22.9
	440260	AI972667	Hs.71130	copine IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-ek	21.9
20	450642	R39773	Hs.71130	copine IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	21.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
40	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157646	Hs.153506	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420511	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
50	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
	424897	D63216	Hs.153684	frizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263*:HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	20.3
	429918	AW873986	Hs.119383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
	441690	R81733	Hs.33106	ESTs	19.9
65	423690	AA329648	Hs.23804	ESTs, Weakly similar to PND099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431556	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	LIM domain only 4	19.2
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
80	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latexin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

	445929	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
5	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	18.7
	418819	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443966	Hs.31595	ESTs	18.4
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
20	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439589	AW602166	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424682	AW604804	Hs.151717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
30	431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
45	421823	N40850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.159983	ESTs	16.9
	432966	AA650114	Hs.325198	ESTs	16.9
55	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:mp12d11.s1 NCL_CGAP_Py3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF085833	Hs.135624	ESTs	16.8
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
60	442054	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocan	16.4
	443801	AW206942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
70	409050	AI815867	Hs.50130	necln (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30098	ESTs	16.0
75	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	WS3048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW089181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AJ093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AI418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	15.4
	443674	AI081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418693	AI750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	15.1
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A45010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	tumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AI699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/HD (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336695	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AJ026838	Hs.30120	ESTs, Weakly similar to NUC1_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	14.5
75	410339	AI916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.145858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
	416836	D54745	Hs.80247	cholecystokinin	14.4
5	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
10	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	A1927288	Hs.196779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob)	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
	433332	A1367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
15	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	14.1
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
20	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	13.9
	418848	AI820961	Hs.193465	ESTs	13.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
25	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
	447384	A1377221	Hs.40528	ESTs	13.9
30	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
35	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
40	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ111041 fis, clone PL	13.7
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
45	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
50	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
55	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
	410001	AB041036	Hs.57771	kallikrein 11	13.6
60	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021955*:Homo sapiens phosphoglucomuta	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	13.6
65	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
70	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
	447082	T85314	Hs.42644	thioredoxin-like	13.5
75	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypotheti	13.3
	433517	AW022133	Hs.189838	ESTs	13.3
80	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (	13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226527	leptin receptor	13.2
5	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
10	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.156880	ESTs	13.2
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
15	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68796	Hs.237731	ESTs	13.1
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI362575	Hs.167133	ESTs	13.0
20	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
25	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
30	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
	417315	AI080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW296451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothi	12.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
40	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
45	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
50	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI568801	Hs.71721	ESTs	12.6
	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
55	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
	427078	AI676082	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
60	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
65	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
	432205	AI806583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
70	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965*:Homo sapiens phosphoglucomuta	12.4
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI459306	Hs.24908	ESTs	12.4
75	441269	AW015206	Hs.178784	ESTs	12.3
	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
80	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	12.2
	400880			NM_000611*:Homo sapiens CD59 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odx (odd Oz/ten-m, Drosophila) homolog 1	12.1
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
15	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	435169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164226	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984625	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730045	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheri	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	426981	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheri	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AI472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	11.5
	412677	AW029508	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI038316		gb:ox48c08.x1 Soares_t0tal_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoiet	11.4
	456804	AI421645	Hs.139851	caveolin 2	11.4
75	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
	433577	AW007080	Hs.8817	ESTs	11.4
80	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEF5_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3



	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
5	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476*gil12737279[ref]XP_012163.1]	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
10	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
15	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
20	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T86534	Hs.14372	ESTs	11.1
	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
25	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
30	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
	412622	AW684708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
35	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104696	KIAA1324 protein	10.9
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
45	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.156110	immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
50	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI623752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	10.8
55	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	H22953	Hs.137551	ESTs	10.8
	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
60	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
65	450206	AI796450	Hs.201600	ESTs	10.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
70	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
75	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW975944	Hs.237396	ESTs	10.7
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
80	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA: cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

	433923	AI823453	Hs.146625	ESTs	10.7
	418196	AI745649	Hs.26549	KIAA1708 protein	10.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
5	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	AI754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmegin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)-like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	AI801098	Hs.151500	ESTs	10.6
	449685	AW296669	Hs.66095	ESTs	10.6
	441111	AI806867	Hs.126594	ESTs	10.6
15	436671	AW137159	Hs.146151	ESTs	10.6
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
	424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	AI694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	451900	AB023199	Hs.27207	KIAA0982 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037766	Hs.146085	KIAA1345 protein	10.5
35	402076			C5002020*:gil1082876[pir][S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	AI380429	Hs.172445	ESTs	10.5
	443684	AI681307	Hs.55098	ESTs	10.5
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyclin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens proslein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-67	10.5
	416182	NM_004354	Hs.79069	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293798	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
75	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
	451593	AF151879	Hs.26706	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	10.2
5	446553	AB021179	Hs.15299	HMBA-inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
15	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
25	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
30	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
35	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	10.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA053564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
55	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
	441054	AA913591	Hs.126480	ESTs	9.9
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31584	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
5	404571			NM_015902: Homo sapiens progesterone induce	9.7
	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278626	Arg/Abl-interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A45010 X-link	9.7
15	417171	BE613486	Hs.81412	tipin 1	9.7
	421709	AA159394	Hs.107056	CED-6 protein	9.7
	415155	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523939	Hs.165258	ESTs	9.6
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.5641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	9.5
	408915	NM_016651	Hs.48950	hepaticellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H46008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AI636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulin 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crik avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
65	412446	AI768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncollin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW288235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
80	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
5	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
	402855		NM_001839*:Homo sapiens calponin 3, acid		9.3
	428465	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D86960	Hs.3610	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558		ENSP00000220478*:SECRETORANIN III.		9.2
15	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
20	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
25	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	9.1
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
30	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
35	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
40	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
45	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
50	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [Hsapli	9.0
	405523		C8001409*:gil7441226 pir  S31212 collage		9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
55	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.9
60	414917	C04863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
65	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
70	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502663	Hs.145037	ESTs	8.9
	403137		NM_005381*:Homo sapiens nucleolin (NCL),		8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
75	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
80	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	necln 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	AI743880	Hs.12876	ESTs	8.8
	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW080798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypolheti	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA564489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:d127e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypolheti	8.7
40	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60	425907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

5	434747	AA837085	Hs.220585	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
	450813	AI739625	Hs.203376	ESTs	8.5
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypothe	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
10	432620	AA777749	Hs.5978	LM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	S-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFP434K1421	8.4
20	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFP586E1923	8.4
25	421622	AB037748	Hs.106204	KIAA1327 protein	8.4
	431160	AW971174	Hs.324330	ESTs	8.4
	449567	AI990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	8.3
30	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFP434D0917 (f	8.3
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431952	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFP586M1418 (f	8.3
35	422295	AF051151	Hs.114408	toll-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	AI799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450.Homo sapiens four and a half L	8.3
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothe	8.3
	453121	AI988264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFP434C0921 (f	8.3
50	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFP564F112 (f	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	8.2
	432695	D63480	Hs.278634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALU7_HUMAN IIII	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypothe	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypothe	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	AI824719	Hs.328700	ESTs	8.2
75	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 59B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334



409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
		AW848214
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
418866	179788_1	T65754 AA229857 AA229658
418876	179960_1	AA740616 AA654854 AA229923
419536	185688_1	AA603305 AA244095 AA244183
419544	185760_2	AI909154 AA526337 AA244193 AI909153
423800	232161_1	AA331156 AA331157 AA331155
426413	266650_1	AA377823 AW954494 AI022688
429163	300543_1	AA884766 AW974271 AA592975 AA447312
430848	324621_1	AW021726 AA487752 AA488085
431121	328275_1	AW971157 AA492575 AA492520
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
434415	385931_1	BE177494 AW276909 AA632849
434579	38916_1	T55958 T57205 AF147346
439518	47334_1	W76326 AF086341 W72300
443161	561305_1	AI038316 AI344631 AI261653
447974	745643_1	R76886 AI453674 R77049

TABLE 59C

Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
Nt_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	Nt_position
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401785	7249190	Minus	165776-165995,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
402076	8117410	Plus	128316-128627
402812	6010110	Plus	25026-25091,25844-25920
402855	9662953	Minus	59763-59909
403047	3540153	Minus	59793-59968
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403149	9799833	Plus	25034-25185
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404571	7249169	Minus	112450-112648
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of prostate tumor to normal adult body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	56.6
419526	AI821895	Hs.193481	ESTs	56.2
420154	AI093155	Hs.95420	JM27 protein	44.0
432441	AW292425	Hs.163484	ESTs	41.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
431616	AA508552	Hs.195839	ESTs, Weakly similar to I35022 hypothe	37.9
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	36.0
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	30.0
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line- pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222896	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	A1918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H7?? transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_001172:Homo sapiens arginase, type II	24.5
	453370	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R18	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AJ267700		ESTs	20.2
	407709	AA456135	Hs.23023	ESTs	20.0
15	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.128816	ESTs	19.4
	409731	AA125985	Hs.55145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
20	410929	H47233	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656*:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	A1765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	A1694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	A1972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	A1202703	Hs.152414	ESTs	14.4
	450893	AW450461	Hs.203965	ESTs	14.4
40	431548	A1834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.3
	430187	A1799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450542	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
50	434656	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	A1127076	Hs.306201	hypothetical protein DKFZp564O1278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
55	453861	A1026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	12.3
	428398	A1249368	Hs.98558	ESTs	12.2
	421059	A1654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	12.2
	443960	A1093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	latexin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.276595	Homo sapiens prostein mRNA, complete cds	11.9
70	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	A1821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	11.6
75	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218885	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AJ277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.5
80	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	10.5
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
5	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	10.3
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
10	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
15	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
20	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
25	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	9.4
	450325	AI935962	Hs.26289	ESTs	9.4
30	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	ALD49610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid	8.2
65	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	426330	L22524	Hs.2256	matrix metalloproteinase 7 (matritysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X76592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453160	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

5	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AI750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI088489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homeo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AU077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
50	439492	AF086310	Hs.103159	ESTs	6.8
	449919	AI574685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI732230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
60	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB039670	Hs.9728	ALEX1 protein	6.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA861697	Hs.120591	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystokinin	6.6
70	447033	AI357412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
75	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
	421077	AK000061	Hs.101590	hypothetical protein	6.4
80	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoeiti	6.3
	453390	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.3
	433610	AA805822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AI922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
	425465	L18964	Hs.1904	protein kinase C, iota	6.2
15	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AI800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
20	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
	437323	AA371145	Hs.194397	leptin receptor	6.1
25	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
30	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmegin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	405523			C8001409:gi7441226 pir S31212 collage	5.9
50	448807	AI571940	Hs.7549	ESTs	5.8
	404642			NM_021965:Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414528	AA148950	Hs.188836	ESTs	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AI739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26613	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970976	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Ah1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	AI241733	Hs.43871	ESTs	5.4
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AI459306	Hs.24908	ESTs	5.4
	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
15	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
20	428354	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
	412677	AW029608	Hs.17384	ESTs	5.3
25	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	AI829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 ferri	5.3
30	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	AI278802	Hs.25661	ESTs	5.3
	441102	AA973905		intermediate filament protein syncoilin	5.3
35	453387	AI990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	AI823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
	447574	AF162666	Hs.18895	lousled-like kinase 1	5.2
40	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	5.2
	429467	NM_004477	Hs.203772	FSHD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	tol-like receptor 5	5.2
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA889120	Hs.110637	homeo box A10	5.2
55	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446795	AI797713	Hs.156471	ESTs	5.1
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 83	5.1
60	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogeni	5.1
	453293	AA382267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409643	AW450866	Hs.257359	ESTs	5.1
65	427723	AJ355260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068658	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	AI358957	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
	433023	AW864793	Hs.87409	thrombospondin 1	5.0
	433862	D86960	Hs.3610	KIAA0205 gene product	5.0
80	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	AI734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659305	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	4.9
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
20	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaean, yeast	4.8
45	408990	AL022395	Hs.49526	I-box and leucine-rich repeat protein 4	4.8
	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA453208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*:SECRETORANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.7
	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALU8_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403046			NM_005656*:Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	4.6
80	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6

	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
5	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
10	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
15	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
20	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
25	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
30	414272	AI651603	Hs.46988	ESTs	4.5
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	4.5
35	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476*:gij12737279[refXP_012163.1]	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
40	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	4.4
	433517	AW022133	Hs.188838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
45	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 fertilin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
50	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
55	448766	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisogu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
60	434022	R18374	Hs.117956	ESTs	4.4
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
65	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostosins (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
70	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
75	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
80	420405	AA743396	Hs.189023	ESTs	4.3
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3



	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155694	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
5	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629666		ESTs, Weakly similar to S64054 hypothe	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
10	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulon 3	4.2
	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	4.2
15	450546	AA010200	Hs.175551	ESTs	4.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
20	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449885	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
25	450377	AB033091	Hs.74313	KIAA1265 protein	4.2
	419647	AA348947	Hs.91816	hypothetical protein	4.2
	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW969657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
30	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
35	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.1
	447752	M73700	Hs.105938	lactotransferrin	4.1
	402855			NM_001839: Homo sapiens calponin 3, acid	4.1
	443161	AI038316		gb:ox48c08.x1 Soares_totat_fetus_Nb2HF8_	4.1
	415827	H17462	Hs.23079	ESTs	4.1
40	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161690	ESTs	4.1
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AJ335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
45	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239499	KIAA0185 protein	4.1
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
50	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.1
	428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
55	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.0
	443273	AI042063	Hs.132156	ESTs	4.0
	428055	AA420564	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AI457338	Hs.29894	ESTs	4.0
60	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
	431117	AF003522	Hs.250500	della (Drosophila)-like 1	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
65	409705	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
	418594	AJ732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
70	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
75	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW277121	Hs.254881	ESTs	4.0
	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
	400695			C11002514:gil11280151[pil]E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

5	428852	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0982 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.9
	442320	AI287817	Hs.129636	ESTs	3.9
15	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:aa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280699	ESTs	3.8
	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
35	443484	AI091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
50	408875	NM_015434	Hs.48804	DKFZP434B168 protein	3.8
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW105663	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
65	448207	AI475490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
70	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
	408312	AF263613	Hs.44198	intracellular membrane-associated calci	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.7
75	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
80	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (I	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.7
	445941	AI267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.6
	412533	AA679863	Hs.69606	ESTs	3.6
10	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AI475858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
15	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	3.6
20	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.6
	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN IIII	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
	433887	AW204232	Hs.279522	ESTs	3.6
25	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
30	435703	AW630133	Hs.83313	GK003 protein	3.6
	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothi	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazar	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA529399	Hs.165258	ESTs	3.5
	410762	AF226053	Hs.66170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exosloses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.5
55	420390	AA330047	Hs.191187	ESTs	3.5
	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
60	413950	AA249096	Hs.32793	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
70	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
75	432589	AL135725	Hs.131708	ESTs	3.5
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

5	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
10	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
15	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synthase	3.4
20	434966	AA657494		gb:nt66f04.s1 NCL_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902*:Homo sapiens progesterone induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheti	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
25	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*:Plasma membrane calcium	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AI655662	Hs.197698	ESTs	3.4
30	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
35	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432866	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
40	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
45	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
50	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
55	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
60	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
65	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
70	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	Klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
75	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
80	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*:HSPC213.	3.3
	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:cx10e09.r1 Soares_t0tal_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
	432363	AA534489		gb:m176g11.s1 NCI_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:z99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chain	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75812	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.2
	452295	BE379936	Hs.28866	programmed cell death 10	3.2
80	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
15	408784	AW971350	Hs.63386	ESTs	3.2
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig), Target Exon	3.2
	405558			ESTs	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
25	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheli	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gbzo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
	438979	AW976218	Hs.32565	ESTs	3.1
70	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
75	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI808583	Hs.125291	ESTs	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
80	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
5	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
15	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434FD91 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.77856	PFTAIKE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Pkey: Unique Eos probaset Identifier number

CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
5	411479	1247077_1 AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	411667	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	414372	143909_1 AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
10	414680	147525_1 AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	415989	156454_1 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416288	1585983_1 H51299 H44619 H46391 R86024 H51892 T72744
	416882	162718_1 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
15	416913	163001_1 AA196390 AA507837 AA196468
	417379	167238_1 AA215702 AA368006 AA215703 BE066555 BE006876
	418304	173658_2 AA226198 AA226513 AA383773
20	418647	177521_1 T65754 AA229857 AA229658
	418866	179788_1 AA603305 AA244095 AA244183
	419536	185688_1 AI909154 AA526337 AA244193 AI909153
	419544	185760_2 AF109300 AI299378 AI202654
	423412	228001_1 AA331156 AA331157 AA331155
25	423800	232161_1 AA769045 AA372590 AW963633
	426226	262918_1 AA377823 AW954494 AI022688
	426413	266650_1 AA380153 AA380233 AW963529
	426503	268283_1 AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
	426775	271683_1 AK001536 AA191092 AW510354 AI554256 AI353968 AA134266
30	426991	27415_1 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI02404 AI085630 AA731340
	428342	290035_2 AA884766 AW974271 AA592975 AA447312
35	429163	300543_1 AW207206 AW341473 AA448195 AI951341
	429220	301384_1 AA448765 C04967 C03045 AA658293
	429258	301917_1 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430935	325772_1 AW972830 AA527647 AA489820 AA570352
	430968	326269_1 AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T59596 BE618035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
40	431429	33313_1 H26383 AW972670 H26359 AA525808
	432093	341283_1 AW972667 AA526539 AI057032 AW167842
	432125	341776_1 AA527941 AI810608 AI620190 AA635266
	432189	342819_1 AA534222 AA632632 T81234
45	432340	345248_1 AA534489 AW970240 AW970323
	432363	345469_1 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432600	350959_1 AA863400 AI991439 AW016017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA626033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542
	432810	354375_1 T55958 T57205 AF147346
50	434579	38916_1 AA657494 AI582663 AI581639
	434966	396504_1 AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	435023	398093_1 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
	437866	44433_2 AW250553 L07876 Z36843 R30893 AI190097 AW965317
55	438147	45074_1 AA830149 AW978407 M85983 AW503637
	439092	468554_1 W76326 AF086341 W72300
	439518	47334_1 AW892676 AA853877 D44747
	439904	479942_1 AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
60	440840	50357_2 AA973905 AI299888 AA917019 H63235 T90771
	441102	509604_1 BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492830 AI376090 AI472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130886 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA54902 D62102 AI0007
	442562	54500_2 AI038316 AI344631 AI261653
65	443161	561305_1 AV655234 AW966332 AA340239
	445808	65133_1 T85314 AI360684 T85528 T91254
	447082	707248_1 AI475858 AW969013
	448212	755099_1 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
70	449625	8113_1 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
	450580	83929_1 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
75	450582	83933_1 AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI834576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
	452260	9074_1 AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AI138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI16834 N25206 AA828301 AI084565 AI302816 AW026905 AA77255
80	452598	92338_2 AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
	452815	93255_1 AL134757 AW079131
	453802	981589_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	455100	1253334_1



457728 393853\_1 AW974811 AA651634 AA650072

5 TABLE 60C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

35 Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

45 Pkey: Unique Eos probeset Identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue  
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	della (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to proleuse [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	3.3	5.9
5	431548	AI834273	Hs.9711	novel protein	15.7	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
10	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
15	451684	AF216751	Hs.26813	CDA14	3.9	5.4
	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
25	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
30	439024	R96696	Hs.35598	ESTs	5.4	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
	451952	AL120173	Hs.301663	ESTs	4.7	4.7
35	41676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476:gil12737279[ref]XP_012163.1]	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
40	429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111802	ESTs	4.8	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
45	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
50	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
	428826	AL048842	Hs.194019	atractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
	429900	AA450421	Hs.30875	ESTs	4.2	4.2
55	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
	409151	AA308105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911527	Hs.11805	ESTs	2.2	4.1
60	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
65	433887	AW204232	Hs.279522	ESTs	4.1	4.1
	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443646	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
70	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
	444755	AA431791	Hs.113823	CipX (caseinolytic protease X, E. coli)	3.9	3.9
75	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoacipale aminotra	3.9	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
80	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

	422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
5	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
10	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7	3.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AI571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
15	451009	AA013140	Hs.115707	ESTs	4.1	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AI357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
20	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
25	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.2	3.5
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AI918950	Hs.123642	EphA3	16.5	3.5
	429302	AI076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
30	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
35	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
40	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
50	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
55	444489	AI151010	Hs.157774	ESTs	3.2	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
	453078	AF053551	Hs.31584	melanin 2	2.1	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
60	434804	AA649530	Hs.348148	gb:ns44f05.s1 NC1_CGAP_Alv1 Homo sapiens	2.1	3.1
	445840	AI277811	Hs.146291	ESTs	3.1	3.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
65	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
70	420154	AI093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
	433285	AW975944	Hs.237396	ESTs	7.7	3.0
75	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
80	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AJ582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisou	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 feri	2.9	2.9
5	428500	AW853261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129536	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451796	AL133019	Hs.27038	Homo sapiens mRNA: cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
15	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor TII, polype	2.8	2.8
20	433865	N29862	Hs.44104	ESTs	2.8	2.8
	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654650	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
40	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436889	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
55	433419	AI830342	Hs.211272	ESTs	2.9	2.6
	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191060	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
70	431474	AL133990	Hs.190642	ESTs	9.3	2.5
	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656: Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ111344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubitinuclein 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	493221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfbt1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gi4507689jref[NP_003298.1] tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL060058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478:SECRETORANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	toll-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

5	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
10	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008:gi7303957 gb AAAF59000.1  (AE00	3.1	2.1
15	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
20	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
25	452959	AI933416	Hs.189674	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
30	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
35	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
40	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
	416208	AW291158	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
45	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
50	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
55	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
60	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
65	443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
70	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
75	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
80	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 618

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AJ141054 AW194991 AA252147 AA319500 A1184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 A1748815 A1763294 AJ333114 A1277384 A1088297 A1468477 A1824624 AW189606 A1631751 Z40749 A1984673 A1671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 A1909153
	419733	187589_1	AW362955 H59488 AJ040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 A1951970 AW044233 N20018 AW663548 T90114 A1139947 AA809643 AA846232 AA581966 AA789002
15	424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 A1268420 A1300495 A1215637 A1300494 A1268551 AA928971 AA179427 AA947684 BE393792 H98018 A1885781 A1188567 A1290558 C15404
	426413	266650_1	AA377823 AW954494 AJ022688
	429258	301917_1	AA448765 C04967 C03045 AA658293
	431676	336411_1	A1685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 A1673378 A1000340 R47500 W16595 AW152297 A1625937 AA002027 A1814851 AA902666 A1039729 AW975053 BE302243 A1240793 AA193203 N5581
	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	A1557914 W81031 AW473764 A1814081 W81068 AW182826 AW173296 A1376594 A1220500 BE257195 BE246486 R55637 C20788 AJ014407 A1248353 AW028015
25	445808	65133_1	AV655234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A1913631 A1498402 T613
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
40	Nt position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt position
	401197	9719705	Plus	176341-176452
	401519	6649315	Plus	157315-157950
	401558	7139678	Plus	103510-104090
45	402802	3287156	Minus	53242-53432
	403047	3540153	Minus	59793-59968
	404641	9795810	Minus	32247-32362
	405685	4508129	Minus	37956-38097
50	406068	9114084	Plus	382-543

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
65	R1:	Ratio of prostate tumor to normal prostate tissue

  

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
75	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	12.6
	401197			ENSP00000229263:HSPC213.	12.6
	426793	X89887	Hs.172350	HiR (histone cell cycle regulation defec	12.6
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
80	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.105768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002357	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AJ080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
20	425174	D87450	Hs.154978	KIAA0261 protein	8.6
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AJ934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AJ984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AJ038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153584	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
	426759	AJ590401	Hs.21213	ESTs	6.8
55	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AJ796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AJ300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AJ971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AJ350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AJ499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AJ745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9



	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	5.9
	431548	AI834273	Hs.9711	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	siatyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
15	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CD44	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103261	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
40	403851			C5002154".gij7299015[gb]AAF54217.1] (AE0	5.3
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
55	444917	R68651	Hs.144997	ESTs	5.1
	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
60	433600	R42833	Hs.22232	ESTs	5.0
	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
65	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
70	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96896	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476:gij12737279[ref]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419455	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE366283	Hs.173987	eukaryotic translation Initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:ztk85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_008732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b5?	4.2
	439518	W76326		gb:ztd60d04.r1 Soares_fetal_heart_NbH:119W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AA58213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567659	Hs.40342	putative nuclear protein	4.1
	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 38 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	CipX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoacidipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypothe	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122669	KIAA0264 protein	3.8
	403100			C2001027:gi7296271 gb AAAF51562.1 (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gb:mf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304505	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmnb33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75958	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
30	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
40	433269	AI343543	Hs.126890	ESTs	3.6
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350:gil6578126[gb]AA17706.1[AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446418	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M50721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb:yg12c04.r1 Soares infant brain 1N1B H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb:yy59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
75	401744			Target Exon	3.4
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

	432741	AJ732358	Hs.185118	ESTs, Moderately similar to A37413 calbi	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AJ207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428466	AF151063	Hs.184456	hypothetical protein	3.4
5	447397	BE247676	Hs.18442	E-1 enzyme	3.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
10	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
15	431689	AA305688	Hs.267695	UDP-Gal-betaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265540	ESTs, Moderately similar to A47582 B-cl	3.4
	403389			C3001393*:g[3327090]dbj[BAA31613.1] (AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
20	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
25	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
30	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
35	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
	426848	H72531	Hs.36190	ESTs	3.3
	439553	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
40	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
50	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
55	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
60	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
65	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
70	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	424273	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
80	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047588	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QVO-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
20	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
30	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNAX-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
40	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA202038	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	414527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e06 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	3.0
	442440	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
80	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		typtophanyl tRNA synthetase 2 (mitochon	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Key: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
		AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
		AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
		AA708749 AA644620 AA652769 AA242975 AA151074 T18890
		R17236 R52580 F11642
		AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
		AI633044 AW016212 AW241143 AA769058 R43272 AW088958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
		AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
		N59027 AA314694 N53937 R08100
		R06054 AA378789 AW956453
		AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
		AW972830 AA527647 AA489820 AA570362
		BE157283 BE157287 AA502438
		AI685464 AW971336 AA513587 AA525142
		AW972667 AA526539 AI057032 AW167842
		AA534489 AW970240 AW970323
		AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
		AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
		AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
		AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
		AW979177 AA846994 AA829672
		W76326 AF086341 W72300
		NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Key: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 N1\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	N1_position
400479	8439786	Minus	115385-116348
400658	8118459	Minus	73525-73544
400750	8119067	Plus	198991-199168, 199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628, 55755-55920, 57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671, 86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39624-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75<sup>th</sup> percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of normal prostate tissue to prostate tumor tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	AI738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	AI791314		gb:ae46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AI280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936.gij3746443[gb]AAC63969.1] (AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N1B H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2



	435190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
	425094	AI955956	Hs.21417	ESTs	4.1
5	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AI028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmet2)	4.1
	404260			Target Exon	4.0
10	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
	449233	BE048401	Hs.196511	ESTs	3.9
15	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
	409679	BE250521		ras homolog gene family, member A	3.8
20	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
25	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gij6679124[ref NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
30	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gij12654691[gib AAH01185.1 AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
	436524	AA922236	Hs.221037	ESTs	3.7
35	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
40	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
	442097	AW015799	Hs.128474	ESTs	3.6
45	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
	400749			NM_003105*:Homo sapiens sortilin-related	3.6
50	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCI_CGAP_GCB1 Homo sapiens	3.5
	405704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
55	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.126326	ESTs	3.4
	445045	AI652676	Hs.147256	ESTs	3.4
60	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KGA1578 protein (Fragm	3.4
	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
	444286	AI625304	Hs.190312	ESTs	3.4
65	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gij2695979[emb CAA70854.1 ] (Y0	3.4
	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
70	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
	418672	L44284	Hs.12915	ESTs	3.3
75	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheri	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I76885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
	458539	AI733837	Hs.145661	ESTs	3.3
80	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
5	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
10	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
15	451686	AA059246	Hs.110293	ESTs	3.1
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: hles3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
20	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	3.1
	402490			Target Exon	3.1
25	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
30	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
	419386	AA236667		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
35	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
40	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
45	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
50	449245	AI636539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
55	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
60	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
65	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	2.9
	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
70	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
75	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:zi199b10.s1 Soares_testis_NHT Homo sap	2.8
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
80	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941	gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656		Target Exon	2.8
	407269	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752 Hs.117341	ESTs	2.8
	433565	AA599763 Hs.112520	ESTs	2.8
	451004	AA044967	gb:z153d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825 Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770		NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239 Hs.189788	ESTs	2.8
	454445	AW749432	gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060 Hs.34382	ESTs	2.8
	427639	AW444530 Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020 Hs.208919	ESTs	2.7
15	406337		C14000021:gil7242973[dbj]BAA92547.1] (AB	2.7
	401884		Target Exon	2.7
	406881	D16154	gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884 Hs.201201	ESTs	2.7
	450044	R66444 Hs.51891	ESTs	2.7
20	403630		C3001708*:gil4758028[ref]NP_004360.1] co	2.7
	445514	AI241280 Hs.148906	ESTs	2.7
	446362	AW612481 Hs.104105	ESTs	2.7
	432492	AW275110 Hs.271106	ESTs	2.7
	430889	U22491 Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330 Hs.118796	annexin A6	2.7
	413155	BE067952	gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041 Hs.199291	numb (Drosophila) homolog-like	2.7
	446523	NM_003063 Hs.334629	sarcolipin	2.7
	449923	BE258051	gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129	gb:DKFZp547F152_r1 547 (synonym: hibr1)	2.7
	405678		CX001454:gil8393794[ref]NP_058681.1] myo	2.7
	432789	D26361 Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689	gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992 Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143 Hs.284284	zinc finger 1111	2.7
	415984	R19046 Hs.5010	gb:yg21f11.r1 Soares infant brain 1N1B H	2.7
	402844		C1000118*:gil9951913[ref]NP_062832.1] pr	2.7
	456666	AA452512 Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120 Hs.244621	ribosomal protein S14	2.7
40	404979		Target Exon	2.7
	412318	AW936911 Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551 Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516 Hs.95097	ESTs	2.7
	441975	AW173248 Hs.344285	EST	2.7
45	457021	AW968934 Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205 Hs.305890	BCL2-like 1	2.7
	439204	AF087987 Hs.42696	EST	2.7
	415642	U19878 Hs.336224	transmembrane protein with EGF-like and	2.7
	446847	T51454 Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AI792583 Hs.135354	ESTs	2.7
	447336	AW139383 Hs.245437	ESTs	2.7
	449045	BE072483 Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530 Hs.112822	OKFZP434B172 protein	2.7
	436030	R02287 Hs.121052	ESTs	2.7
55	449589	AW752437 Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AI345995 Hs.127383	ESTs	2.6
	415054	AI733907	gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913 Hs.293896	pregnancy-associated plasma protein-E	2.6
	409583	AW440117 Hs.256879	ESTs	2.6
60	410483	BE163567	gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083	wee1 (S. pombe) homolog	2.6
	426629	AI203933 Hs.97142	ESTs	2.6
	415831	H15145 Hs.30509	ESTs	2.6
	412281	AI810054 Hs.14119	ESTs	2.6
65	434898	AW500458 Hs.29956	KIAA0460 protein	2.6
	422229	AF134414 Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061	gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215667 Hs.175044	ESTs	2.6
	438548	AA813125 Hs.146335	ESTs	2.6
70	450399	AW511049 Hs.202007	ESTs	2.6
	420833	R47948 Hs.188732	ESTs	2.6
	453903	AW296606 Hs.232777	ESTs	2.6
	443650	AI698330 Hs.151444	ESTs	2.6
	427419	NM_000200 Hs.177888	histatin 3	2.6
75	423741	AA330362	gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101 Hs.40730	ESTs	2.6
	441358	AW173212 Hs.129041	ESTs	2.6
	402706		Target Exon	2.6
	436054	AI076262 Hs.119813	ESTs	2.6
80	402749		Target Exon	2.6
	442472	AW806859	gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002 Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872	gb:oo57d07.s1 NCI_CGAP_Lu5 Homo sapiens	2.6
	405564		Target Exon	2.6

	406003		Target Exon	2.6	
	459584	AI910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.6
	445060	AA830811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gil403440[gb]AAA73168.1 (M817	2.6
	416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypothe	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA225522		gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	Hs.170058	ESTs	2.6
20	441063	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	AI125263	Hs.170410	ESTs	2.5
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AI693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yl79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.5
45	404678			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429906	AL080137	Hs.193743	ESTs	2.5
	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
50	438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048462_1	AW176091 H24234
	408432	1058667_1	AW195262 R27868 AW811262
	409579	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
65	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
	411829	1260309_1	AW865749 BE179419 BE179492
70	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
	415054	151827_1	AI733907 AA159708 AI732614
75	415098	1522174_1	D59687 D59694 D59656 D59589
	415131	1523680_1	D61119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35594 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08951
	419896	1888662_1	Z99362 Z99363
	420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599
			CO2215 AI6525
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
15	436190	41555_1	AK001059 AA633055
	438535	45946_1	L09078 L03145 L09084 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
20	447518	724787_1	T80061 AI382804
	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
25	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072258 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380836_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
50	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
65	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
	403649	8705159	Minus	27141-27247
75	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
80	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

5	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079,102261-102443,102895-103202
	405564	2114222	Minus	16766-17344
	405678	4079670	Plus	151821-152027
	405735	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

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Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

25	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to normal adult body tissue		
30	Pkey	ExAccn	Unigene ID	Unigene Title
	420154	AI093155	Hs.95420	JM27 protein
	425747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen
	419526	AI821895	Hs.193481	ESTs
	432441	AW292425	Hs.163484	ESTs
35	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheri
	407202	N58172	Hs.109370	ESTs
	432101	AI918950	Hs.123642	EphA3
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen
	425075	AA506324	Hs.1852	acid phosphatase, prostate
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1
	410929	H47233	Hs.30643	ESTs
	400287	S39329	Hs.181350	kallikrein 2, prostatic
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr
45	415989	AI267700		ESTs
	426336	AA503115	Hs.183752	microseminoprotein, beta-
	450693	AW450461	Hs.203965	ESTs
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of
	407168	R45175	Hs.117183	ESTs
50	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport
	454119	BE549773	Hs.40510	uncoupling protein 4
	428819	AL135623	Hs.193914	KIAA0575 gene product
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278
55	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheri
	433444	AW975324	Hs.129816	ESTs
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL
60	401424			NM_001172:Homo sapiens arginase, type II
	432435	BE218886	Hs.282070	ESTs
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1
65	407275	AI364186		gbqw34h07.x1 NCL_CGAP_U14 Homo sapiens
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma
	432473	AI202703	Hs.152414	ESTs
	410330	AW023630	Hs.159425	ESTs
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH
70	452792	AB037765	Hs.30652	KIAA1344 protein
	418848	AI820961	Hs.193465	ESTs
	400292	AA250737	Hs.72472	BMP-R1B
	433647	AA603367	Hs.222294	ESTs
	453160	AI263307	Hs.239884	H2B histone family, member L
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624
	431474	AL133990	Hs.180642	CEGP1 protein
	429220	AW207206		ESTs
	428134	AA421773	Hs.161008	ESTs
80	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu
	434792	AA649253	Hs.132458	ESTs
	433466	AA508353	Hs.105314	relaxin 1 (H1)
	439176	AI464444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr
	428398	AI249368	Hs.98558	ESTs

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
	429918	AW873986	Hs.119383	ESTs	9.1
5	440260	AJ972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450642	R39773	Hs.7130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55899	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI980741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146625	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieli	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415785	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
	449821	AI671141	Hs.211122	ESTs	6.8
55	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site faml	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
10	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
15	434485	AI623511	Hs.118567	ESTs	5.8
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesteron induca	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo	5.5
	426581	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R18	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	M83941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
80	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0



	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
5	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.0
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100:gil5852342[gb]AAD54015.1] (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
10	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
	414422	AA147224	Hs.249195	Homeo box A13	4.9
15	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
20	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
25	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheli	4.7
30	452843	AI796769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
35	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
40	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
45	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
50	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418835	AI655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
55	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78958	Hs.14411	ESTs	4.5
60	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
65	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
75	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*:PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
5	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
	420111	AA255652		gb:zs21h11.1 NCI_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
10	405348			C7001664:gil12698061 dbj BAB21849.1  (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
15	432887	AI926047	Hs.162859	ESTs	4.3
	420905	AA521307	Hs.186651	ESTs	4.2
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
20	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
	450597	AI701635	Hs.207077	ESTs	4.2
	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
25	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
30	440594	AW445167	Hs.126036	ESTs	4.2
	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
35	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
40	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449507	AA004825	Hs.103281	ESTs	4.1
45	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
50	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
55	440840	AW629666		ESTs, Weakly similar to S64054 hypothe	4.0
	442338	AI761976	Hs.156080	ESTs	4.0
	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
60	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
65	421312	AA824627	Hs.291670	ESTs	4.0
	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partia	4.0
70	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
	452221	C21322	Hs.288057	hypothetical protein FLJ2242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
75	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
80	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothe	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
5	435878	R08330	Hs.20152	ESTs	3.9
	446862	AV660697	Hs.282700	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403			Target Exon	3.9
	448779	BE042877	Hs.177135	ESTs	3.9
10	420533	AI809510	Hs.118971	ESTs	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	423453	AW450737	Hs.128791	CGI-09 protein	3.9
15	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AWB48047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	Hs.190325	ESTs	3.9
	421129	BE439899	Hs.89271	ESTs	3.9
20	424332	AA338919	Hs.101615	ESTs	3.9
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	3.9
	447033	AI357412	Hs.157601	ESTs	3.9
	439306	BE220199		WD40 protein C1a01	3.8
	410352	AW969725	Hs.150444	KIAA0373 gene product	3.8
25	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	3.8
30	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE617907	Hs.97635	ESTs	3.8
	438379	N23018	Hs.171391	C-terminal binding protein 2	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
35	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	Hs.97266	protocadherin 18	3.8
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	Hs.191791	ESTs	3.8
	437718	AI927288	Hs.196779	ESTs	3.8
40	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	426981	AL044675	Hs.173081	KIAA0530 protein	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
45	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	3.7
50	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	423096	AA732684	Hs.278428	progesterin induced protein	3.7
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420564	Hs.101760	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	453293	AA382267	Hs.10653	ESTs	3.7
	436671	AW137159	Hs.146151	ESTs	3.7
60	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	Hs.44743	KIAA1435 protein	3.7
	420092	AA814043	Hs.88045	ESTs	3.7
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	Hs.5722	hypothetical protein FLJ23316	3.7
65	419875	AA853410	Hs.93557	proenkephalin	3.7
	431231	AA653552	Hs.116532	ESTs	3.7
	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
70	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	Hs.145037	ESTs	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
80	450630	AA010429	Hs.191939	ESTs	3.6
	411067	AI681006	Hs.71721	ESTs	3.6
	436326	BE085236		aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
10	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18964	Hs.1904	protein kinase C, iota	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517":g[4758712]ref[NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
15	435177	AI018174	Hs.42936	ESTs	3.5
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
20	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.1.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
25	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769":BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
65	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
70	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
80	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
5	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
15	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
20	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83683	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
	423595	R82826	Hs.220702	ESTs	3.2
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhiHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338*:gll7459502 pir jS74665 outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.65731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
	415862	R51034	Hs.144513	ESTs	3.2
	420959	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI456682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
75	423855	AA331761	Hs.254859	ESTs	3.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

	407426	AF129533	gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	ESTs	3.1
	418037	AJ990212	ESTs	3.1
5	419197	N48921	KIAA1615 protein	3.1
	420179	N74530	ESTs	3.1
	433610	AA806822	ESTs	3.1
	436295	N73895	gb:zab2d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	ESTs	3.1
10	418858	AW961605	hypothetical protein RG083M05.2	3.1
	446469	BE094848	homogentisate 1,2-dioxygenase (homogenti	3.1
	431992	NM_002742	protein kinase C, mu	3.1
	405510		ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
	410869	AW808361	gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
15	425354	U62027	complement component 3a receptor 1	3.1
	425480	AB023198	KIAA0981 protein	3.1
	441492	AI149998	ESTs	3.1
	447078	AW885727	ESTs	3.1
20	459324	AW080953	gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.1
	433852	AI378329	ESTs	3.0
	448658	H71739	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	glycosyltransferase	3.0
	424690	BE538356	eukaryotic translation initiation factor	3.0
25	405264		NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	ESTs, Weakly similar to I38022 hypothe	3.0
	434497	AI821803	ESTs	3.0
	420355	AW968263	ESTs	3.0
30	403481		Target Exon	3.0
	412988	BE046680	gb:tn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	transmembrane, prostate androgen induced	3.0
	416642	T96118	ESTs	3.0
	418948	AI217097	gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	ESTs	3.0
	430459	BE178539	ESTs	3.0
	439182	AF086030	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	ESTs	3.0
	448686	AA158659	hypothetical protein FLJ14744	3.0
40	453455	AA063553	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	ESTs	3.0
	427302	AA400540	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	ESTs	3.0
	450963	AI864668	ESTs	3.0
45	432336	NM_002759	protein kinase, interferon-inducible dou	3.0
	459535	AV654907	gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	hypothetical protein FLJ13197	3.0
50	420407	AA814732	lipopolysaccharide-specific response 5-li	3.0
	426743	AA383833	ESTs	3.0
	442326	H92962	hypothetical protein MGC14817	3.0
	449913	AA004696	ESTs	3.0
	454096	AW062757	gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	leptin receptor	3.0
	407137	T97307	gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087	ESTs	3.0
	429084	AJ001443	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	ESTs	3.0
60	423784	AK000039	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
	435677	AA694142	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	hypothetical protein FLJ14600	3.0
	418819	AA228776	ESTs	3.0
	428634	AA811845	Kelch motif containing protein	3.0
65	431869	AA521136	ESTs	3.0
	435008	AF150262	ESTs	3.0
	448880	AW205507	ESTs, Highly similar to I38587 retroviro	3.0
	451391	AA017410	ESTs	3.0
	452959	AI933416	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
80			AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
			AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528

5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355085 Z43062 R13213 H14422 H51299 H44619 H46391 R86024 H51892 T72744 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671315 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597 AA215404 AI950909 BE464132 AW271459 N74332 AI262061 T65754 AA229857 AA229658 AI217097 AW886090 W38035 W38792 AA232835 AW936043 AA603305 AA244095 AA244183 AA255652 AA280911 AW987920 AA262684 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AF109300 AI299378 AI202654 AA337221 AA336756 AW966196 AA377823 AW954494 AI022688 AA380153 AA380233 AW963529 AK001538 AA191092 AW510354 AI554256 AL353968 AA134266 AA418703 AA418711 BE071915 BE071920 BE071912 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA83419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340 AA884766 AW974271 AA592975 AA447312 AW207206 AW341473 AA448195 AI951341 AW968485 AW968670 AA480922 BE350425 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339 AJ003429 AJ003367 AA564825 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA648618 AW974389 H51771 N73895 AJ001872 BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281 AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706 AW270601 AW873282 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188 AA830149 AW978407 M85983 AW503637 BE220199 W01813 AF086118 N70760 BE221405 AW628666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877 AA910403 AI815593 W58361 AW162520 AI816550 N99828 BE079873 AI110738 AF074645 AV653771 BE089370 AI458682 H24240 R14537 R18426 AW867082 AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053 AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467 H00789 R76925 AW1828 AA001793 AA001871 NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AI039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AI692689 R14223 R18395 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AA495800 AA495737 AA010736 AA654716 AA640726 BE173515 BE173560 AI902860 T79703 T96307 AI079725 AW998716 AW022148 N68020 AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW753456 AW753036 AW854868 AW854862 AW835767 AW835537 BE160187 AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464 AA493662 AW897396 BE154814 AI911066 AI933734 AI680888 AJ003599
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TABLE 64C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NI\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
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5	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9955004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of BPH tissue to prostate tumor tissue			
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	428134	AA421773	Hs.161008	ESTs	9.4
	446336	AW815036	Hs.151251	ESTs	9.3
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	400533			ENSP00000209376*-PRED65 protein (Fragmen	8.7
	418310	AA814100	Hs.86693	ESTs	8.7
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	8.1
45	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
	400080			Eos Control	7.4
	459846	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
50	418387	R18085		gb:yg16b12.r1 Soares infant brain 1N1B H	7.2
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
	404967			Target Exon	6.9
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
	412988	BE046680		gb:hm42h03.x1 NCI_CGAP_RDF2 Homo sapiens	6.8
	400440	X83957	Hs.83870	nebulin	6.6
60	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
	400086			Eos Control	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
65	419015	T79262	Hs.14463	ESTs	6.3
	453789	AA628517	Hs.118502	ESTs	6.2
	424940	AA985308	Hs.283902	ESTs	6.1
	403667			Target Exon	6.1
	429014	AI800518	Hs.118158	ESTs	6.0
70	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter	6.0
	419999	AI760942	Hs.191754	ESTs	6.0
	405348			C7001664:gi12698061 dbj BAB21849.1  (AB	6.0
	404003			Target Exon	5.9
	453200	AA033832	Hs.212433	ESTs	5.7
75	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432319	AW510770	Hs.128386	ESTs	5.7
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
	443361	AI792628	Hs.133273	ESTs	5.6
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	5.6
80	439079	AF085937	Hs.38348	ESTs	5.5
	422081	AW136820	Hs.196011	ESTs	5.5
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
	423529	T87318	Hs.120411	ESTs	5.5



	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
	454958	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
15	435375	AI733510	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
20	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gi 4758712 ref NP_004659.1  al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stratagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
	441620	R59595	Hs.26675	ESTs	4.2
70	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	408500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	430124	AW204994	Hs.253450	ESTs	4.2
80	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
5	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo	4.0
10	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW569118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
15	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
20	454806	AW872430	Hs.273743	ESTs	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
25	407834	AW084991	Hs.26100	ESTs	3.9
	400398	AF137396	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482:gij9790241[ref]NP_062628.1  S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
40	434381	AA631834		gb:nrp77h05.s1 NCL_CGAP_P2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AI637649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AI470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Refina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455057	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
5	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517*:gil4758712[ref NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
	403510			Target Exon	3.5
20	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI399732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
50	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA069050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothe	3.2
	418986	AI123555	Hs.81795	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:gil129092[sp P23270 OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203833	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429559	AA454993	Hs.138343	ESTs, Weakly similar to I7885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA577981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AI754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
15	441817	AW969705	Hs.293332	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
25	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
30	441492	AI149998	Hs.146346	ESTs	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypothe	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AI939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762C0076	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140::Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AI381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

## 55 TABLE 65B

	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
60	Pkey	CAT Number
	408304	1050848_1
		Accession
		AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515
		AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288
		AW810263 AW810325 AW810443 AW8
65	409189	110687_1
		AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512
		AA085119 AA085208 AA085045
	410559	1208283_1
	410790	1221131_1
	410859	1225123_1
70		Accession
		AW754192 W00554 AW857797 AW754203 AW754197 AW754193
		AW803357 AW803423 AW812233 R06814
		AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
		AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
		AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1
	411518	1248692_1
	411552	1249255_1
75	412701	1322288_1
	412988	1342150_1
	413081	1348563_1
	413525	1374635_1
	416009	1566379_1
80	416422	1593811_1
	418059	171879_1
	418387	174731_1
	418948	180808_1
		Accession
		H60457 H68709 H73528 H54335 R87154
		AA211586 F35799 AA211641 F29720 AW937387 AW937408
		R18085 AA219028 R17712 Z44345
		AI217097 AW886090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW052757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

45

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probe set
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nl position:	Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	Nl_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
65	403305	8099945	Plus	114632-114805
	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	105655-108050
	403433	9719511	Minus	72225-72437
	403481	9965004	Plus	93496-93633
70	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442, 1545-1697
	403805	8140491	Minus	51483-51742, 53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
75	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034, 25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
80	405321	3419846	Minus	44654-45210
	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:zw34h07.x1 NCI_CGAP_U14 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-05 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PREDE65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothe	5.3

	423101	M83941	Hs.123542	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	454958	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
5	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
10	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71885 Ste20-lik	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
15	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420633	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
20	457374	AA493682		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
	450497	H64159	Hs.15328	ESTs	4.8
25	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
30	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
35	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	405348			C7001664.gij12698061 dbj BAB21849.1  (AB	4.6
40	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123542	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
45	449821	AI671141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
50	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
55	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
60	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
65	432765	AI003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	458912	AI911066		ESTs	4.2
70	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	450597	AI701635	Hs.207077	ESTs	4.1
75	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	438875	AA827640	Hs.189059	ESTs	4.1
80	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
	435136	R27299	Hs.10172	ESTs	4.0
5	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, moto	4.0
10	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
15	412988	BE046680		gb:hn42h03.x1 NCL_CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
20	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	440450	AI333129	Hs.156147	ESTs	3.8
25	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
30	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
35	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	432101	AJ918950	Hs.123642	EphA3	3.7
40	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	435345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.7
50	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
55	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
60	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
65	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
	426917	AA913814	Hs.172854	DKFZP58680923 protein	3.6
70	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
75	401132			C12000517*:gij4758712[ref]NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCL_CGAP_Ew1 Homo sapiens	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5



	430665	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
5	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
10	404848			ENSP00000240769:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.4
15	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
20	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170685	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
65	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th
	434512	AW139932	Hs.188941	ESTs
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-
	433444	AW975324	Hs.129816	ESTs
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti
	415861	Z43123	Hs.144513	ESTs
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174
10	432527	AW975028	Hs.102754	ESTs
	427773	AA412290	Hs.98124	ESTs
	441817	AW969706	Hs.293332	ESTs
	416812	H91010	Hs.44940	ESTs
	417958	AA767382	Hs.193417	ESTs
15	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL
	416423	H54375	Hs.268921	ESTs
	418037	AI990212	Hs.86447	ESTs
	419197	N48921	Hs.27441	KIAA1615 protein
	420179	N74530	Hs.21168	ESTs
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen
	405548			Target Exon
	423595	R82826	Hs.220702	ESTs
	412533	AA679863	Hs.69606	ESTs
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds
25	405264			NM_030813:Homo sapiens suppressor of po
	410869	AW808361		gb:MR1-ST0111-111099-003-004 ST0111 Homo
	425354	U62027	Hs.155935	complement component 3a receptor 1
	441492	AI149998	Hs.146346	ESTs
	447078	AW885727	Hs.9914	ESTs
30	435021	AA922192	Hs.54709	ESTs
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC
	450580	N40087		ESTs
	432319	AW510770	Hs.128386	ESTs
	453713	R20640	Hs.79133	cadherin 8, type 2
35	445784	AI253155	Hs.146065	ESTs
	416642	T96118	Hs.226313	ESTs
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W
	433796	AA810867	Hs.186997	ESTs
	439182	AF086030	Hs.21621	hypothetical protein DKFp762O076
40	404995			ENSP00000251890:Monocytic leukemia zinc
	444794	AI419991	Hs.145225	ESTs
	443634	H73972	Hs.134460	ESTs
	420133	AA426117	Hs.155543	ESTs
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197
45	426743	AA383833	Hs.245022	ESTs
	442326	H92962	Hs.124813	hypothetical protein MGC14817
	449913	AA004696	Hs.333016	ESTs
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo
50	419622	AA452054	Hs.119338	ESTs
	449745	AI668593		gb:yl38a05.x5 Soares breast 3NbHbSt Homo
	428412	AA428240	Hs.126083	ESTs
	426200	AI039624	Hs.98388	ESTs
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600
	431869	AA521136	Hs.190176	ESTs
55	451391	AA017410	Hs.40568	ESTs
	452959	AI933416	Hs.189674	ESTs

TABLE 68B

60	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
<hr/>			
65	Pkey <sub>i</sub>	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
70	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	412988	1342150_1	BE046680 BE046738 BE044958
75	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
80	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	424200	236595_1	AA337221 AA336756 AW966196
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912

	428342	290035_2	A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404 A1085530 AA731340 AW968485 AW968670 AA480922 BE350425 AJ003429 AJ003367 AA564825 H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320 AA648618 AW974389 H51771 N73895 AJ001872 AAB30149 AW978407 M85983 AW503637 BE220199 W01813 AF086118 N70760 BE221405 AA910403 A1815593 W58361 AW162520 A1816550 N99828 BE079873 A1110738 AF074645 AV653771 BE089370 A1458682 H24240 R14537 R18426 AW867082 AA001793 AA001871 A1668593 A1820774 R86205 H39971 H22177 H26241 A1692589 R14223 R18395 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303 A1339732 AA010300 AW515041 AA768334 N29860 AA25874 AA425118 AA865829 AW936878 AA495800 AA495737 AA010736 AA654716 AA640726 BE173515 BE173560 A1902860 T79703 T96307 AL079725 AW998716 AW022148 N68020 AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW753456 AW753036 AW854868 AW854862 AW812866 AW812746 AW812747 AW812884 AW812763 AW812722 AW835767 AW835537 BE160187 AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 AW854538 AW854418 AW854412 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464 AA493662 AW897396 BE154814 A1911066 A1933734 A1680888 AJ003599
5	430635	319643_1	
	432765	353907_1	
	433523	368873_1	
	434763	392847_1	
	436295	41733_1	
	439092	468554_1	
	439306	47088_1	
10	440947	505904_1	
	442481	543588_1	
	445432	63943_1	
	448044	747196_1	
	449570	81018_1	
15	449745	814534_1	
	450317	831956_1	
	450580	83929_1	
20	450582	83933_1	
	450687	84327_1	
	452462	918580_1	
	453682	977454_1	
	454037	996287_1	
25	454096	1007449_1	
	454171	1049240_1	
	454457	1207274_1	
	454665	1228599_1	
	454860	1237732_1	
30	454968	1247029_1	
	455067	1252050_1	
	455276	1272541_1	
	455646	1348557_1	
	455710	1352368_1	
35	457374	328758_1	
	458912	823104_1	

TABLE 66C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 Rt: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelID	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kalikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AJ420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kalikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kalikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425528	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin)-prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M33119	Hs.89584	insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.126749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothei	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFP434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
	432101	AI918950	Hs.123642	EphA3	9.1
10	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypol	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
15	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	8.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.5
20	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
25	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0666 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
30	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	429505	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	432586	AA568548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
	450377	AB033091		KIAA1265 protein	6.6
60	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
	448045	AJ297436	Hs.20166	prostate stem cell antigen	6.0
80	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP56680846 protein	5.8
5	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.7
10	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	5.4
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-8 protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
25	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
30	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
35	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptotagmin 2	5.0
	403046			NM_005656*:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
	450164	AI239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
50	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.105778	ATPase, Ca transporting, type 2C, member	4.7
	431724	AA514535	Hs.283704	ESTs	4.7
60	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22527	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.5
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
75	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S6B401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
5	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AJ694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheli	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
10	442501	AA315267	Hs.23128	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
15	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
20	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430845	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
	432363	AA534489	Hs.18895	gbm176g11.s1 NCL CGAP_Co3 Homo sapiens	4.1
25	447574	AF162666	Hs.18895	lousled-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
	422890	Z43784	Hs.101307	ankyrin 3, node of Ranvier (ankyrin G)	4.0
30	417379	AA196390	Hs.279727	gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228899	Hs.279727	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.183161	ESTs; homologue of PEM-3 [Clona savignyi	4.0
	418821	AA436002	Hs.79953	ESTs	4.0
	438825	BE327427	Hs.301804	ESTs	4.0
35	433233	AB040927	Hs.78353	KIAA1494 protein	4.0
	415276	U88666	Hs.90790	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.89969	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185	Hs.102754	ESTs	4.0
40	450402	BE218027	Hs.112110	ESTs	4.0
	432527	AW975028	Hs.282070	ESTs	4.0
	419733	AW362955	Hs.25318	Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.31595	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.233765	ESTs	3.9
45	450680	AF131784	Hs.34892	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.292911	ESTs	3.9
	430122	NM_013342	Hs.40109	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.81086	KIAA1323 protein	3.9
	429259	AA420450	Hs.61152	Plakophilin	3.9
50	407813	AL120247	Hs.193417	KIAA0872 protein	3.9
	417067	AJ001417	Hs.40334	solute carrier family 22 (extraneuronal	3.9
	410227	AB009284	Hs.293246	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.105887	ESTs	3.9
	427176	AW381569	Hs.92381	ESTs	3.9
55	448826	AI580252	Hs.178471	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.9029	ESTs, Weakly similar to Homolog of rat Z	3.8
	432675	AI791855	Hs.32793	ESTs	3.8
	419713	AW968058	Hs.6793	nudix (nucleoside diphosphate linked moi	3.8
	427479	BE410092	Hs.98613	KIAA0798 gene product	3.8
60	443162	T49951	Hs.20509	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.21187	ESTs	3.8
	439963	AW247529	Hs.274251	platelet-activating factor acetylhydrola	3.8
	419083	AI479560	Hs.246315	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.87539	HBV pX associated protein-8	3.8
	419465	AW500239	Hs.79428	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
65	432274	AK000382	Hs.300496	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951	Hs.108708	ESTs	3.8
	430589	AJ002744	Hs.164159	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
	418004	U37519	Hs.5947	aldehyde dehydrogenase 3 family, member	3.8
70	416655	AW968613	Hs.127337	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.35198	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.42346	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.111138	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.88323	mel transforming oncogene (derived from	3.7
	417061	AI675944	Hs.98541	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
75	423337	NM_004655	Hs.254835	axin 2 (conductin, axil)	3.7
	418838	AW385224	Hs.294101	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.246315	KIAA0633 protein	3.7
	408063	BE086548	Hs.33010	calcinurin-binding protein calsarcin-1	3.7
	422072	AB018255	Hs.42346	KIAA0712 gene product	3.7
80	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

5	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synthase	3.6
	422424	A186431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
10	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
15	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274255	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
	429686	A1871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
20	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
25	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	A1336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
30	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
35	427723	A1355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
40	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
	437617	A1026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
45	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
50	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
55	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
60	433891	AA613792		gb:nc97h03.s1 NCI_CGAP_Py2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	A1248720	Hs.114390	ESTs	3.3
65	412628	A1972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
	433345	A1681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
70	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
75	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*gi12737279[ref]XP_012163.1]	3.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
80	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upt3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	A1249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2



	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
15	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10574 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
	436278	BE396290	Hs.5097	synaplogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	438705	AJ049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278952	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA: cDNA DKFZp564N0763 (f	3.0
45	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AJ298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.292833	ESTs, Weakly similar to t38022 hypotheti	3.0
	429956	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78106	phosphodiesterase 8B	2.9
	412826	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
80	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
5	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
15	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
20	422202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
	418166	AI754416		Cdc42 effector protein 3	2.8
25	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
	425320	U29344	Hs.83190	fatty acid synthase	2.8
30	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
40	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
45	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulf	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
55	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
70	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
	409650	T08490	Hs.288969	HSCARG protein	2.7
75	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
80	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

5	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	riban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
15	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulin 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
20	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102545	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.255301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
30	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
40	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRV (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
50	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
55	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AJ373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
60	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW961400	Hs.333526	HER2 receptor tyrosine Kinase (c-erb-b2,	2.5
70	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC087 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450628	AW382884	Hs.204715	ESTs	2.5
75	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
80	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
	414556	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWUSNF related, matrix associated, acti	2.5
10	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.5
	443837	AI934625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
	435021	AA922192	Hs.73962	ESTs	2.5
15	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
20	449458	AI805078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.181444	hypothetical protein	2.5
	424369	R87622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.5
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.5
	427515	T79526	Hs.179516	integral type I protein	2.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

35	Pkey	CAT Number	Accession
40	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 AW341473 AA448195 AW207206 AI951341 AA969259
	429220	15103_7	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
	412446	63467_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
45	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
50	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AW722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
55	437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA68546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422
60	432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554063 AI826259 AA568548
	438869	52134_1	AF075009 R63109 R63068
	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768485 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
65	436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
70	428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA809524 AA635311 AA649040 AI392620 Z40708 AI885564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036987 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
75	424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810905 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
	450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
80	451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
	432363	1234917_1	

5	422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AI538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10054 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
10	417379	1610005_1	AA196390 AA507837 AA196488
	407819	7392_2	AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
	419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 B28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
15	432675	1237917_1	AW973834 AI791932 AI791855 AI732640 AA558833 AA558987 AI821610
	447620	687223_1	AI973051 AI400921 AI796154 AW241817 AW230951
	409151	4123_1	NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435620 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
20	409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW266868 AI268977 BI168133 BM352065 AI262769 BF941976 AI056920 BE125470 BE732690 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
25	433891	647290_1	AW182329 AA613792 T05304 AW858385
	414922	1563_2	BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AI562079 AI700926 AI700561 BF063058 AW196387 AI132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827
30	414222	18695_1	BC021085 AI527872 AI526296 AL557087 BI255090 AU141439 AI560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI70885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726966 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI22949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219705 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI204449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI727535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AI564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA405317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106
35	426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG507710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191902 BF132635
40	434194	62680_1	AF119847 AA437261 AA436987 AI132965
	432908	452541_1	AF150424 AI861896 AA570057 AV738855
	412652	18858_2	AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI091780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
50	437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA338371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092229 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF467021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
55	418166	18858_1	AK055915 BE867252 AI523348 AA765350 BF466858 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW052986 BI962893 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732
60	431416	120918_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974
	447881	44623_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28518 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AA438839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
65	407192	2200202_1	AA602964 AA609200
	434747	117643_1	AW976537 AI033582 AA837085 AA745261 AA648395
	410297	2990_1	BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA28261 AI60355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025801 AA452120 AI150479 AI016166 AA779515 AA561791 BM474307 BI911169 BG575154 AW953303 T33504 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 RT0463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N98979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AI418710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 RT0550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI855262 R55325 AI468927 R34681 H96211 Z39807 BF954386
70	424339	50559_1	NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833

445636	8561_5	BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA866998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961054 AI018062 H80618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322 AI041403 Z49148
406789	0_0	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AI567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
400263	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562865 AI099178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF669652 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859,56389-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165995,166189-166314,166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833,5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AI821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
5	400292	AA250737	Hs.72472	BMP-R1B	31.4
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
10	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
15	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
20	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
25	437052	AA861697	Hs.120591	ESTs	22.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
30	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	14.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820861	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
55	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	della (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
5	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000282	Hs.130732	hypothetical protein FLJ20285	10.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
10	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975844	Hs.237396	ESTs	10.0
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
	443180	R15875	Hs.258576	claudin 12	9.5
20	406964	M21305		FGENES predicted novel secreted protein	9.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
25	440594	AW445167	Hs.126036	ESTs	9.4
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA554458		KIAA0666 protein	9.2
30	428728	NM_016625	Hs.191381	hypothetical protein	9.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
35	418836	AI655499	Hs.161712	ESTs	8.8
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
40	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	8.7
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
45	416239	AI038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP5641052 protein	8.4
	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420611	Hs.153934	ESTs	8.3
50	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
55	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
60	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	7.7
65	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
70	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	7.6
	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	432933	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2



5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
	412350	AJ659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
10	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
15	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
20	420297	AJ628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
25	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
30	410762	AF226053	Hs.66170	HSKM-8 protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
35	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
40	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
45	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
50	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
60	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
65	435706	W31254	Hs.7045	GLD04 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
70	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.5
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	5.5
	403046			NM_005656*:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
75	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
80	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
5	417318	AW953937	Hs.240845	ESTs	5.3
	429467	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	UV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
	450832	AW970602	Hs.105421	ESTs	5.1
15	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
20	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
25	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	HA0164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635385	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432353	AA534489		gb:mf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.7
50	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Stralagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X65724	Hs.2839	Norie disease (pseudoglioma)	4.7
	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538225	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
75	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433555	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
5	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
10	417958	AA767382	Hs.193417	ESTs	4.4
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
20	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
30	432675	AJ791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI248720	Hs.114390	ESTs	4.2
	410297	AA148710		lumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340805	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	teptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476:gil12737279[ref]XP_012163.1	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ublnuclein 1	3.9
	429163	AA884766		gb:ram20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AI249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphatase synth	3.8
15	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426891	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AI186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429886	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA305342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AI861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AI806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*:HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulum 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
55	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
60	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPIC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
75	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gbno97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA: cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300295	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
70	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_016569	Hs.267182	TBX3-iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to t38022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase 1	3.2

5	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	A1023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	A1382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275: Homo sapiens keratin 15 (KRT1	3.2
10	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	3.2
	422173	BE385828	Hs.250619	phorbol-like protein MDS019	3.2
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
15	419829	AJ924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371: Homo sapiens hydroxysteroid (1	3.2
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
20	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
25	437179	AA393508		serologically defined colon cancer antig	3.2
	418700	AJ963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
30	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638: Homo sapiens hypothetical prot	3.2
	452941	AL110347	Hs.31074	N-sulfoglucosaminase sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
35	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
40	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AJ187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
	448044	AJ458682		gb:tk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
45	421254	AK001724	Hs.102950	coat protein gamma-coop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161065	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	3.1
50	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
	439864	AJ720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105964	ESTs	3.1
55	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
60	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437296	AA350994	Hs.20281	KIAA1700	3.1
	452627	AJ122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
65	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
70	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
75	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406827	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
80	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445586	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
15	408298	A1745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	A1452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	A1584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	A129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	A1675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:zn24c08.s1 NCI CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas,	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	A1200281	Hs.123910	ESTs, Highly similar to B34087 hypothe	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	nlban protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749865		ESTs, Weakly similar to I38022 hypothe	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	A1015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	A1373544	Hs.331328	intermediate filament protein syncollin	2.8
	433312	A1241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF176265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	A1984625	Hs.9884	spindle pole body protein	2.8
75	418196	A1745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
80	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	A1557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
	440080	AW051597		ESTs	2.8
15	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10500	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
25	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
50	432745	AI821926		gbnl78f05.x5 NCL CGAP_Pr3 Homo sapiens	2.7
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(fh	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000081	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron of trichorhinophalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AB23987	Hs.182285	ESTs	2.7
	411950	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7



	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
15	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
	404913			NM_024408*-Homo sapiens Nolph (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
35	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.6
	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
50	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47357	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp5660134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.260858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410645	Hs.164649	hypothetical protein DKFZp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
75	458946	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Aubergier b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-HRNA synthetase	2.5
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
15	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
25	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synth	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W05656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [Hs	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153	
			BG285837 AI720344 BF541715 AA355086 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	

449625	249224_1	B1918168 AW779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG886750 N45526 BG986917 T61382 R49391 R45432 A1203107 R35004 F07491 R25094 R35360
412446	63467_1	BC021735 A1669212 A120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF950659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 B1035538 BF908052 BF908057 BF090026 BF943158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 A1633838 AA617929 BF947001 B1035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 A1702161 AW341832 BE222503 N71836 A1026061 AW953116 AW083132 A1979261 AV725377 A1423288 A1640707 AW675518 A1032611 A1818044 A1295508 A1911386 A1270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF080433
453160	6028_5	BC009612 NM_003526 B1597616 AV761592 AV760377 AL601008 B1604131 BE645918 BG187760 BG181525 BG210634 BG192999 A1263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 A1143991 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R24557 A1337047 AA948360 A1638005 AA459950 A1624915 A1638047 A1467856 A1521826 AA860305 A1932315 AW003092 AW271756 AW779380 AA609879 A1634791 A1493770 A1565211 Z41145 A1627952 AA303734 BE349457 AW196765 AA255527 BE089727
437124	59408_1	AL050013 BG939500 AW969191 AA769925 A1377973 A1625545 AA811365 AA521114 N24705 A1379579 AA424899 A1684671 AA829715 A1453010 N35401 AA677452 AA504340 A1209149 AA883574 A1379062 A1084455 A1280147 AA644327 BF432508 N27873 A17364 N34880 A1147024 T85860 A1219716 AA960926 H25544 B1857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 A1292318 AA829886 N95742 A1218758 H25588 N36282 AA024987 N36687 B1919187 N49471 AA889970 AW166152 AA68546 A1262504 AA452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 A1016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 B1756612 AA508234 R49885 BF850422
438669	52134_1	AF075009 R63109 R63068
428342	6712_1	AK056315 A1015524 AA724079 B1713519 A1377728 AW293682 A1928140 A1092404 A1085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 A1332765 AW500888 AW576556 A1859571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 AW070509 A1521500 AL042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 A19392620 Z40708 A1985564 AW263513 AA913892 A1693486 AW263502 A1806164 AW291137 B1061872 B1059498 AA134476 AW084888 AA036967 AW370823 T55263 B1002756 AA489664 BF827261 W74741 BF963166
450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 A1819354 AW974068 A1393635 A1580846 A1024796 AW020098 B1491127 A1393644 N74993 AW472959 BM478854 B1597437 H12165 A1458612 BE543192
432586	6633_1	BC022881 AU150944 BG50783 AW754175 AW857737 A1911659 A1050036 AA554053 A1826259 AA568548
450377	12109_1	AB033091 AL502043 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 A1679751 A1873695 BG700891 B1553517 R05018 BG779771 BG534451 AA479402 AW961580 BF061430 A1857643 A1768486 AW512118 AA479302 AW770384 AW072470 A1041596 A1049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF671621 BF350794 BF351375 BE925699 A1050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 B1036602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 A1693720 AA743364 A1915793 N48185 A1573107 AA043474 A1351615 A1969490 A1910763 R50866 A1699181 N73808 H08164
436063	5483_1	AK000028 AA494483 A1298674 AA720773 AV761529 A1884670 A1936202 AW294235 D61652 BF881184 A1711384 N27154 A1926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
424036	6226_1	NM_033445 BC001193 A1885871 BF794032 AA476620 AA810906 AA810905 A1291244 A1885097 A1359708 A1335629 H97396 A1344589 AA300377 AA457566 AW771833 BE465621 A1364068 A1364452 A1648505 A1918342 A1928670 AA886580 AL531029 AA886344 A1186419 B19329056 BM045465 AL531028 BG437151 BE668021 AA179427
407819	7392_2	AK055626 A1800896 BF939022 BE644718 A1954754 BE218177 BE348567 A1962406 AW293122 A1968798 A1457321 BE327228 BG913531 AW933055 T30280 R54166 Z43366 BG819153 BF031119 BE646274 BF940881 R18246 R42185
409151	4123_1	NM_004892 AF047442 BE275338 BF724863 B1917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 A1902726 AA354813 B1092644 BG778400 B1260001 BG007325 A1267455 AA426574 A1160782 A1472186 AA255500 AA434006 BG435520 A1356111 H00525 AV749060 BG944497 BG282031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW968448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
422890	61426_1	AK057805 AW162343 A1190479 A1093318 BE048820 A1198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z42566 AW572911 AW964436 AW04030 A1632565 BE502530 B1792383 BF056928 AA449241 A1651825 AA805324 A1264863 A1969818 AA948267 A1953735 A1263703 BF056387 AW594171 A1867447 AA319159 A1033440 AW956110 A1366013 A1867923 BG911906 D81142 C15616 AL538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 B1819428 AA583393 AA583376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
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BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769205 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084 BG256892 H10532 NA6614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W06152 BF115102 AI633815 BF921562 AA094230 BE092587 W66151 AA526153 AI672156 BF914496 R12579 BF852352 AA699760 T57386 BF903022 R09933 AA678298 BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672 N27807 AA256634 BE276324 AF263306 BF951698 T66089 F11783 F11794 H29379 R19493 H18042 AL133995 AW134660 AI299437 AA057405 AA917450 AI002692 T09262 R43839 H29290 T65008 N78357 AI221207 AI659856 AA913591 AI220302 NM_000786 U23942 BI01050 BG773455 BI561558 BI460206 BG714348 BM126447 AU129411 AU129401 AI119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 AI217668 AA399409 BE182318 BM128040 AI693998 AW615411 AW070426 AI124550 AW778736 AA477781 AW263013 AI459619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA504786 BF432722 BI916393 BM470755 BI333211 AA095636 BI256415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48858 T91611 H42019 BI869421 BG502073 BG425943 W37290 W31363 BE004451 BF208311 BI048717 N78122 AA226597 AI525334 AI953821 AA657925 AA935436 AW957068 BC000222 AL136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI227161 BG820180 AA454463 AA255685 N31549 AA326504 BC019924 BG257230 BI092368 BI869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF868779 AI755222 AA452272 AW241170 AU156565 F28259 T16319 AA362508 N64153 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 AI922439 BE270975 AL119339 BF956085 AI565178 AL1554305 AL573240 AL572917 AI129627 AL546640 BE392285 AI092843 AI371057 BE302410 AI608753 AW674261 AI750057 AI052649 N47822 AL516249 AI589903 BG258439 AI123662 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 AI051112 AI783806 AL569622 AA070466 BF229936 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 AI361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 BI262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 BI085686 AA564566 AI221630 D52045 C14510 AA029390 W60153 H98743 AI682641 H28485 AA723093 AI081730 AA641309 AA587083 BI224818 AW204722 AI309186 AI215122 AI200785 BE467373 BM352502 AI304400 AI193071 AI742483 AW003408 AI400201 AI656740 AW665173 AI215120 AI147599 AI803429 AI076110 AI754349 AW205103 AI262491 AI808243 AI281007 AI051273 AI004801 AW768918 AW103289 AI474637 AI264446 AI699509 BE704420 AA989278 AA918256 AA830956 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94863 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 AI813809 AA933607 AA129695 AA548261 AA714393 AA775005 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51696 D55942 D52740 AI000118 AL516304 AL534259 N54940 AL579194 AI669399 AI342925 BE939201 AA633000 BI222963 AI619676 AW190306 BF035010 AW087897 AI864969 T57243 R48211 AA113880 R26594 C14467 C14444 BI195459 BE886346 BE720780 AL568073 BG389833 BE891549 BI223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304 AI380443 AI240179 AA977516 AA884643 AW079380 AW294316 AI913755 AI864320 AI685770 H25135 AI972654 AI538592 AI174783 R12271 R83569 AI274757 AI559500 AW022192 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60556 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769205 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 68C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104, 152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (	2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA286520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90808	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*:CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
15	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gbryb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
40	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
45	406506			Target Exon	1.97
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptojanin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414785	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiotensin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.76
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.65
70	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL036668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

5	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.109706	hematological and neurological expressed	1.65
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs;similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypothe	2.33
	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
45	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
50	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406964	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
	408989	AW361666	Hs.49500	KIAA0746 protein	1.43
60	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-rel simian leukemia viral oncogene hom	2.25
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
70	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AI065648	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI597655	Hs.49265	ESTs	3.08
	422424	AI186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Ecos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession



453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745542 AA412583 AA355375 BG6547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI288436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AW70033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AW723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65028 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG07601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG428986 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA534798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882 AA156151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
442006	1239046_1	

TABLE 69C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402463	9796896	Minus	8818-8952
400494	9714719	Plus	169845-170272
401234	9929642	Plus	120173-120337
406506	7711374	Minus	6843-8077
405025	7107727	Plus	105267-105343, 106184-106294, 106387-10653
405121	8102330	Minus	35816-36004, 36587-36684
400666	8118496	Plus	17982-18115, 20297-20456

TABLE 70A:

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigenelD:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of the mean of the vessel AI's to the mean of the HUVEC AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	0.99
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06
412636	NM_004415		desmoplakin (DPI, DPII)	1.25
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.36
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.50
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 tis, clone H	1.55
414572	AU077174	Hs.288181	cathepsin H	1.64
415314	N88802	Hs.5422	glycoprotein M6B	1.70
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	1.75
406973	M34996	Hs.198253	major histocompatibility complex, class	1.88
456974	M12529	Hs.169401	apolipoprotein E	1.90
430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.91
406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of m	1.97
422048	NM_012445	Hs.288126	spodalin 2, extracellular matrix protein	1.99

5	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
10	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	AI193115	Hs.16611	tumor protein D52-like 1	2.27
	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	2.31
15	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudodysostosis)	2.38
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.39
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
20	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
	426716	NM_006379	Hs.171921	sera domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
25	410532	TS3088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
30	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
35	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	2.73
40	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
45	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
50	413305	NM_00426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425622	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
55	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
	414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
	424651	AI493206		ESTs	3.17
60	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone H1409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	perlestin(OSF-2os)	3.24
65	447384	AJ377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
70	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI091195	Hs.65029	growth arrest-specific 1	3.35
75	451529	AI917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
80	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
	407938	AA905097	Hs.85050	phospholamban	3.48
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	Integrin, alpha 8	3.52
	404277			NM_019111*:Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.106924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.85
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
	434868	RS0032	Hs.159263	collagen, type VI, alpha 2	3.90
15	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
20	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW539251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78065	complement component 7	4.37
	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
30	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
35	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.88
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
45	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probe set identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF130965 BG681115 BG740377 BI712964 BG000656 AA128470 BM438324 H27408 BE831630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW365566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AJ951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873593 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 CD4715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW597139 BE865474 BE185187 BE156621 BF715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA126330 BG681425 BE705078 R20904 BG880059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE057786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI668869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247695 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

5	45042	30254_1	BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90699 AW365145 W38382 AI498487 AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570 AW964381 BG007409 BM314056 AA465642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267360 N64249 W67500 F07962 AA322394 BI489987 BE644965 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280 424651 46029_5 BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA635644 AI493206 AA669979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495			
			TABLE 70C			
			Pkey: Unique number corresponding to an Eos probeset			
			Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.			
			Strand: Indicates DNA strand from which exons were predicted.			
25	404277	1834458	NL_position: Indicates nucleotide positions of predicted exons.			
			Pkey	Ref	Strand	NL_position
30	404277	1834458	Minus	91655-91946		
35	TABLE 71A:	774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES				
40	Table 1A lists	774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.				
45	Pkey:	Unique Eos probeset identifier number	ExAccn:	Exemplar Accession number, Genbank accession number	UnigeneID:	Unigene number
50	Unigene Title:	Unigene gene title	R1:	75th percentile of ewing sarcoma to 85th percentile of body map		
55	Pkey	ExAccn	UnigeneID	Unigene Title	R1	
60	104659	AW969769	Hs.105201	ESTs	70.3	
65	101447	M21305	Hs.105201	gb:Human alpha satellite and satellite 3	64.7	
70	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5	
75	115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8	
80	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7	
85	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6	
90	110278	AF061573	Hs.19492	protocadherin 8	46.1	
95	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4	
100	116752	AL008583	Hs.91622	neuronal pentraxin receptor	40.9	
105	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6	
110	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9	
115	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5	
120	121362	AF050147	Hs.97932	chondromodulin I precursor	34.7	
125	131291	NM_004350	Hs.170019	nunt-related transcription factor 3	33.0	
130	101063	D54745	Hs.80247	cholecystokinin	31.7	
135	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylser	28.7	
140	122651	AW975398	Hs.293836	ESTs	28.0	
145	100299	D49493	Hs.2171	growth differentiation factor 10	26.5	
150	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2	
155	123619	AA602964	Hs.1395	gb:nc97c02.s1 NCL CGAP_P12 Homo sapiens	26.1	
160	124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 (Clona savigny)	23.1	
165	116301	AW969706	Hs.293332	ESTs	22.6	
170	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII	22.3	
175	106533	AL134708	Hs.145998	ESTs	21.3	
180	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	20.8	
185	131313	R96290	Hs.75874	ribosomal protein L44	18.7	
190	116790	AW161357	Hs.24835	microtubule-associated protein tau	18.2	
195	105316	AI671245	Hs.1594	hypothetical protein FLJ14594	17.8	
200	102123	NM_001809	Hs.13649	centromere protein A (17kD)	16.7	
205	126218	AL049801	Hs.58291	Novel human gene mapping to chromosome 13	16.3	
210	119791	AA554907	Hs.7215	ESTs	16.3	
215	113003	AW292315	Hs.158330	neuropeptide Y receptor Y5	16.3	
220	102836	U94320	Hs.74376	olfactomedin related ER localized protein	15.5	
225	126799	AW753865	Hs.26369	hypothetical protein FLJ20287	14.8	
230	105298	BE387790	Hs.27669	KIAA1563 protein	14.6	
235	107160	AA314490	Hs.184411	albumin	14.2	
240	115313	AA808001	Hs.103538	ESTs		
245	123308	C14187				

	126077	M78772	Hs.210836	ESTs	14.0
	100598	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40565	Hs.31564	ESTs	13.8
	106498	AI221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;catyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
10	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
15	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104968	AI249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
	123049	BE047680	Hs.211869	diclkopf (Xenopus laevis) homolog 2	10.6
25	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BES38082	Hs.8172	ESTs, Moderately similar to A46010 X-in	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
	110730	N67655	Hs.26411	ESTs	10.3
30	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
40	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
45	121910	AI204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
50	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-in	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown [H.sapie	8.8
55	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AI347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AI823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP586D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypothe	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (	7.6
	118036	AA71862	Hs.196008	Homo sapiens cDNA FLJ111723 fis, clone HE	7.6
	131170	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
15	101050	AJ077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
	118013	AJ674126	Hs.94031	ESTs	6.9
	120147	AJ917116		hemoglobin, beta	6.8
30	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	106301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AJ373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132255	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
55	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
60	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypothe	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yl32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.8
70	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI458004	Hs.278956	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
80	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
5	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
	106668	R49390	Hs.254129	KIAA1678	5.4
10	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
	131185	BE280074	Hs.23960	cyclin B1	5.4
15	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
20	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	5.3
25	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothi	5.2
	120830	AI568170	Hs.96886	ESTs	5.2
30	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
	116680	AW902848	Hs.273829	ESTs	5.2
35	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothi	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	116814	H50834	Hs.77899	gb:yp86a10.s1 Soares fetal liver spleen	5.0
50	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	125769	AA083456		gb:zn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AV080510	Hs.97056	hypothetical protein FLJ21634	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALLUS_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcionin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

5	113974	AW959756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
10	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothe	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
15	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
20	106489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypothe	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
25	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
30	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
35	115167	AA749209	Hs.43728	hypothetical protein	4.3
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
40	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
45	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
50	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
55	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	4.2
	130832	AW836006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
60	125960	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-IRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
65	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73964	EphA4	4.2
	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
70	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothe	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
75	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
80	129948	AJ537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.263316	ESTs	4.1



	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid)	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovirus	4.0
5	127153	AJ732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128559	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
10	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo)	4.0
	126965	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	4.0
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
15	128797	NM_002975	Hs.105927	stem cell growth factor, lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
20	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M82843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_	4.0
25	126522	W31912	Hs.21168	gb:zc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
30	105808	AJ133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
35	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
40	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	3.9
	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
45	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
50	105476	AL117352	Hs.77196	Human DNA sequence from clone RPS-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
55	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.8
	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
60	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA256874	Hs.77494	deoxyguanosine kinase	3.8
65	127262	AA828125		gb:rod71a09.s1 NC1_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UJ-H-BI3-ata-a-12-0-UI.s1 NC1_CGAP_Su	3.7
	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126862	R12014	Hs.20976	ESTs	3.7
70	116203	AW137166	Hs.87306	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
75	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AJ241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
80	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypothe	3.6
15	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_Nb1H19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X18866	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
20	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypothe	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1N1B H	3.5
	117265	AA451966		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	AJ002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	Insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
60	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
80	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
5	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	108650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal olfact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares infant brain 1NIB H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:tk3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	3.3
	123284	AA488988	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GC81 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326663	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14205 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
5	133761	AF041430	Hs.75922	brain protein l3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
15	109517	AJ631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AJ769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA928960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
30	132305	AJ806090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA371165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
35	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
45	134964	AJ803516	Hs.272891	hippocalcin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease H1, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373052		nuclear receptor subfamily 1, group 1, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AJ652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
60	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW283689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AJ908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AJ914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
75	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
80	123485	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LJM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hm88a05.x1 NC1_CGAP_Kd11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
15	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133666	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gbzce81h08.s1 Pancreatic Islet Homo sapi	3.0
40	122219	AA436002	Hs.183161	ESTs	3.0
	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	126559	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gbrae38l04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	126887	H20832		gbym48d03.s1 Soares Infant brain 1NIB H	3.0
70	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

80 Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey CAT Number Accession

108451 13765\_27  
 107908 46987\_1  
 5 123619 371681\_1  
 131495 142008\_1  
 10 101445 1650\_5  
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 15 117297 647718\_1  
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 125165 1852047\_1  
 116790 19864\_1  
 20 103038 15024\_1  
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 55 127262 231725\_1  
 127315 37938\_1  
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 126872 142695\_1  
 65 126887 1572189\_1  
 128132 177108\_1  
 126967 169750\_1  
 120325 166688\_1  
 112511 17406\_2  
 70 127496 340470\_1  
 126872 142695\_1  
 75 126887 1572189\_1  
 128132 177108\_1  
 126967 169750\_1  
 120325 166688\_1  
 112511 17406\_2  
 80 127496 340470\_1  
 126872 142695\_1

106012	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R35203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
5	127705 966283_2 127728 3398_5 129012 22280_4	AJ003322 AJ003324 AW404061 R09654 T67160 N50566 N53259 R81936 D78695 D78806 D78780 C17009 AA004406 AA122102 R70625 AA148932 H59583 H81146 H08378 H49863 H21182 H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R21924 H01290 H01283 H42464 W31947 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AA92481 AA088608 R69918 R36334 H80281 N58483 AI075154 AI086754 AA595787 H81051 H01187 AI057251 T96992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 AI088338 AI373324 H66992 R96235 AI494132 R16678 AA088178 AA705356 AA962143 AA148933 R09231 AI160937 R70525 T46980 AI200046 H02301 AA367587 R35968 T97106 D78703 R78072 D78668 D63268 R28197 AA085579 R63766 R92415 W00998 R80766 R67875 R27583 R09343 H13646 R27682 T89007
10		AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 AI93667 AI341984 N92658 T32870 R52664 N50428 AW089291 AI934175 AI423737 D60665
15	106498 245223_1	AA226198 AA226513 AA383773 R18656 AW968014 AA262288 AW968002 X93079 AJ002788 R51324 AI381600 D80031 AW500520 AW593740 F09382 AA810597
20	120934 177521_1 115197 42406_1 129706 81501_1	AA262174 AA810595 AA810596 AA443241 R23784 R67255 R00047 AI457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864 AI953638 R31669 AW769278 R82398 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605 AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W39371 R99823 R77956 H61601 R98785 R09738 H78317 H53537 H81056 T53780 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI702300 R30775 H68996 AI014957 AA369082 AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453 H00188 R21233 H03055 R53822 AA367588 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H60972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R82759 C19002 H01715 W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N99687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805255 AI458777 AA974369 AI866929 AI886032 AI823925 AI823566 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI355825 AI2668 AA894603
25		AW105585 AI824555 AW339175 D20479
30	131019 223488_3	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193
35	131170 8113_1	AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
40	123470 8785_29	AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 AI093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 AI673095 AA599106 AW601545 AI538739 AI538730 AI521786 AW366369 AW021010
45	123532 genbank_AA608733 125032 genbank_T74884 123808 genbank_AA620552 102398 entrez_U42359 118129 genbank_N57493 109841 genbank_H01052 118922 220560_1	AA362576 AI289927 AA382592 AA608733 T74884 AA620552 U42359 N57493 H01052 AW206193 AW137594 AI953685 AI919143 AI424371 AW007698 AW025681 AI954289 R40438 AW070364 AI679653 AI679081 AI623213 AI652310 AI631411 AI565384 AI566734 AA149597 AI538172 AI040831 AI770021 AI914287 AA279311 W73001 AI493117 AI693374 AI802007 AI990645 N29752 R94559 AA806475 AA806828 R90998 R94558 AW300112 W24097 AW003016 N91920
50	113119 genbank_T47910 104799 genbank_AA029703 113560 genbank_T91015 129794 39565_1	T47910 AA029703 T91015 AF093097 AI869509 T27070 AA326718 AA024743 W23922 AA479593 AI765668 W23908 U92986 AA081632 N50578 AA065245 AW365046 AW365014 AA961091 AA150231 H53426 AA234651 N50522 T79343 T87399 N91858 H41179 AW009453 AA024744 T27069 AI346379 H88431 AA152289 R45373 AA477432 AI745607 AI807602 H41152 AA065244 AI242569 AI091032 AI251849 F03857 H88369 AI174488 AI002696 H53427 T87293 N91869 W35270 AA453723 AA453705 AW071829 AI393866 AW071807 W23592 AI342074 D31158 AA833756 AI991896 AA447791 AI864125 AW377239 AA295365 AI687970 R34076 F07607 AA521310
55		AW499865 R94584 R21283 AA350256 H68126 M21305 N24829 X94563 H58818 AA211777 AA401807 AA195191 AA190578 AI632307 AA195227 AA743633 AI823408 AI832203 AI653114 AA205307 AW021913 AI687980 AI674198 AI675563 AI417935 AA707350 AA135157 AI434721 AI151038 AI038305 R52643 AA780141 AW207645 D19691 AI474370 AA401739 N22905 N70378
60	124250 314220_1 101447 entrez_M21305 117357 genbank_N24829 103392 entrez_X94563 135029 H58818_at 105225 genbank_AA211777 121292 genbank_AA401807 105909 82840_1	D30715 AA251089 AA598484
65		
70	100237 entrez_D30715 114988 genbank_AA251089 123423 genbank_AA598484	
75		

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigena Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigena number
	Unigena Title:	Unigena gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

Pkey	ExAccn	UnigenelD	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932	cydin D1 (PRAD1: parathyroid adenomas
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi
	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1
	447761	AF061573	Hs.19492	protocadherin 8
	428183	AW969726	Hs.98381	ESTs, Weakly similar to serine protease
10	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri
	104559	AW969769	Hs.105201	ESTs
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop
15	100299	D49493	Hs.2171	growth differentiation factor 10
	116301	AW969706	Hs.293332	ESTs
	106533	AL134708	Hs.145998	ESTs
	131313	R96290	Hs.75874	ribosomal protein L44
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594
20	113003	AW292315	Hs.7215	ESTs
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei
	123308	C14187	Hs.157208	ESTs
	120147	AI917116	Hs.211869	hemoglobin, beta
25	123049	BE047680	Hs.211869	diclkopf (Xenopus laevis) homolog 2
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr
	105301	AW352357	Hs.7457	MAGE1 protein
	128478	AA708205	Hs.100343	ESTs
	106111	AW875398	Hs.6451	PRO0659 protein
30	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor
	120830	AI568170	Hs.96886	ESTs
	127664	AA806164	Hs.116502	ESTs
	102725	AB026187	Hs.159156	protocadherin 11
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas
35	130637	AA356764	Hs.17109	integral membrane protein 2A
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA
	125770	AA143045	Hs.81665	w-kil Hardy-Zuckerman 4 feline sarcoma v
40	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
	420462	AF050147	Hs.97932	chondromodulin I precursor
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor
	416836	D54745	Hs.80247	cholecystokinin
45				

Table 72B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
131307	3138_1	NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
131313	93372_1	R95290 H02411 C18327 AA367588 AA367557 H89632 C17954 AA568860 AI752983 AA699451 H04260 AI28118 AW193364 N94503
		AA029995 T40536 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226
		AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R65618 H73711 R58545 D79189 AW265710
		R77664 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H63662
	116301	52669_2
		AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807205 AW663917 AA454645
		AA489238 BE241958 AA743491
60	103080	17092_1
		AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880
		BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077
		W05266 AI824103 AI499061 AA642944 AI042556 AA906539 W60380 AI571777 AI135581 AA112340 N75459 AA592929 AI085348 AI278890
		AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160503 AI074344 AI344561
		AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI659596
		AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779
		AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077
		AA148042 AI740837 BE087278 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141
		BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329
		BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W46412 AW771113 AI700678 AA502628 AA133137 BE274186
		BE396090 BE613371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970
		AW298822 AW080962 AI073747 W24123 AA577596 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347
		AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162
		W49709 AW514883 AA100676 AI366087 AD069474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333594 AI289794
		AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI660881 AI366117 AA403090 AI272818
		AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079958 AI752231 AA076431 AA113245
		AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535600 AA064665 AA705388 AA064623 AA962503 AI924926 AW131206
		AW275281 AI280632 T29597 W48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 N72201 AW510563 AW079132
		AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526
		AA487486 R92970 AA934071 AI080448 AA063257 C05786 N99099 R42969 AA807065 AA662686 AA533833 AA662304 H51748 BE539444
		AI382164 AI814595 BE537043 AI168307 BE408935 AA453606 R89428 AA936527 AA936890 AW369618 AW264602 R18074 AI474189
		AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086552 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692



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410102 117657\_1  
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414761 14860\_1

416836 16233\_1

420462 19379\_1

428183 287965\_1  
439221 46993\_1

447761 7355\_1

AA730357 AI128690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087  
AA773947 AA469192 AI199289 AI127085 H89232 N30719 AI028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061  
N59622 AI360625 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407  
AA736720 AA664587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60546 AA483039 AA507705 AA480448  
AI768654 AA658955 AA730803 AA330312 AW021127 BE172031 AW961052 AA339070 AA648172 BE172892 AA174175 AA492012 AA491590  
AW118733 AA484130 AA730783 AA730510 D62577 D62828 AI469294 AI801343 N53447 AA740226 AI831983 AA516146 D79799 AI758212  
AA484040 H38039 AI038772 AI039410 AA528387 AA730576 AA527231 AA748111 D62946 U38439 AA721708 H22130 AA559229 H51620  
AA283355 AA730970 R01595 N72450 AA469123 AA579389 AA480477 AA283306 AA347822 AA328013  
AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA664359 AI91039 AA084598 AA081641  
AA316181 BE439545 AC005053 AF186249 AW386101 AC004969 AA730199 AA032221 AI686139 AI167942 AA809228 AI184070 AI394674  
AW969977 AA032279 AW079284 AA513174 AA888312 AI453179 AA483363 AA528432 AA579511  
AU077228 U61145 AL044256 AA206185 AL044975 NM\_004456 X95653 AW890905 AA332806 AW965453 BE299226 U52965 BE275009  
AA428252 AA769212 AA312778 AA810901 AA461315 AI969286 AI953668 AW296248 AI291422 AA704747 Z44716 BE541235 AW608806  
AA588583 AW403788 AW408386 AA053521 T87571 AA581163 BE183241 T97906 R89149 AI808196 BE618521 AI970278 AI652680 AW130143  
AI970272 AW197254 BE550449 AI628403 AA010143 AW005107 AA251815 AA805836 N53459 AA055309 AA643678 AI345616 AI345618  
AI635728 AI871286 AI018437 AI262514 H75287 AI033155 AI203388 AA205802 AI475265 AW594186 AI696059 AI333312 AW264710 AA876764  
AA864892 AA173156 AI292066 T79837 W93995 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T89364  
AI090913 N55098 AA101673 AA626665 AA251840 N68857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310  
BE244495 AI365179 T99536 AI203088 Z40549 AW139858 AA599627 R91847 AA483681 AW068982 H51746 AA091201 H13030 AA459732  
T99430 AI051764 R45991  
D54745 AU077189 NM\_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571  
H19813 AI745597 AI769202 AI205982 AW205841 R64324 AI201975 H46993 C18067 R71189 N29729 AI799838 AI091209 H87455 R82443  
AW970995 AW072136 N40841 H13148 AI219052 N30191 T28007 AI817428 AA503602  
AF050147 NM\_007015 AB006000 AB005999 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194  
BE222414 BE046984 AW470357 AW339338 C02526 AW590220 AI298082 AW296998 AI333135 AI867816 AA730514 BE348513 AA405500  
AW136179 AA327834 BE327350 BE327366  
AW969726 AA424028 AI266636 AI271571 AA423988 AI266634 AA702780 AA452037 AI424866 AA742931 AA483361  
AA737106 N35765 N35779 AF086045 N30152 AW374028 AI478237 AA923562 AI382236 AA846668 AI627389 AI371709 H98083 H95983  
H26576 H95984 AA745021 AA639180 H26575  
AF061573 NM\_002590 AA780138 AW135620 AI197884 AA483348 R05468 AW969724 H29216

Table 73: Sequences

Seq ID NO: B1 DNA sequence  
Nucleic Acid Accession #: NM\_053056.1  
Coding sequence: 210..1097

5	1	11	21	31	41	51	
	CACACGGACT	ACAGGGGAGT	TTTGTGTAAG	TTGCAAAGTC	CTGGAGCCTC	CAGAGGGCTG	60
	TCGGCGCAGT	AGCAGCGAGC	AGCAGAGTCC	GCACGCTCCG	GCGAGGGGCA	GAAGAGCGCG	120
10	AGGGAGCGCG	GGGCAGCAGA	AGCCGAGAGCC	GAGCGCGGAC	CCAGCCAGGA	CCCACAGCCC	180
	TCCCCAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGCG	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAATGT	GTGCAGGAAG	360
	AGGTCTGCCC	GTCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCGAGGAAC	420
15	AGAAGTGCGA	GGAGGAGGTC	TTCCCGCTGG	CCATGAACTA	CCTGGACCGC	TTCTGTGCGC	480
	TGGAGCCCGT	GAAGAAAGAGC	CGCTGCAGC	TGCTGGGGGC	CACCTGTCATG	TTCTGTGCGCT	540
	CTAAGATGAA	GGAGACCATC	CCCTGACCG	CCGAGAAAGCT	GTGCATCTAC	ACCGACAACCT	600
	CCATCCGGCC	CGAGGAGCTG	CTGCAAATGG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTGGA	660
	ACCTGGCCGC	AATGAGCCCG	CACGATTTC	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
20	CGGAGGAGAA	CAAAACAGATC	ATCCGCAAC	ACGCGCAGAC	CTTCGTTGCC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCATTTC	AATCCGCCCT	CCATGGTGCC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCAAGC	CCTGAACCTG	AGGAGCCCA	ACAACCTCCT	GTCTACTACT	CGCCTCACAC	900
	GCTTCTCTC	CAGAGTGATC	AAGTGTGACC	CAGACTGCCT	CCGGGCTGCG	CAGGAGCAGA	960
	TCGAAGCCCT	AAGGAGCCCG	AGCCTGCGCC	AGGCCGAGCA	GAACATGGAG	CCCAAGGCCG	1020
25	CCGAGGAGGA	GGAGAGGAG	GAGGAGGAGG	TGGACCTGGC	TTGCACACCC	ACCCACGTGC	1080
	GGGACGTGGA	CATCTGAGGG	CGCCAGGCAG	GCGGGCGCCA	CCGCCACCCG	CAGCGAGGGC	1140
	GGAGCGCGCC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCAGA	1200
	AGGGAAGCT	TCATTCTCCT	TGTTGTGGT	TGTTTTTTCC	TTTGTCTTTT	CCCCCTTCCA	1260
	TCTCTGACTT	AAGCAAAAGA	AAAAGATTAC	CCAAAACTG	TCTTTAAAG	AGAGAGAGAG	1320
30	AAAAAATAAA	TAGTATTGCG	ATAACCTGTA	GCGGTGGGGG	AGGAGGGTTG	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TGTTTTTTAT	ATTAATGTAC	TTGTTTCTCT	1440
	GTTGTAAGAA	TAGGCATTAA	CACAAAGGAG	GCGTCTCGGG	AGAGGATTAG	GTTCCATCCT	1500
	TTACGTGTTT	AAAAAAAGC	ATAAAACAT	TTTAAAAACA	TAGAAAAATT	CAGCAAAACA	1560
	TTTTTAAAGT	AGAGAGGCTG	TTAGGTAGA	AAACATATT	CTGTGCTTT	TCCTGATAAA	1620
35	GCACAGCTGT	AGTGGGGTTC	TAGGCATCTC	TGTACTTTGC	TTGCTCATAT	GCATGTAGTC	1680
	ACTTTATAAG	TCATTGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAAAC	TCTTCACCTT	1740
	ATTCTATGGT	GAAGTCACTT	CTTGGTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCCTT	1800
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40	CTACTATAAA	GAGAAGACGA	AATAGTGACA	TAATATATTC	TATTTTATA	CTCTTCTCTAT	1980
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	TTCCCTTTCT	TTAAAGAAGT	TGAAGTTTAG	GAATCCTTTG	GTGCCAACTG	GTGTTTGAAA	2400
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	ACCAAAAGAA	TTTGACCCCC	GCTGCGGGCC	CACGTGGTTG	GGGCCCTGCC	CTGCGAGGGT	3900
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	CAAGTCTGAG	GGTCTGGGCG	GCGGGCGGCT	GGGTCTGTGC	ATTTCTGTGT	GCACCGCGGC	4200
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Seq ID NO: B2 Protein sequence  
Protein Accession #: NP\_444284.1

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797

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Seq ID NO: B3 DNA sequence  
 Nucleic Acid Accession #: XM\_044166  
 Coding sequence: 1..1576

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Seq ID NO: B4 Protein sequence  
 Protein Accession #: XP\_044166.2

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 PMVTGRREDV ATARREIISA AEHFSMIRAS RNKSGAAGFV APALPGQVTI RVRVPYRVVG 240  
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 EYNNENDFLA GSPDAIDSR YSDANRVHOP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360  
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5 Seq ID NO: B5 DNA sequence  
Nucleic Acid Accession #: NM\_000909.1  
Coding sequence: 209..1363

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    ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTTGAAAA 240
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15  TGATTGTGAT CTGCGCTTGG CCATGATATT TACCTTAGCT CTTCCTTATG GAGCTGTGAT 360
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    CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540
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    GCCTTTCCTG ATCTCAACAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGATGC 780
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30  GCAGTTCTTC TTCACTTTT GTGATTTCGG GTCTCGGATG GATGATTATG AAACAATAGC 1260
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Seq ID NO: B6 Protein sequence  
Protein Accession #: NP\_000900.1

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    CVSTVTSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIVLVAASS LPFLIYQVMT 180
65  DEFFQNVILD AYKDKYVCFD QPPSDSHRLS YTTLLLVLYQ FGLCFIFIC YPKIYIRLKR 240
    RNNMMDKMRD NKYSSETKR INIMLLSIVV AFVAVCWPLPT IFNTVFDWNH QIIATCNHNL 300
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70 Seq ID NO: B7 DNA sequence  
Nucleic Acid Accession #: NM\_002590.2  
Coding sequence: 204..3416

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80  TCCCTTGTCA GCTCTTCAGC CTCTGCTGGG TGCTCTCAGT GSCCCAGAGC AAAACAGTCC 300
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    TGCTCCGGGT GCGCGAAGGC GACGGGCAGC TGACCGTCGG GGACGCGCGC CTGGACCGCG 480
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5  
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 AGTCCCTTCC TGGCAGGTAC CTGTCCCGGA AGAAGGAGC CAATGAAAAT GTGTAATCCC 3420  
 ATGCTGCATG TCTTCACACA TATACAGTCT ACTCGAGAA GCCCTAAGT TATTGACCGG 3480  
 TTTCAAGTGT GTATATATA ATATGCAAGA TGTGCCITAC AATGAAGTTG TTGGAAGCTA 3540  
 TTTCAATCA CATTGTGAT GTTGTGATT TGCAACAAA AATGTAGTTA ATGTAATTT 3600  
 TATGAATGT GTGCAATATT TAATTTTCT TATGCTATTG ACTTGATT CAATTGCGGC 3660  
 TTGCCATTTT CTAGTGTGTT TTAACCTGTA CATTTGTGTA TGTAAATGTT GTATATAATG 3720  
 AAATTTTGT ATATTTTAT ATAATAAAG CTAAGTGGGA AGTTATTGCC AAAGGAAGT 3780  
 TCTGTAGAG AAAAACAACA ACATGTTGGA ATTACTTAAT TGAATTTAT CTTCACCTG 3840  
 AAAACAACCTA GTGTTTGA GAAATTTGCT TGCCAAGTAT AACTGTGATA TCTTGACTCT 3900  
 GTGGTAGATT TCAAGTTCAA TGTTATTTAA TTACATTTGG TTTTCGTA ACCGTGTCAC 3960  
 TTATAAGCAC AGTAATAAAA GATTGTGCTAT GTGTTTGAAG AAAAAAAAAA AAAAAAAA 4020  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: B8 Protein sequence  
 Protein Accession #: NP\_002581.2

65  
70  
75  
80

1 11 21 31 41 51  
 MSPVRRWGSF CLFPLQLFSL CWLVSVAQSK TVRYSTFEED APGTVIGTIL EDLHMKVSGD 60  
 TSFRLMKQPN SSLLRVREGD QQLTVGDAGL DRERLQGAAP QCVLAFDVVS FSQEQFRLVH 120  
 VEVEVRDND HAPRFPRAQI PVEVSEGAIV GTRIPLEVPV DEDVGANGLO TVRLAEPHSP 180  
 FRVELQTRAD GAQCADLVLL QELDRESQAA YSLELVAQDG GRPPRSATA LSVRVLDAND 240  
 HSPAFQGAIV AEVELAEDAP VGSLLLDLDA ADPDEGENGD VVFAFGARTP PEARRLFRLD 300  
 PRSGRTLAG PVDYERQDTY ELDVRAQDRG PGPRAACTKV IVRIRDNDN APDIAITPLA 360  
 APGAPATSPF AAAAAAALG GADASSPAGA GTPEAGATSL VPEGAARESL VALVSTSDRD 420  
 SGANGQVRCA LYGHEHFRLO PAYAGSYLVV TAASLRERI AEYNLTIVAE DRGAPPLRTV 480  
 RPYTVRVGDE NDNAPLPTRP VYEVSVRENN PPGAYLATVA ARDRDLRNG QVTVRLLEAE 540  
 VGRAGGAVST YVSDPATGA IYALRSFDYB TLRQLDVRIQ ASDGGSPQLS SSALVQVRVL 600  
 QDNDAFVLV HPAPANGSLE VAVPGRTAKD TVVARVQARD ADEGANGELA FELQQQEPRE 660  
 AFAIGRRTGE ILLTGDLSE PPGRVFRALL VISDGGRPPL TTTATVSFVV TAGGGRGPA 720  
 PASAGSPERS RPPGSRGLVS GSVLQMDTFL IVIIVLAGSC TLLLAIIAI ATTCNRREKE 780  
 VRKGGALREB RPGAAGGGAS APGSPPEAR GAGPRPMFMD VLTFFPTGKA PFGSPAADAP 840  
 PPVAAAEVPS GSEGGSATGE SACHFEGQOR LRGAHAEPYG ASPGFGKEPA PPVAVWKHGS 900  
 FNTISGREAE KPSGKDSGKG DSDFNDSDSI ISGDALKKOL INHMQSLWA CTAECKILGH 960  
 SDRCSWSPCS GPNAPSPHP PAQMSTFCKS TSLPRDLRR DNYQAQLPK TVGLQSVYEK 1020  
 VLHRDYDRTV TLLSPPRPGR LPDLQBIGVP LYQSPPGRYL SPKKGANENV

Seq ID NO: B9 DNA sequence  
Nucleic Acid Accession #: AL121939.12  
Coding sequence: 185..1426

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5      1      11      21      31      41      51
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GCTCAGGCTG GCTGAGAGGC TCCAGCTGTC AGCGTCCCGC CCGCCTCCT CGGGAGCTCT 120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAGGCTG GCAGACAAA ATTAGAAGAT 180
10     CAAAATGGAA AATATGCTGC TTTGGTTGAT ATTTTTCACC CCTGGGTGGA COCTCATTTA 240
TGATCTGAA ATGGAATGGG ATTTTATGTG GCACCTGAGA AAGGTACCCC GGATTGTCTG 300
TGAAGGACT TTCCATCTCA CCAGCCCCGC ATTTGAGGCA GATGCTAAGA TGATGGTAAA 360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCAACT CCCAGCCTTT CTGAATTGGA 420
GGATTATCTT TCCTATGAGA CTGTCTTTGA GAATGGCACC CGAACCTTAA CCAGGGTGAA 480
15     AGTTCAAGAT TTGGTCTTG AGCCGACTCA AAATATCACC ACAAGGGAG TATCTGTTAG 540
GAGAAAGAGA CAGGTGTATG GCACCGACAG CAGGTTGAGC ATCTTGGACA AAAGGTTCTT 600
AACCATTTC CCTTTCAGCA CAGCTGTGAA GCTTTCACG GGCTGTAGTG GCATTCTCAT 660
TTCCCTCAG CATGTTCTAA CTGCTGCCCA CTGTGTTTCA GATGGAAGG ACTATGTCAA 720
AGGGAGTAAA AAGCTAAGGG TAGGGTTGTT GAAGATGAGG AATAAAGTG GAGGCAAGAA 780
20     ACGTCAGGT TCTAAGAGGA GCAGAGAGA AGCTAGTGGT GGTGACCAA GAGAGGGTAC 840
CAGAGAGCAT CTGAGGAGA GAGCGAAGGG TGGGAGAAGA AGAAAAAAT CTGGCCGGGG 900
TCAGAGGATT GCCGAAGGGA GGCCTTCCCT TCAGTGGACC CGGTCAAGA ATACCCACAT 960
TCCGAAGGGC TGGGCAGGAG GAGGCATGGG GAGCGCTACC TTGGAATCA ACTATGCTCT 1020
25     TCTGGAGCTG AAGCGTCTC ACAAAAGAA ATACATGGA CTGGAATCA GCCCAACGAT 1080
CAAGAAATG CCTGGTGGAA TGATCCACTT CTCAGGATTT GATAACGATA GGGCTGATCA 1140
GTGGTCTAT CGGTTTGGCA GTGTGTCYGA CGAATCCAAT GATCTCCTTT ACCAATAYTG 1200
CGATGCTGAG TCGGCTCCA CGGTTCCGGG GGTCTATCTG CGTCTGAAAG ATCCAGACAA 1260
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CGGGTTTCA AAGGACTACA ACGTTGCTGT TCGCATCACT CCCCTAAAAT ACGCCAGAT 1380
30     TTGCTCTGG ATTCACGGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAAC 1440
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CAATGCCAAG TATATACTCT TCTTACATG GTGATGAGTT TCATTGTAG AAAAATTTTG 1680
35     TTGCTCTTCT AAAAATTAGA CACACTTAA ACCTTCAAAC AGGTATTATA AATAACATGT 1740
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TTGTGTAATA AATGTGAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAGTTTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGTCTAT 1920
GCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTTAGTTT AGTTTITTTG 1980
40     AAGAAATACA AATCAGAAGA AAAAGCAAGC ATTATAAACA AAACATAATA CTGTTTIACT 2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCTT 2100
ATGAAATAAA CCTAGTTTAA AATAGGGGAA GCTGAGACAT TTTAAGATCT CAAGTTTITA 2160
TTTAACTAAT ACTCAAAATA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCACAAAT 2220
45     TATGAATGAT CATGTGTGTA AAGCCACATT ATTTTATGCT ATACATTCTA TGTATGAGGT 2280
GCTACATTTT TAGGACAAAG AATTCTGTAA TCTTTTCAA GAAAGAGTCT TTTTCTCCTT 2340
GACAAATCC AGCTTTTGTG TGAGGACTAT AGGGTGAATT CTCTGATTAG TAAATTTAGA 2400
TATGTCTTTT CCTAAAAATG AATAAAATTT ATGAATATGA CTTAAAAAAA AAARWCGACG 2460
CGGCCGGA TTTAGTAGTA GTAGTCGACC CGGGAATTC GACCGGTAC CTGACGGCGT 2520
ACCAGC
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Seq ID NO: B10 Protein sequence  
Protein Accession #: CAC35071.1

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55     1      11      21      31      41      51
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VOGIEQKEL PTPSLSELED YLSYETVFEN GTRTLTRVKV QDLVLEPTQN IITKGVSVRR 120
KRQVYGTDSR FSILDKRFLT NFFPSTAVKL STGCSGILIS PQHVLTAARC VHDGKDYVKG 180
60     SKKLRLVGLLK MRNKGSGKKR RGSKRSRREA SGGDQREGTR EHLRERAKGG RRRKKSGRGQ 240
RIABGRPSFQ WTRVKNTHIP KGWARGGMD ATLDYDYALL ELKRAHKKKY MELGISPTIK 300
KNPFGMIHPS GFDNDRADQL VYRFCVSUDE SNDLLVQYCD AESGSTGSGV YLRKDPDKK 360
NWKRIIAVY SGHQWVDVHG VQRDYNVAVR ITPLKYAQIC LWHGNDANC AY
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Seq ID NO: 11 DNA sequence  
Nucleic Acid Accession #: NM\_002035.1  
Coding sequence: 108..1106

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70     1      11      21      31      41      51
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CTGCCGCCCTT CCTCGTGGCC TTCTGTCTGC TGCTGTACAT GGTGTCTCCG CTCATCAGCC 180
CCAAGCCCTT CCGCCTGCCG GGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
75     GGAAGTGCAT TGCTATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGACAGAA 300
ATGAGGATAA GCTGCTGACG GCAAGAGAAG AAATTGAAAT GCACCTTATT AATGACAAA 360
AGTGGTGTCT TTGCATATCA GTTGATGTAT CTCAGACTA TAACCAAGTA GAGAATGTCA 420
TAAACACAGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAATTTGT GCAGGAATGG 480
CAGTGTGAGG AAAATTTGAA GATCTTGAAG TTAGTACCTT TGAAGGTTA ATGAGCATCA 540
ATTACCTGGG CAGCGGTGAC CCCAGCCGGG CGGTGATCAC CACCATGAAG GAGCGCGGG 600
80     TGGGCAGGAT CGTGTGTTG TCTTCCAGG CAGGACAGTT GGGATTATTC GGTTCACAG 660
CTACTCTGCT TTCCAAGTTT GCCATAAGGG GATTGGCAGA AGCTTTGAG ATGGAGGTGA 720
AGCCATATAA TGTCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGCTTGT 780
CGAAGAAAA CAGAACAAAG CCTTTGAGA CTGACTTAT TTCAGAGACC ACATCTGTGT 840
GCAACACAGA ACAGTGGGCC AAACAAATTG TTAAGATGTC CATAACAGA AATTTCAACA 900
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GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960
CTTCTATTAC TGAGGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT 1020
TGTTTTACCT TGGAAGTTTT GACAGCATAG TTCGTGCTG CATGATGCAG AGAGAAAAAT 1080
CTGAAAATGC AGACAAAACCT GCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTITCCAAA 1140
TAATTTGAAC AGCTTGCTGC TAAATGGGAC CCAATTTTGG GCCTATAGAC ACTTATGTAT 1200
TGTTTTCGAA TACGTAGAT TGGACCACTG CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG 1260
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TTGATTTTCT AGGCTTTGTG GTAGAGAGGT GAAGGTATGA GAATTAATAG CGTGTGAACA 1380
AAGTAAAGAA CAGGATTCCA GAATGATCAT TAAATTTGTT TCTATTATT CTTTTTGGCC 1440
CCCTAGAGA TTAAGTCCAG AAATGTACTT TCTGGCAGAT AAAGAAATCT TGAGGACTTT 1500
GTTTAAACCT TCCATAAAAA AACAAATTTT GGTTCCTCGG GTTCTCTCTC TCTGTCTCTC 1560
TGTCCTCTG TCCTCTCTG TCTCTCTCTC TCTCTCTCTC TCTCTTCTT TCTTTGTGTA 1620
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GTGTGCTCA GGACTCACTC TGCTGCTGGT GGAAGCTCAT GGCTTCTCTC TCTCTTTGAT 1740
CCCATAAAGC TACGAGGGGG ACGGGAGAGG GCAGTGCAAT GGGAGTAAA GAGATATTTT 1800
CCAGTAGCAA AAGCAATGCT TTCTTGCTT TAGACTCAAA TGCTTAGGGA ACGTTTCATT 1860
TCTCATTCAT GGGGAAAGGC AGCCTCCTTA AATGTTTTCT GAAGAGCGGT AAAATCTAGA 1920
AGCTTAAAGAA TTACAGTTT CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCAT 1980
TAGCATCTA CTGTGTTTTT CCATCTCTT CTTTCCAATT TTGCTTATAC TGCTGTAATA 2040
TTTTGTAAA AAAAAAATAA AAGGAAAAAA AAGACCAGCT AAAATTTTGG ACTTGACTTT 2100
TTAACTTAAC TCATGAATTA ATTAAGCAA ATGAAAAAAT TAAAAAGTGT GACTTTTTCT 2160
CGGAGCATAT ATGTAGCTTT TAGGAAAGGC TGATGATGGT ATAAAGTTTG CTCATTAAGA 2220
AAAAAAGACA AGGCTGATT TGAAGAGAGT TGCTTTTGAA ATAAATGAT CA

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Seq ID NO: B12 Protein sequence  
Protein Accession #: NP\_002026.1

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35

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1 11 21 31 41 51
| | | | |
MLLLAAFLV AFVLLLYMVS PLISPKPLAL PGAHVVTGG SSGIGKCIAT ECKYQGAPIT 60
LVARNEDKLL QAKKEIEMHS INDKQVVLCT SVDVSQDYNQ VENVIKQAE KLGPVDMLVN 120
CAGMAVSGKF EDLEVSTFER LMSINYLGSV YPSRAVITTM KERRVGRIVF VSSQAGQLGL 180
FGFTAYSASK FAIRGLAEAL QMEVKPYNVY ITVAYPPDTD TPGFAENRT KPLETRLISE 240
TTSVCKPEQV AKQIVKDAIQ GNFNSLSGSD GYMLSALTCG MAPVTSITEG LQVVVTMGLF 300
RTIALFYLGS FDSIVRRCMQ QREKSENADK TA

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Seq ID NO: B13 DNA sequence  
Nucleic Acid Accession #: CAT Cluster

40  
45  
50

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1 11 21 31 41 51
| | | | |
CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTAA TTTTAAAAAT 60
CGGCAAAATA TTGGTGCCCT TCCCGAAATT TGGTCCCGG CTCCCTTATA GGATAATTGG 120
TTTGATTGG TTAAGTCCAA TTATTAAATG CTGGGTTTC AAATTCAGG CTGGAAGGAC 180
CAACCATTTA AAAACCTTCA AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAATAAT 240
CCAGCATTG GTTTGACATA TTCCAGAGC TCAATCTGCG AGTGTTCAC ATGCACATAC 300
AAGATCCAGA GTCTCATGTT AAAATCATT ACATACCCAG AAAGACCACC ACTTTGCAGG 360
TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
AAGAACACAT AAGATGCCCT CTTCATCAA ATGCACCTGC TTGTGAATTA ATGCACCTGT 480
AAATGAACA ATGCAATCAG TCTTTTATAA TGCACTGTTT AATTGAGAT TCAAGTATT 540
CTATTCTTG GAAAAAATTT TAAGATCAA AATAAAGAA AATAAAAGT GCATACAGTT 600
AAACATTCCA AAAAAAAAAA AA

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Seq ID NO: B14 DNA sequence  
Nucleic Acid Accession #: XM\_086767.1  
Coding sequence: 276..611

60  
65  
70  
75

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1 11 21 31 41 51
| | | | |
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CAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC 120
TGGCTGGGT TATCAAGCCA AGCTATTAA AGGTGTTTTA AAAGAAAGGA TGGAAAGGAAG 180
ACCTCTTAGG ACCACTGTGT TTTGGATAC AAGTGTACA TATCCATTCT GTAGCCTATT 240
ATTTGTCTT CAGTATAAAT GTTCCAGATA AAATATGAT GGTATGGCTG TTTTCATTTA 300
AATTATTAAA TCAGCTTGGG ATGATTGAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT 360
TTTATAAAT TCAAGAAGTC AAGATTCTTG CTCAATTTTA TAATGACTTT GTAAATATT 420
CAAGCATTTG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCCACA TGCACATACA 480
AGATCCAGAG ACTCATGTTA AAATCATTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540
ATAATATTGT ACTTAAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600
AGAACACATA AGATGCCCTT TTCCATCAAA TGCACTTGCT TGTGAATTAA TGGACTTGTA 660
AATGAACAA TGCAATCAGT CTTTATAAAT GCACGTGTCA ATTTGAGATT CAAGTATTTC 720
TATTCTCTTG AAAAAATTTT AAGAATCAA AATAAAGAAA ATAAAAATG CATACAGTTA 780
AACATTCC

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Seq ID NO: B15 Protein sequence  
Protein Accession #: XP\_086767.1

80

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1 11 21 31 41 51
| | | | |
MMDGSFSFKL LNQLGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNISS IGLTYFQSSN 60
LQCTCTYKI QRLMLKSLTY PERPPLCRYN IVLKDREEVF LNPNTCTPKN T

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Seq ID NO: B16 DNA sequence



Nucleic Acid Accession #: CAT cluster

```
1      11      21      31      41      51
5      |      |      |      |      |      |
      TTTTITTTT TTTTITTTT TTAATGCAA AGGAGCAACA AAATTTATTG ACTGAATTAA 60
ACACAACAGT AAAATGGCAG TGTTGTAATT TCATTTTCAG ATGTTTGAAT GGAACAAGAA 120
AAGTGCTATT AGCCCAAGCT TCTTACATTC ATTAAGAGAG TGACTATCAA AAACAGCAAC 180
ATGCACAATG GTACATATGC ACAAATGGA ATTATATCAA CAAATATACA AAATACCCAA 240
AATAAAATAT TTACAGGTTT AAAAATATAA ACATTGATTC CTCTATCCCA TTAAACCATT 300
10     GGAGTGGAGA AAGGAGGAAA GACCCTATTG CTATTAGAA TCCTTTTAA AACAGTTT 360
TAAACATAG AATTAGTTCT AGGAGACAAT TTTTGATGTT TTTCAGGGGT TTAACATTCT 420
ATTATAAAAA TAACATCTAT AAACCTACTA ACAATTTTCC TCCTGTGCAC AAAATAATA 480
CTGCCAAAC CTGTCCTCAA AGACATGCCT GACTTTCAGG AAAGCTAATT ATGGAATGG 540
AGTTTCTCGT TTGGGTATC TTTGTTACTA TTTTCAAATA ACCAGCACT CCCTATATTA 600
15     CACTGAGATA CTTTATATAA ATAACTGGG CGAAACCTGA AGTTCACAA GAGCCTGCTA 660
GGTAGCTGGT TCAAGTACA AATGATAGGA ATTGACTTTG CCAACAACAT CAAAGCATTT 720
TTCCCTGATA TTCCTGATAG ACCTACCACT ATCAGATCCT CCATATCAA TAAGATTTAT 780
CCTGGAAGCA ATGAAATGT TAAATATTAC TTTGCTAGAG TTTCTCTCC TTTATTAGA 840
20     AATAAATGTG TAGTGGGGAC CAGTGGTTGT AATGTAGATA CTTGAGAAGT TTCATTGATT 900
CCTTCAGACC CATGCCG
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Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM\_022898.1

Coding sequence: 268..2739

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25     1      11      21      31      41      51
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GAAAGAGCAA AATAAAGAG AAGAAGAGGA GGAAGAGAGG GAAAGAGAGG AAGGGAAGAA 120
AAACACCAAC CCGGGCAGAG GAGGAGGTGC GCGCGCGCGG CCGCGCGCGG CAGCGCGCGG 180
AGCGGCGGGG CGCGGCTCG GACCCCTCC CCGGCTCCC CCATCAGTG CAGCTCTCG 240
GGCGATGCCA GAATAGATGC CGGGCAATG TCCGCGCGCA AACAGGSCAA CCGCGCAGC 300
TTGTCCAGA GGGAGTCAT CACCCAGAG GCTGACCATG TGGAGGCGG CATCTCGAA 360
GAAGACGAGG GTCTGGAGAT AGAGGAGCCA AGTGGCTCG GGTGATGCT GGTGGGCCC 420
GACCTTGACC TGCTCAGCTG TGGCAGTGT CAAATGAATC TCCCTTGGG GGACATCTG 480
GTITTTATAG AGCACAAAG GAAGCAGTGT GCGCGCAGCT TGGGTGCTG CTATGACAAG 540
GCCCTGGACA AGGACAGCCC GCCACCTCC TCACGCTCG AGCTCAGGAA AGTGTCCGAG 600
CCGGTGAGGA TCGGGATCCA AGTCACCCC GACGAAGATG ACCACCTGCT CTCACCCAG 660
AAAGGCATCT GTCCCAAGCA GGAGAACATT GCAGGTAAAG ATGAGCCTTC CAGCTACATT 720
TGCAACATC GCAAGCAGCC CTTCAACAGC GCGTGGTTCC TGCTGCAGCA CGCGCAGAAC 780
ACGCAAGGCT TCGCATCTA CCGGAGCCC GGGCGCGCCA GCAGCTCGCT CACGCGCGG 840
CTCACCATCC CGCGCGCGCT CGGCGCGGAG GCGCTGGGCG AGTCCCGCT CATGAATTTC 900
CTGGGCGACA GCAACCCCTT CAACCTGCTG CGCATGACGG GCCCATCCT CGGGAACCA 960
CGGGCTTGG GCGAGGGCGG CCGTCCGCGG ACGCGCGCTC TCTTCAGTCC CCGCGCGCG 1020
CACCACCTGG ACCCGCAGCG CTTCACTGCC GAGGAGATGG GGCTGTGTCG CCAGCAGCCC 1080
AGTGCCTTGG ACCGAGTCTA GCGCTGAAC CCGATGGCCA TCGACTCGCC CGCATGAGC 1140
TTCTCGCGGC GCTTCCGCGA GCTGGCGGGC AACAGCTCCA CGCGCGCGCC CGTGTCCCG 1200
GGCGCGGCA ACCCTATGCA CCGGCTCCTG AACCCCTTCC AGCCAGCCC CAGTCCCGG 1260
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CCAGCCAGA GCAAGTCTGT CGAGTTCTGC GGCAAGACCT TCAAGTTCCA GAGCAATCTC 1380
ATCGTGCACC TCGCGAGTCA CACGGCGGAG AAGCCCTACA AGTGCCAGCT GTGCGAGCAC 1440
GCGTGTCTGC AGCGCAGCAA GCTCAAGCGC CACATGAAGA CGCATGCA CAAGGCGCGC 1500
TGCTGGCGG GCGGCTCGA CGACGGGCTC TCGCGCGCCA GCTCCCGCA GCGCGGACC 1560
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GGCTTAGCG CACTGCCGCA GTACGGCGAG CTCCTGGCG ACGAGCAGAA CGCGCGCGC 1920
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CCTTACAGT GCGAGCTGT CAACTAGCG TGCGCGCAGA CGACAGAGT CACGCGCCAG 2580
ATGAAGCGC AGCGGAGAT GCGCAAGGAG GTGTACGCT GCGACATCT CCAGATGCC 2640
TTCAAGCTT ACAGCACCTT GGAGAAACAC ATGAAGAAAT GGCACGCGA GCACTTGTG 2700
ACTAAGAGG TCAAAATCGA CAGGCGCGAG AGGAGCTAAG CGCGCGGGC CCGGCGCCCC 2760
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CACGCGCAC CCGCACCCG CGTGTCCCG GGGCCAGGG GAGGCGCAC TCCACCTAA 2880
CCTGTGTCT GAAAGTCTTA TGGAAACCG AGGGTTGATT AAGGCAGTAT AAATTGTGA 2940
GCCTTTTAA TGTGCAATAA TTCTGTATT TATTGGGTTT TGTAATTTT TTGGCATGT 3000
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TAAAGTTGTT TACTTTTCA TTCTTCTT TTTTGTGTC TGAATAAAA AGTGGCATGC 3300
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GAGATGTAGC ACTCATGTGC TCCCGAGTCA AGCGGCCTTT TCTGTGTTGA TTTCCGGCTTT 3480  
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Seq ID NO: B18 Protein sequence  
Protein Accession #: NP\_075049.1

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1 11 21 31 41 51  
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PGPASSSLPT RLTIPLPLGP EAVAQSLPMN FLGDSNPFNL LRMTGPILRD HPFGEGRLP 240  
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5 PESSFSMDSE LSRNRENGGG GVPGVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPOYG 540  
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GRRSDTCEYC GKVFKNCSNL TVHRRSHTGE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK 780  
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Seq ID NO: B19 DNA sequence  
Nucleic Acid Accession #: NM\_000399.2  
Coding sequence: 339..1769

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Seq ID NO: B20 Protein sequence  
Protein Accession #: NP\_000390.2

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LQGVTSFAST TABSSVTSAS PNPLATGLGL VCTMSQTPD LDHLYSPPPP PFPYSGCAGD 180  
LYQDPSAFLS AATTSTSSSL AYPPPPSYPS PKPATDPLGL PMIPDYPGFF PSQQRDLHG 240  
TAGPDRKPPF CPLDILRVPP PLTPLSTIRN PTLGGPSAGV TGPQASGGSB GPRLPSSGSA 300  
AAAAAAAAY NPHELLPLRPI LRPRKYPNRP SKTPVHERPY PCPAEGCDRR FSRSEDELTRH 360  
IRIHTGHKFF QCRICMNFNS RSDHLTTHIR THTGEKPFAC DYCGRKPARS DERKRHTKIH 420  
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Seq ID NO: B21 DNA sequence  
Nucleic Acid Accession #: NM\_004962.2  
Coding sequence: 457..1893

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	AAGGCAGGCG	GCCGACTCGG	GCTCGGCTCG	GCTCTGCGCT	GCTCCGGAGC	GCTGTGACCG	240
	CTGGCGGGGG	GCTCGGGCGG	CCGGTACCAC	CGGACCGCGC	GCCCGGGTGC	CTGCTCCGCT	300
	AAGCCCTCTG	CCCCGCGCGG	ACCTCGGTAT	CCAGCGCCCT	GCTGCCCGGG	CTCTCCCGCG	360
	GCGCCCTACT	GCGCGAGAGT	CAGTCCGCAG	CCTCCGGTGC	GCCAGCGCTC	GCCTTCCTCC	420
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10	AGCCCGGGAC	CGGGGCCCCA	GCTGCTGCTG	CTGCTGCTGC	CGTTGTTTCT	GCTGTTGCTC	540
	CGGATGTGGG	CGGCGAGCCA	CAGGGCCCCC	GCCTGGTCCG	CACTGCCCGC	GGCCGCCGAC	600
	GGCCTGCAGG	GCGACAGGGA	TCTCCAGCGG	CACCTGGGGG	ACGCGGCCCG	CACGTTGGGC	660
	CCAGCGCCCC	AGGACATGGT	CGCTGTCCAC	ATGCACAGGC	TCTATGAGAA	GTACAGCCGG	720
	CAGGGCGCCG	GGCCGGGAGG	GGGCAACACG	GTCCGACAGT	TCAGGGCCAG	GCTGGAAGTG	780
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15	CTTACGGCCA	CTTTCCACTT	CTACTCAGAG	CGGCTCGGT	GGCCTCGAGC	GCTCGAGGTG	900
	CTATGCAAGC	CGGCGGCCAA	GAACGCTTCA	GGCGGCCCGC	TGCCCTGGG	CCGCCCCACA	960
	CGCCAGCACC	TGCTCTTCCG	CAGCCTCTCG	CAGAACACGG	CCACACAGGG	GCTACTCCGC	1020
	GGGGCCATGG	CCCTGGCGCC	CCCACCGCGC	GGCCTGTGGC	AGGCCAAGGA	CATCTCCCCC	1080
20	ATCGTCAAGG	CGGGCGCGCG	GGATGGCGAG	CTGCTCCTCT	CGGCCAGCT	GGATTCTGAG	1140
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25	AGGCCCGCGC	GGCCCAAGCG	ACAGCACTTC	CACAAGCACC	AGCTGTGGCC	CAGCCCCCTC	1440
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30	TGTGAGTTCC	CCATGCCCTAA	GATCGTTTGT	CCATCCAAAC	ATGCCACCAT	CCAGAGCATT	1740
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	AACTCCCTTG	AGTCTCTCTT	CCTGGATGAG	AATCGGAATG	TGGTTCTGAA	GGTGATCCCC	1860
	AACATGTCCG	TGGACACCTG	TGCTGCGCGG	TGAGACCACT	CCAGGGTGGG	AAGAAGCCAC	1920
	GCCCAGCAGA	GCTGCTCTCT	CGGAGCCCTC	TGCAACCAGG	ACTTGTGGTG	CAGCTGCAGA	1980
35	CACAGAGCAC	AGCTCATGGG	CAACATCACT	GGGGCCCGA	GAGAGCTGTC	CGCCAGTGCA	2040
	TCATTAGGGG	GTCTTTTCTT	GCTAGTGACT	AGCCCCCTAA	ATGCCAGCCT	GAGTACCTGA	2100
	AGGAATCTGG	GAAATAGGCC	TGGCCTGAAA	TGGGCCCATC	ATTCAATCCC	ACTGTTCTGA	2160
	AGGCTTGAAA	ACAAAACATA	TCCACAACAT	TGGCTTGATG	TGATCATCAT	CTCATAACTG	2220
	AGCAAGAAGA	CTATGCAAAAT	CTTAGGGGCG	TCGCTCCCTG	CACACGGAAG	GAACCTCTGT	2280
40	TAAATGCTCA	GTTCAGAAAC	CTTTGGGCCA	CATAGTGATT	TGGAAAAACA	GGATAATCGT	2340
	GGTGTAAATG	AGTGTTCCTT	TTCAAAGTCC	ACTGCAGAGC	TTTTATCCAT	ATGTTATGCA	2400
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	CATGCATATT	GAATAAACAC	ATATAGTAAC	GTGGGAATAC	TAAAAAATAA	CCAAGATTCT	2580
45	ATATTTTGTG	AAATTATACT	TTCTATACTG	TAGATTGTGT	ATGTTATGTG	TTTTTATGGA	2640
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Seq ID NO: B22 Protein sequence  
Protein Accession #: NP\_004953.1

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	GDAATLGPSS	AQDMVAHVHM	RLYEKYSRQG	ARPGGNTVR	SFRARLEVD	QKAVYFNLIT	120
	SMQDSMILIT	ATFHFSYSEPP	RMPRALEVLC	KPRAKNASGR	PLPLGPPTRG	HLLFRSLSQN	180
55	TATQGLLRCA	MALAPPPRGL	WQAKDISPIV	KAARRDGELL	LSAQLDSEER	DPGVPRPSPY	240
	APYILLVAND	LALSEPNSVA	VTLQRYDFPP	AGDPEPRAAP	NNSADPRVRR	AAQATGFLQD	300
	NELPGLDERP	PRAHAQHFKH	HQLWPSPPFA	LKPRPGRKDR	RKKGQEVFMA	ASQVLDPFDEK	360
	TMQKARRKQW	DEPRVCSRRY	LKVDPADIGW	NEWIISPXSF	DAYYCAGACE	FPMPIKVRPS	420
60	NHATIQSIIVR	AVGIIPGIPE	PCCVPDKMNS	LGVLFLENR	NVVLKVYPNM	SVDTACAR	

Seq ID NO: B23 DNA sequence  
Nucleic Acid Accession #: AK026322.1

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	ACATATCCCT	GCTTCTTCCC	ATATTAGTA	AAGTTAGTGT	GGATGCTGGA	TTGTTTAAAT	180
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70	TAGTTGAATT	ACTTGCAAAAT	CAGCTTGATC	ATTCTGAGAC	TTGTTTAAAT	CTTTTGTGCA	300
	AAAGGCTATG	CTATTCAAG	TATAATAAAA	CCTAGTTTAA	GTTTTATCCT	ATAACTAAGG	360
	CATGTGTTC	ATTGTAATGT	CTCCAACCTT	GTGTGAACCT	TGAAATTTGT	TCAGCTCCCA	420
	ATTTGCGAGT	AATTTTTTTT	GTTCAGCCTT	GCACTCTCAT	CCTACTCAAG	TGTGGCTCTG	480
	TATCCAAACA	CAGTCTTGGA	GATCTCATGA	AGATTCTGTA	AACTTTGTCT	CTGCAGGATA	540
75	CCTTCTTTTG	TGGTTATGTG	CCCTGAAAAC	TCCAGCCTCC	GTGCTCTCAA	TTCACTGAAA	600
	CTACTACTCT	GCTTGGAATC	CCCTCTTATA	CAATGGTCTA	CCAAGTGACT	GCAACACAGAA	660
	ATCTAAGGGA	ATTTCAAGAG	TCACCTCAT	TATTTTCTCT	TTTTTCAGGG	ATTATAGTAG	720
	TACTATACCA	CTGTGACGCC	AATGTGTGAG	AATGTTGGTT	TCATACATT	TCTCCAATTC	780
80	TTTCTTGTTA	CAGGAGCCTC	CATTACTTTT	CAACAGTAA	TGCAGTTGCA	GTGCTCTCTC	840
	CTTTTCTCTA	TTATGTGTTT	ATCTCTGGCA	GTTTGAGCCA	AGAGAGGGCA	CGGAGAAGTA	900
	CAATGAGTATG	AGAGCACTTC	TGTTGAGGCT	CAITCAATTGA	CCCTACCCCT	AGTGCTTTAT	960
	GAATGTGTGC	TGCAGATGTC	ATACAGCATC	ACAGCTTCTT	CTCTAATTTA	TGAGCCATAA	1020
	TTTTTTTTTT	TGTAATTTTA	TTGTATTACC	TGCTTGGTTG	CAAGAGGATG	ATGAGGAGGA	1080
	CTACTATAGG	ATRAATTTGT	TTTTATAGAG	CAATTTCTCA	TGGGTACAGA	GGGATAGTAC	1140

TCCATTTC TCACGTATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200  
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5 Seq ID NO: B24 DNA sequence  
Nucleic Acid Accession #: cat cluster

1 11 21 31 41 51  
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TTCTTTTCCC TCTTCTCTT TACCTTTCTT GGTCTGATC CTTCTGTACT CAGTTCCOCT 240  
15 AAATTATTGG ACTACAACT AATATACTAG AAAAGCATAC ACTTATTTTA TTTGAATGCA 300  
GAAATGCTAT CTATCAGTAT ATATACATAA GAATGTATAT TACAGTATAT CTATATATAC 360  
TTAACACTGT AACCTTCAGT ATTCCTCCAGT TAGCGTACCT AACTCTCCTG TGGGTTATGT 420  
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TGCCCCATAA GTAAATAGTA TAGCCACATT CTGAACATAT CAAAAGTACA AACTTAGGAG 600  
20 GAGTGTATGT ACAAATATGT AAAATTTTAT GAAAATGAAC ATGTTTTTAT GATGTTATTT 660  
CTAGTTTATA AGAATGTGAT GACTGCTTTG CTTCATTTAT GTACGTTCCC ATTATATTCT 720  
TGCTGTCAAT CAATCACAAA TTTATATCAG ATTAGGATAA ACTAAGCCAT TTTATGTATT 780  
TTATTTTAAA CCTTATTTTG GCAGAGTAAT TCCTTAGAAT TGGAAAAGCT GTTACTTTGA 840  
AATTACCAAT TATATACAAA ACATAGAAAT GTATTGTAGC TACAAAGACA ACCAAGCATT 900  
25 TTCTGTGTTT TAATGAATAT CTAAAAACT ACATTTAGTT TATTTTACTC AGTTTGTAAA 960  
TGATTTTTTT ACTGGCTCTA TTGCCCTTAA ATAACCTAAGA GATTAATGAT TCTTTGTATA 1020  
ATTTTCCTTT TCTTTGTTCT TTTTITTAAC TTTCCGACAG TTATATCTAT AGTTTGTATA 1080  
ACAATTTCTT ATGATTTCTG GATAACTGAA AACAACATAA GGTGTTGGGC ATTAGAAAAT 1140  
AATTGTAGC AGTAAGATTA CTGATGTAAT ATGATGTTG GACTGAAGTA TTTCTTTATA 1200  
30 AACATTCTAT TTGATTTTAA GCAAAATGTA TGTAAAGCA TGTTTTACA TCAGTAAAGT 1260  
CATTGTGCGA CCTTCGGGAA ATGAAAGGTT TTTACCTAGA TACTGTAAGT TACACCTCCT 1320  
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GTTACAGAGC AGTTGGTACT TTGTAACCCA GACTTACAGT TTAATAATAT CAAGTTAGCT 1500  
35 GATGTTTCAT TATAATAAAA ATACTATTTT GCTTAAGAGT TGTATTACAA ATATTGTGTC 1560  
TTAACATTAG AAATAGCTGT TTTAAATTGT AGTTAACATA TTAACCTTTT CAGAAAAAAA 1620  
GCATGGTTTA TTTTAAATAA TGAAATAGAG AACATAATAC GTAATGTTCA GTATAACAGC 1680  
TGAGTTAAAA CATCTGCCAG GATTAACATC AGTGCCTTTT TGCCAAATGCA TAGAGGCATT 1740  
40 TTTCTCTAAG TATGAGGCTT AATGATAACT ATTCCTTTGT ACACATTCAA GTCACTCCCA 1800  
TACAAGTAAC TAGTGGGTGA TATGTTTAC TCCAAAGGGT GTATTAATTC TGAATGCTAA 1860  
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45 Seq ID NO: B25 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1144

1 11 21 31 41 51  
50 ATGGAGCGCG GAGTGCACCT CGGTGCAGCG GCGCGCGCG AGGACGACCT CTTCTGCAC 60  
AAGAGCCTGA GCGCTCCAC CTCCAAGCGC TTGGAAGCGG CTTTCCGCTC CACGCCCCCG 120  
GGCATGGACC TGTCCTCGGC GCGCGCGCT CCGGAAACGC CGCGCTCTC CTCTCGTCG 180  
CCCCTGGGCT GCTTCGAGCC GGCTGACCCC GAGGGGGCAG GCGTCTGTT GCGCGCGCT 240  
GGAGGAGGCG GCGCGCGCAG CCGCGGAAGT GCGCGCGCG GCGCGCGCG GGTGGGTGTC 300  
55 CCGGGCTGCT TAGTAGTTTC AGCGCGGCTT GGGGGCGACC CTAGCCTAAG CAGCCTGCGG 360  
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AGCAGCGGCG GCGAGCAGAG CCGGACGAC GACAGCGAG GTGCTGCGA GCTCGTGTG 480  
CGGGCGGAG TAGCGACCC GCGGGCTCC CCGGAGCGG GAGGTGGTGG CCGGAAGGCA 540  
GCGAGGGCT GCTCCATGCG CCACCTCCAC GCGGGCGCCA GCGTCCCCC GGGGGGCTC 600  
60 GCGCGCGCG GCGCGCGGCG TAGCAGCAGC GGTAGCAGTG GCGCGGTTGG CCGTAGCGGT 660  
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65 GAGGAGATGC GCGCGCTAGT CGCTACCTC AACCAGGGCC AGGCCATCTC GGTGCTCTC 960  
CTGCCAGCT CCGCGGCTG AGCGGCAGCA GCTGCTGCC TCACCCCGGC GCTCGGCGCC 1020  
TACGAGCAG CAGCGGCTG CCGTTTACG GCGGACTGC CCGCGGCTG CTCTGCGCG 1080  
GAGAAGTGCG CCTGTTTAA CAGCGCTCC TCCAGCTCT GCAACAGTG CAGGAGAAAG 1140  
CCTT

70 Seq ID NO: B26 Protein sequence  
Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
75 MERGMHLGAA AAGEDDLFLH KSLASASTSKR LEAAFRSTPP GMDLSLAPPP RERPASSSSS 60  
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AGAALCLIKY ESASRGSVAE SSGGEGSPDD DSDGRCELVL RAGVADPRAS PGAGGGGAKA 180  
AEGCSNAHLH GGSVPPGGL GGGGGGGSSS GSSGGGGGSG SSGSGSSSSS SSSSKKSKEQ 240  
80 KALRLNINAR ERRRMHDLND ALDELRAVIP YAHSPSVRL SKIATLLAK NYILMQAQL 300  
EEMRELVAYL NQQAISAAS LPSSAAAAA AAALHPALGA YQAAGYFFS AGLPPAASCP 360  
EKCALFNSVS SSLCKQCTEK P

Seq ID NO: B27 DNA sequence  
Nucleic Acid Accession #: cat cluster

Seq ID NO: B28 DNA sequence  
Nucleic Acid Accession #: NM\_002581.2  
Coding sequence: 368..5251

	Coding sequence: 368..5231								
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35	CAGATAAAGG	AGCGGGGAGA	GAAATTAATT	GCCCAACCAG	AGGAGTTGGG	CTGTATTTTT		180	
	CAAAGGCTGG	GAGAGTGGAG	CACACACCTT	GAGGAGGAAA	GCAGAGAAAG	AAGAAAAAAA		240	
	GCAAGTGAAG	GGGGGCTCGC	CGCAAGAGGG	TGAAGAAGCG	AAGAAAGTGC	AGGCGCCGAG		300	
	GCTCCCAAAG	CTGGCAGCTC	CGGGTGGGCG	TGCAGGGGCG	AAGGGGGGGG	CGGGGGGAAC		360	
	CTCGGACATG	CGGCTCTGGA	GTGCGGTGCT	GCACCTGGGG	CTGCTGAGCG	CGCGCTTGGG		420	
40	CTCGGGGCTG	CGCGAGGCTG	CCCGCGCGGC	CCGGAGAGAC	CCGCGGGCGC	GGCGACCCCC		480	
	GGCGCCCGCC	GGCGGCGCGG	CCACCTCTGC	CACCGCGCGC	CGCGGGCCGC	CGCGCTCTGC		540	
	CGCGCGCGCC	GGCGGCGCGG	GGGCTGCTGC	GGAGAGCGTG	CGCTCTCCCC	GGCGGGCGCA		600	
	GCAGCGGGAG	GCAGAGGGGG	CCACCGAGGA	GCAGGAGCCG	CGGAGCGGCG	CGCTCTATTT		660	
	CAGCGGGCGA	CGCGAGCAGC	TGCGAGTCTC	CGGGGGCGAC	CTCGAGCTGC	CGCGGACCGC		720	
45	GTTCAAGCTG	CAAGTGTGAG	TGCGAGCGGA	GGGGGGCCAG	AGGTCTCCGC	CAGTGATCAC		780	
	AGGGCTGTAT	GACAAATGTT	CTTATATCTC	ACGTGACCGA	GGATGGGTGC	TGGGCATCCA		840	
	CACCATCAGT	GACCAAGACA	ACAAAGACCC	ACGCTACTTT	TTCTCCTTGA	AGACAGACCG		900	
	AGCCCGCCAA	GTGACCAACA	TCAATGCCCA	CCGCAAGTAC	CTCCAGGCGC	AGTGGGTATA		960	
50	CCTAGCTCGC	ACCTATGATG	GGCAGTTCAT	GGAAGTCTAT	GTGAATGGTG	CCAGGTGGCC		1020	
	CACCTCTGGG	GACAAGATGG	GTGGCATATT	CAGCCCACTG	ACCCACAGAT	GCAAAGTGCT		1080	
	CATGTTAGGG	GGCAGTCCCC	TGAATCACAA	CTACCGGGGC	TACATCGAGC	ACTTCACTGT		1140	
	GTGGAAAGTG	GCGAGAGTCT	AGCGGAGATC	ACTGCTTGAC	TTGTGAACCC	ATGGCGCCCA		1200	
	CATGTCTCAG	CCTCAGCTCC	TCTCTCAGGA	GAACTGGGAC	AATGTGAAGC	ATGCCCTGGT		1260	
55	CCCCATGAAG	GATGGCAGCA	CGCCCAAAAT	GGAACTCAGC	AATGCCCAAG	GCCTTCTGTG		1320	
	GGACACGAGT	CTGGAGCCTC	CTCTGTGCGG	ACAGACATTG	TGTGACAAAC	CAGAGGTCTAT		1380	
	TGCCACCTAT	AATCAGCTCT	CAAGTTTCGC	CAGCCCCAAG	GTGGTGCGCT	ACCGCGTGAT		1440	
	CCACCCTCTA	GAAAGATGAT	ATAAGAACCC	GAGCGTGAAG	CGCGAGCAGC	TGGACTTCCA		1500	
	GCACCATCAG	TGCGCTGAGG	CTCTCAAGCA	ATACAACATC	TCTCGGGAGC	TGGACGTGCT		1560	
60	GGAGCTGAGC	AATCTCTCCG	CGTCCGCGCG	CTCATCTCTG	GCACAATCTG	ACATCAGCAA		1620	
	GATTGGGGAT	GAGAACTGTG	ACCCCGAGTG	CACACCAACG	CTGACGGGCG	ACGACGGCGG		1680	
	GGATTTCGCG	CACCTGCGCC	AGCTTGCCCT	CTGGAAGAGG	CAGCAACAA	GGGTGTGTGA		1740	
	CATGAGCTGC	AACATGAAGC	GGTTCAACTT	TGATGGTGGG	GAGTGCTGTG	ACCCGTGAAT		1800	
	CAATAGATGC	ACTCAGACTT	CGTTTGACCA	CGACTCTCCA	CACAGAGCACT	ACTTGGATGT		1860	
65	TACCTAGAGT	AAGAAATCTC	TTAATATGCG	TGGATCAACA	CATCTCAACT	TTTTCTTTGC		1920	
	AAAATCCTCA	GAGGAGGAGT	TGGCAGGAGT	AGCAACTTGG	CCATGGGACA	AGGAGGCCCT		1980	
	GATGCACCTA	GGTGGCATTG	TCTTGAACCC	ATCTTTCTAT	GGCATGGCTG	GGCACAACCA		2040	
	CACCATGATC	CATGAGATTG	GTCCACAGCT	GGGCGCTCTAT	CACGCTCTCC	GAGGCATCTC		2100	
	AGAAATCCAG	TCTGTCAGAT	ACCCCTGCAT	GAGAGCAGAG	CCCTCTCTTG	AGACTGGAGA		2160	
70	CTCTGCAAGC	GATACCAAGC	CAGCGCCGAT	ACACAGTCC	TGTGGTGACG	CAGGGCGCAG		2220	
	AAATGACACC	TGTGCGTTTC	ATAGCTTCTT	CAACACTCTC	TACAACACTT	TCAATGAGTA		2280	
	TGCGATGACG	GACTGTAGCG	ACTCTTTCAC	GCCCAATCAA	GTGCGCAAG	TGATCTGTGA		2340	
	CTGTCAGCTG	GCTTACCAAG	GCTGCGCAGC	CTCCAGGAAA	CCAGCGCCCTG	TGSCCCTCGC		2400	
	CCCCCAATTT	CTGGGCAACA	CAATCGGACT	TGTGACACATG	GAGTGTGTCC	CACCTATAGA		2460	
75	TGCGCAATTT	TTTGAAGAG	AATTGGGATC	AGCATGTCTAT	CTTTGCTCGG	AAGGGAGATG		2520	
	CCTGTGTCAG	TATGCTTCCA							

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GTACCAGTAT TGGGTCATAA CTATTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT 3180  
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ACAAATGGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTTCT GCCGACAAGA 3300  
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ATTCCTGGAT CAGTGGGCAT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCCAGG 3480  
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TGTATTGTG CACCTGGTGA OGGATGGGAC ATATTATGGG GACCAAAAG AGGAGACCAT 3720  
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TCCACCAAAA TTCCATGGGC TCTACAGTG TACTAATGGC TTCCAGTTCA ACAGTGAGTG 4680  
TAGGATCAAG TGTGAAGACA GTGATGCTC CCAGGCACTT GGGAGCAATG TCATTCAATG 4740  
CCGAAAGAT GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGAGATGC AAGGCCAGTG 4800  
CTCGTTTCCA AAGTGCCTG ACAGCAACT CAAACTGCAG TGCCCTGATG GCTATGCCAT 4860  
AGGTCGGAG TGTGCCACT CGTGCTGGA CCACAAAGC GAGTCCATCA TCCTGCCAAT 4920  
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CTGCACCTGCT GGTCTCAAGT GGTATCTCA CCTGCTCTG ATTCACTGTG TCAAGGCTG 5040  
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TGACGTTGGG GATTGCTGCA CCTCCACAGT GAAGACCAAA AAGGTCAACC CATTCCTAT 5160  
GTCTGTGAC CTACAGGTG ACTGTGCTT TCGGACCCCG CAGGCCCAAG AACACAGCCG 5220  
GAAGAGCTG CCGGCGTACA GCCATGGCTA AGGAAGGACA AGAAGTTGTC AAGAATTC 5280  
CAAGGCCAGG ACCCAGATCC CTTTGGTATT GATTTCACAG TCAGCTGCTC AACGGAATGG 5340  
CCTCTCCACA CCAGGGATCC TTAGCACCCA ACCGGTCTGC CTTTAATTTT ACCCAGGAAG 5400  
GACTCACAAT GGGCGAATG AACCAAGTTT CGCCATGCTG GATGATGAAA TGGATTCCCA 5460  
TCCAAAGTC TGAGATGGAT TGATATACA GTGTGCAGTC CCAGAGCCTC CTAATAATTCT 5520  
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Seq ID NO: B29 Protein sequence

Protein Accession #: NP\_002572.1

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50  
55  
60  
65  
70  
75

1 11 21 31 41 51  
| | | | |  
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AAAAGRAWEA VRVPRRRQQR EARGATEEPS PPSRALYFSG RGEQLRVLRA DLRLPRDAFT 120  
LQVWLRAEGG QRSAPVITGL YDKCSYISRD RGWVVGHIHTI SDQDNKDPRY FPSLKTDRAR 180  
QVTTINAHRS YLPGQWVYLA ATYDQGFMLG YVNGAQVATS GEQVGGIFSP LTQKCKVLM 240  
GGGALNNHYR GYIEHPSLWK VARTQREILS DMETHGAHTA LPQLLLQENW DNVKHAWSM 300  
KDGSSPKVEP SNAHGFLDIT SLEPLLCGQT LCDNTEVIAS YNQLSSFRQP KVVRYRVVNL 360  
YEDDHKNPTV TREQVDFQHH QLAERAFKQYN ISWELDVLEV SNSSLRRRLI LANCDISKIG 420  
DENCDPECNH TLTGHDGDCG RHLRHPAFVK QHNGVCDMD CNYERFNFPG GECCDPEITN 480  
VTQTCFDDPS PHRAYLDVNE LKNILKLDGS THLNIFFAKS SEELAGVAT WPDKEALMH 540  
LGGIVLNPSP YGMPGHHTM IHEIGHSLGL YHVRIGISEI QSCSDPCMET EPSFETGDL 600  
NDTNPAKHK SCGDPGPGND TCGHFSFPNT PYNNFMSYAD DDCTDSFTPN QVARMHCYLD 660  
LVYQGNQPSR KPAPVALAPQ VLGHITDSVT LEWFPPIIDGH FFERELGSAC HLCLEGRILV 720  
QYASNASSEM PCSPSGHWSP REAEGHPDVE QPCKSSVTRW SPNSAVNPHT VPPACPEPQG 780  
CYLELEFLYP LVPESLTIWV TFVSTDWDS GAVNDIKLLA VSGKNI SLGP QNVPCDVPLT 840  
IRLWDVGEEV YGIQIYTLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVVR DPPLQMDVAS 900  
ILHLNRKFVD MDNLGSGVYQ YWVITISGTE ESEPSPAVTY IHGRGYCGDG IIQKDQGEQC 960  
DDMNKINGDG CSLFCRQEV FNCIDEPSRC YFHDGCVCE EPEQKTSIKD CGVYTPQGFL 1020  
DQWNASVSV HQDQCPGVV IIGQPAASQV CRTKVIDLSE GISQHWYPC TISYPYSQLA 1080  
QTTFWLRAYF SQPMVAAYV VHLVTDGTY GDQKQETISV QLLDTKDQSH DLGLHVLSCR 1140  
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AEQSCVHFAC EKTDCPELAV ENASLNCSS DRYHGAQCTV SCRTGYVLQI RRDELKISQ 1260  
TGPSVTVTCT EGKWNKQVAC EPVDCSIPDH HQVYAASFSC PEGTTFGSQC SPQCRHPAQL 1320  
KGNNLLTCLM EDGLWSFPEA LCELMLCLAPP PVPNADLQTA RCRENKHKVG SPCKYKCKPG 1380  
YHVPSSRSKS KRAPKTQCT QDGSWQEGAC VPTVCPPPP KFHGLYQCTN GPQFNSECR 1440  
KCEDSDASQ LGSNVHCRK DGTWNGSFHV CQEMQGCQSV FNELNSNLKL QCPDGYAIGS 1500  
ECATSCLDHN SESIILPMNV TVRDIPHWN PTRVERVUCT AGLKWPHPA LIHCVKCEP 1560  
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Seq ID NO: B30 DNA sequence

Nucleic Acid Accession #: NM\_032808.1

Coding sequence: 61..1008

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1 11 21 31 41 51  
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5 GTGGAGCCCT ATGCTTCCG CGGCCTCAAC TACCTGCGCG TGCTCAATGT CTCTGGCAAC 180  
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 ATCCGGGACC GCAAGGCCCA GCAGGTGTTT GTGGACGAGG GCCACACGGT GCAGTTTGTG 480  
 TGCCGGGCGG ATGGCGACCC GCGGCCCGCC ATCCTCTGGC TCTCACCCCG AAAGCACCTG 540  
 GTCTCAGCCA AGAGCAATGG GCGGCTCACA GTCTTCCCTG ATGGCACGCT GGAGGTGCGC 600  
 TACGCCCAGG TACAGGACAA CGGCACGTAC CTGTGCATCG CGGCCAACGC GGGCGGCAAC 660  
 GACTCCATGC CCGCCACCT GCATGTGCGC AGCTACTCGC CCGACTGGCC CCATCAGCCC 720  
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35 Seq ID NO: B31 Protein sequence  
 Protein Accession #: NP\_116197.1

40 1 11 21 31 41 51  
 MLHELLRLQE IQLVGGQLAV VEPYAFRGLN YLRVLNVSGN QLITLLEELVF HSVGNLETLI 60  
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 IRDRKAQVF VDEGHTVQFV CRADGPPPA ILWLSPRKEL VSAKSNRLT VFPDGLTEVR 180  
 YAQVDNGTY LCIAANAGGN DSMPAHLHVR SYSPDWPHQP NKTFAFISNQ PGEGEANSTR 240  
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45 Seq ID NO: B32 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

50 1 11 21 31 41 51  
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 AACCAAGACC CTGCTTCCCA GCCCAGAGGT GGAGGAGGGC GGTCAAGGTT GGGTCTACAG 240  
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 GAAAGTGCCG GGGGTGGTCC TTGGAACAACA GTTGGGCTGT TCTTGGCAGG AATAGTAGAC 360  
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60 Seq ID NO: B33 DNA sequence  
 Nucleic Acid Accession #: NM\_006174.1  
 Coding sequence: 71..1408

65 1 11 21 31 41 51  
 GAAAGGCTAT CGGTAACAAC TGACCTGCCA CAAAGTTAGA AGAAAGGATT GATTCAAGAA 60  
 AGACTATAAT ATGGATTAG AGCTCGACGA GTATTATAAC AAGACACTTG CCACAGAGAA 120  
 TAATACTGCT GCCACTCGGA ATTCTGATTT CCCAGTCTGG GATGACTATA AAAGCAGTGT 180  
 AGATGACTTA CAGTATTTTC TGATTGGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT 240  
 GGGGAATCTA CTTATTTTAA TGGCTCTCAT GAAAAAGCGT AATCAGAAGA CTACGGTAAA 300  
 CTTCTCAGC GGCATCTGG CCTTTCTGA TATCTTGGTT GTGCTGTTTT GCTCACCTTT 360  
 CACACTGACG TCTGTCTTGC TGGATCAGTG GATGTTGGC AAAGTCAATG GCCATATTAT 420  
 GCCTTTTCTT CAATGTGTGT CAGTTTGGT TTCACTTTA ATTTTAATAT CAATTGCCAT 480  
 TGTCAAGTAT CATATGATA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540  
 CTTTCTGATA GCTACTGTCT GGACACTAGG TTTTGCCATC TGTTCCTCCC TTCAGTGTT 600  
 TCACAGTCTT GTGGAACCTC AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATT 660  
 ATGTGTTGAG TCATGGCCAT CTGATTCATA CAGAATTGCC TTTACTATCT CTTTATTGCT 720  
 AGTTCAGTAT ATCTGCCCC TAGTTTGTCT TACTGTAAGT CATACAAGTG TCTGCAGAG 780  
 TATAAGCTGT GGATTGTCCA ACAGAGAAAA CAGACTTGAA GAAATGAGA TGATCAACTT 840  
 AACTCTTCTT CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900  
 GAGTATTCTA TTCTCAAAA AACACAGAAG AAGATATAGC AAGAAGACAG CATGTGTGTT 960  
 ACCTGCTCCA GAAAGACCTT CTCAGAGAG CCACTCCAGA ATACTTCCAG AAAACTTGG 1020  
 CTCTGAAGA AGTCAGCTCT CTTCAATCCG TAAGTTCATA CCAGGGGTCC CCACTGTCTT 1080  
 TGAGATAAAA CCTGAAGAAA ATTCAGATGT TCATGAATTG AGAGTAAAC GTTCTGTATC 1140



AAGAATAAAA AAGAGATCTC GAAGTGTITT CTACAGACTG ACCATACTGA TATTAGTATT 1200  
 TGCCTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAACTCT 1260  
 TATTTCAAAT AGGCATTCTA AGTTGGTGTA TTGCATTGTG CATTGTGTGG GCATGATGTC 1320  
 CTGTTGTCTT AATCCAATTC TATATGGGTT TCTTAATAAT GGGATTAAAG CTGATTTAGT 1380  
 GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence  
 Protein Accession #: NP\_006165.1

1 11 21 31 41 51  
 MDLEDEYYN KTLATENNTA ATRNSDFPVW DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60  
 LILMALMKKR NQKTTVNFLI GNLAFFSDILV VLFCSPPFTLT SVLLDQWMPG KVMCHIMPFL 120  
 QCVSVLVSTL ILISIAIVRY HMIKHPISNN LTANHGYFLI ATVWTLGFAL CSPLPVFHSN 180  
 VELQETFGSA LLSSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240  
 GLSNKENRLE ENEMINLTLL PSKSGSPQVK LSGSHKWSYS FIKKHRRYS KKTACVLPAP 300  
 ERPSQENHSR ILPENFGSVR SQLSSSSKFI PGVPTCFEIK PEENSVDHEL RVKRSVTRIK 360  
 KRRSVFPYRL TILILVFAVS WMPLHLFHV TDFNDNLISN RHFKLVYVIC HLLGMMSCCL 420  
 NPILYGLNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence  
 Nucleic Acid Accession #: NM\_014279.1  
 Coding sequence: 286..1689

1 11 21 31 41 51  
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCGCG CCAGCCCAGC 60  
 CCTGCCACGC CCTGCCCGGA GCGAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120  
 CGGAGGCTTC GCGGACGAGA GCGCGGCGCG CGCCCGCTCC GGGTGCTGAA TCCAGGGGTG 180  
 GGGACACGAG CCAGGCGCGG CCGCGGAGCG CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240  
 TCGCGCTCCA CGCAGCGCGC GCGCGGCGCG CACCCAGGGC CCGCATGCCC AGGTCTGTGG 300  
 AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCTCTA GCCTCCTCTT CCTCATCTCT 360  
 ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420  
 AGCTCTGCCC AGGACACGGA GGGCAGGTGT ATCTGCACAG TGGTGGCCCC ACAGCAGACC 480  
 ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCGAG TACTGGAGAA GTGCAGAAC 540  
 ATGTCTCAAT CCATAGAGGT CTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600  
 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAACTTCA AACAGGTGGA GGAGAGTCAT 660  
 AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAGCGGA AAATGGATGA ACTTAGGCCT 720  
 TTGATACCTG TGTGGAAGA GTACAAGGCC GATGCCAAAT TGGTATTGCA GTTTAAAGAG 780  
 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATTTG CGCCTATGAC 840  
 TACGATGAAC TTCAGAGCAG AGTGTTCAAT CTGAAGAAA GGCTCCGTGC ATGCATGCAA 900  
 AAACCTAGCTT GCGGGAAGTT GACGGGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC 960  
 TCGAGGTTTG GATCCTGGAT GACAGACCTT CTGCGCCCTG AAGGCGATAA CCGGTGTGG 1020  
 TACATGGAGC GATATCAAAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGACTTTC 1080  
 ATGAACACGG ACAATTTTCA CTCCCAACCG CTCCCAACCG CCTGTGCGGG CACGGGGCAG 1140  
 GTGGTCTACA ACGGTTCTAT CTACTTCAAC AAGTTCAGG GCCACATCAT CATCAGGTTT 1200  
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCTTGG ACTATGCCGG TTACAACAAC 1260  
 ATGTACCACT ACGCTCGGGG TGGCCACTCG GACATCGACC TCATGGTGGG CGAGAGCGGG 1320  
 CTGTGGGCGG TGTAGGCCAC CAACCAAGAA GCTGGCAACA TCGTGTGAG TAGGCTGGAC 1380  
 CCGGTGTCCT TCAGAGACCT GCGACCTTGG AACACAGACT ACCCAAGCG CAGCGCGGGG 1440  
 GAGGCGCTTCA TCGTGTGCGG CACGCTGTAC GTACCAACCG GCTACTCAGG GGGTACCAAG 1500  
 GTCCACTATG CATACAGAG CAATGCCTCC ACCTATGAAT ACATGACAT CCCATTCCAG 1560  
 AACAAATATC CCCACATCTC CATGTGTGAC TACAACCCCA AGGACCGGGC CCTGTATGCC 1620  
 TGGAAACAAG GCGACACAGT CCTCTACAAC GTGACCTCTT TCCACGTGCT CCGCTCCGAC 1680  
 GAGTTGTAGC TCCTCTCTCC TGGAGGCCAA GGGCCCAAGT CCTCACCACA AAGGGACTCC 1740  
 TGTGAAACTG CTGCAAAAAG GATACCAATA ACTATAACAA TACCGATCTT GAAAAATCAT 1800  
 CAGCAGTGGG GATTCTGACA TCGAGGGATG GCATTACCTC CGTGTCTCTC CCTTTCGAGC 1860  
 CGCGGGGGCA CAGAGCTGCG AAGAAATCCG CGTATTTGCA GCTGGAAGT CAGCCCAAGG 1920  
 CGCCCGCGTT TTCTCCCGCG CCTGTCCCTT CTCTGTGCAA ACAACATACT AAGAGGGCGA 1980  
 GGCATGACT GTTGCCAGT TCTCACCGGG GAAAAACCCA CTGTAGGAT GGCATGAACA 2040  
 TTTCTTAGA TCGTGTGTCAG CTCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100  
 CTRGCACCCG GCGTAGGCT AGTGTAACTC GCATCCCAT CAGTGTCCGT TCTTGTACTG 2160  
 TGTGTCTGTC TCTTAGATTA ACCGTGCTGA GGTCCACAT AGCTCTGCGA CCTGTGTCTA 2220  
 GTACATACTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGTGTGCCC ACATTGTTT 2280  
 AACTCGCTGA CCCCGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCTT TGAGGTGGTA 2340  
 ACTTCGTATG TTAGTTTAT GCGATGATTG TTGTAATATG AATGCCGTAG TTTGGATTAA 2400  
 TAAGTGGATG GTTTTTGTTT CTAATAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460  
 CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTCTTGT TAAATTAGCT 2520  
 AATCATGTA ACCGAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGGTTT CCGATGGGAC 2580  
 AGGAAGTCA TACGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAGTAA AAAACAAAGG 2640  
 CAACTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAGG 2700  
 AAAAAAAGG AAAAAAAGG AAAAAAAGG AAAAAAAGG A

Seq ID NO: B36 Protein sequence  
 Protein Accession #: NP\_055094.1

1 11 21 31 41 51  
 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPPE SQVYSSAQD SEGRICITVV 60  
 APQQTMCSDR ARTKQLRQLL EKVQNMSSSI EVLDRRTQRD LQYVEKMENQ MKGLESKFQK 120  
 VESBKHQHLA RQFKAIKAKM DELRPLIPVL EYKADAKLV LQFKEEVQNL TSVLNEHQEE 180  
 IGAYDYDELO SRVSNLEERL RACMQKLACG KLTGISDPVT VKTSGSRFSG WMTDPLAPEG 240  
 DNRVWYMDGY HNNRFVREYK SMVDFMNTDN FTSRLPLPHW SGTGQVVYNG SIYFNKQFQS 300  
 IIRFPLKTE TILKTRSLDY AGYNNMYHYA NGGHSIDILM VDESGLVAVY ATNQNAGNIV 360

VSRLDPVSLQ TLQTNWTSYP KRSAGEAFII CGTLVVTNGY SGGTKVHYAY QTNASTYEYI 420  
DIPFQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLFH VIRSDEL

5 Seq ID NO: B37 DNA sequence  
Nucleic Acid Accession #: NM\_006334.1  
Coding sequence: 286..693

1 11 21 31 41 51  
10 GCGCGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60  
CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120  
CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180  
GGGACACGAG CCAGGCGCGC CCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240  
15 TCCGCGTCCA CCGACCGCGC GCGCGGCCAG CACCCAGGCG CCTGCATGCC AGGTCGTTGG 300  
AGGTGGCAGC GAGACATGCA CCGGCGCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360  
ATGGGCACTG AACTCACTCA AGTGTGCCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420  
AGCTCTGCCG AGGACAGCGA GGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480  
ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540  
20 ATGTCTCAAT CCATAGAGGT CTTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600  
AAGATGGAGA ACCAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660  
AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACCTAAAA GAGTTTTTTC AATGCTGCAG 720  
TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTTCGA 780  
CCATGCATT TTAATATTAT TTTCCAATAC TTAGCACCAT TTCCTAAGG AACCTTGAAT 840  
25 ACAACACAGA TCCTCCTTTG CATGCGACTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900  
TGTCATGCA TTTTGTGAAA AAGAAAGAAA AAAAAAACTT CGTGTATGTG ACTCAAAGCA 960  
TGTAACCTTA AGATGTTGCA TTCTAAACTG ACAATAAGA CCTTCCCC

30 Seq ID NO: B38 Protein sequence  
Protein Accession #: NP\_006325.1

1 11 21 31 41 51  
30 MPGRWRWQD MHPARKLLSL LFLILMGTEL TQVLPNPEE SQVYSSAQD SEGRICITVV 60  
APQQTMCSDR ARTKQLRQLL EKVQNMSSQI EVLDRRTQRD LQYVERMENQ MKGLESKFQK 120  
35 VEESHKQHLA RQPKG

40 Seq ID NO: B39 DNA sequence  
Nucleic Acid Accession #: NM\_058199.1  
Coding sequence: 286..795

1 11 21 31 41 51  
40 GCGCGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60  
CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120  
45 CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180  
GGGACACGAG CCAGGCGCGC CCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240  
TCCGCGTCCA CCGACCGCGC GCGCGGCCAG CACCCAGGCG CCTGCATGCC AGGTCGTTGG 300  
AGGTGGCAGC GAGACATGCA CCGGCGCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360  
50 ATGGGCACTG AACTCACTCA AAATAAAAGA GAAACAAAG CAGAGAAGAT GGGAGGGCCA 420  
GAGAGCGAGA GGAAGACCAC AGGAGAGAAG AACTGAAAG AGCTTCCCTT GTTTTGCTG 480  
GAAGCCACAG CTGGCTCCCT GGCTCTGCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540  
GTGGGGTTAT GTGCTCCCGC TTACCTCAG AGCCCTTCTC CTGGTGCTGC CCAGACGATC 600  
AGCCAGTCCC TCTTGGAGAG GTTCTGCATG GCCTCTAGGA GAGAAGTTT CTGGCCCA 660  
55 GGAAGGCTG GTGGAGGCTG GTGGTTGTGC ACTGTTGCTG GACAGATGCA TTCATTATG 720  
TGACACACCA CACACACACA TGACACACA GGGGAGCAGA TACTGCAGA GAAGAGCCAA 780  
CCAGGTCCCTG ATTAGTGGCA AGCTGCCCA CAAAGGGCTA TGCCCTGTGTC TTATTGAGAC 840  
ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTGGAC ATGGCCGAC CAAAGGGCCC 900  
TCCAAGCCTT AATGGCACCC TGAAGCCTCC ATGCCAGGC CAAAGATGTC TTTTCTCC 960  
TAAAAA AAAA

60 Seq ID NO: B40 Protein sequence  
Protein Accession #: NP\_478106.1

1 11 21 31 41 51  
65 MPGRWRWQD MHPARKLLSL LFLILMGTEL TQNKRENAE RMGGPESERK TTGEKTLNEL 60  
PLFCLAHAG SLALPRMCSF NPNPAVGLCR PAYPQSPSPG AAQTISQSL ERFMASRRE 120  
VFLAPGRPG GWMLCTVAGQ MHPMCTH THAHTGEQIP AEKSQPGPD

70 Seq ID NO: B41 DNA sequence  
Nucleic Acid Accession #: AY038071.1  
Coding sequence: 1..1686

1 11 21 31 41 51  
75 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60  
CCAACCTTGC TCTCTCTTA CTGCATCGAC AGCATCTTGG GCGGAGGAG CCGTGCAAA 120  
ATGCGGTTGC TGGGAGCGCG GCAGAGCTTG CTGTCTCCGC TGACCAAGCG CGCCGACCG 180  
80 GAAAAGGCGG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTCGAGGC CGAGCTGCAC 240  
CTGCGGCCCA AGCTGCGCGC CTGTATCGGC CCGGCGGGG GCGCCTCTT TCAGGCTGCG 300  
GCAGCGCGCG CGCGGGCGCG GCGGCGGGCG GCGGAGCGCG CCGCCACGGC CAGGCGGGT 360  
CCACGCGGGG AGGCCCTTCC GCGGCCACCG CCAACCGCGC GGGCCGGGGA ACGGCGGAC 420  
GGCGCGGGG CGCGCGCGCG AGCCCGGGCC GCGGCGCGCG CGGCTGGGA CAGCTCAAG 480  
ATCAGCCAGG CGCCGCGAGT GAGCATCAGC CGCAGCAAGT CGTACCGGGA GAACGGGGCG 540

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CCCTTCGTGC CGCCGCGCCG CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCACGCAC 600
CCGGAGGAGC GCCTCGGCGT GGCCGCGCGC CCGGGCAGCG CCCC GGCTGC GGGTGGTGGC 660
ACCGGACCGG AGGACGACGA GGAGGAGCTG CTGGAGGAGG AAGAAGATGA GGACGAGGAA 720
GAGGAACTGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACAGACGCCG CGCGCTGCTC 780
AAGGAGCCCC GCGCTGTGCT TGTGGCCGCG ACTGGCGCCG TGGCCGCGAG AGCTGCGGCT 840
GCAGTGGCCA CAGAGGGGCG GGAGCTGTCA CCAAGGAGG AGCTGCTGCT GCACCCGGAA 900
GACGCTGAGG GCAAGGACCG CGAGGACAGC GTGTGCCTCT CTGCGGCGAG CGACTCGGAG 960
GAGGGGCTGC TGAACGACGA ACAGAGGCGC TACCGCACCA CGTTCACCA CTACCACTG 1020
GAGGAACTGG AGCGGGCCTT CCAGAAGACG CACTACCCGG ACGTCTTCAC CAGGGAGGAA 1080
CTGGCCATGA GGCCTGACTT GACCGAGGCC CGAGTCCAGT TCTGTTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGACAGC GCGCAGACCC ACCCCCTGG GCTGCCCTTC 1200
CGGGGCGCGC TCTCCGCCAC CCACCCGCTC AGCCCTACC TGGACGCCAG CCCCTTCCTT 1260
CGCACCAACC CGCGCTCGCA CTCGCTTGG ACTGCCGCTG CCGCCGCGCC CGCCGCGCGC 1320
TTCCCGAGCC TACCTCCGCC TCCGGGCTCG GCCAGCCTGC CGCCAGCGG GGC CGCGCTG 1380
GGCTGAGCA CTTCCTCGG AGCGGCACTG TTCCGACACC CAGCTTTCAT CAGCCCGGCA 1440
TTCCGAGGC TCTTTTCCAC AATGGCCCCC CTGACCAAGC GGTGACCCG GCGCGCGCTC 1500
CTGAGACAGC CCACACCCGC CGTGGAGGCG GCAGTGGCAT CCGGCGCCCT GCGCGACCCG 1560
GCCACGCGCG CCGCAGACAG ACGCGCTCT AGCATAGCCG CGCTGAGGCT CAAGGCCAAG 1620
GAGCAGCGCG CGCAGCTCAC GCAGCTCAAC ATCTGCGCG GCACCAAGCAG GGGCAAGGAG 1680
GTGTGC

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Seq ID NO: B42 Protein sequence  
Protein Accession #: AAK93901.1

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1 11 21 31 41 51
MSNQYQEEGC SERPECKSKS FTLLSSYCID SILGRRSPCK MRLLGAAQSL PAPLTSRADP 60
EKAVQGSFSPK SSAPFEAEHL LPPKLRLRYL PGGRLLQGA AAAAAAAAAA AAAAATATAG 120
PRGEAPPPPP PTARPERPDP GAGAAAAAAA AAAAANDTLK ISQAPQVSIS RSKSYRENGA 180
PFVPPPALD ELGGPGGVTH PEERLGVAGG PGSAPAAAGG TGTEDEDEEL LEDEDEDEEE 240
EELLEDEDEE LLEDDARALL KEPRRCPVAA TGAVAAAAAA AVATEGGELS PKEELLHPE 300
DAEGKDGEDS VCLSGSDSE EGLLKRKQRR YRTFTSYQL BELEAFQKT HYPDVFTRFE 360
LAMRLDLTEA RVQVWFQNRK AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASFPF 420
PHHPALDSAW TAAAAAATAA FPSLPFPPGS ASLPPSGAPL GLSTFLGAUV FRHPAFISPA 480
FGRLESTMAP LTSASTAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAAQLTQLN ILPGTSTGKE VC

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Seq ID NO: B43 DNA sequence  
Nucleic Acid Accession #: CAT cluster

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1 11 21 31 41 51
CGCTGCCCC CCGTTGCTT CTCTCTCTC CTTCTGCGCT GCGTGTCTCG CCGTCTTTGG 60
TTCCGCGCGT TCGGTGCGCC CTCTCTGGG TTCGCTTCA CCTCCGCTC GGCTGTGCT 120
CTGCTCTCTC CCGCTCTCAT GCCCTTTCA GCTCTACTC TGGTGTGCT CCGCTCCCTC 180
GCTCTGTTCT CTGTCTCTC TCTTCCCGG TCGTGTCTC GCTCTCTGT GTTCCCTCTC 240
GTCTGTGTTT TGGGTGCTG CTCTGCGTCC TGCTCTTTC TCTTGGGTT CCGCGCGCTT 300
CCTGTTTGG TCCCTCTGCT TCTGCGCGG TTCTGTGTG CCGCGCGCGC CCGTCTTTC 360
TTGGTGTCTT GCTCTGCTC TCTGTCTGT GTTCTCGGC GTCTGTGCT TCTCTCTTT 420
ATCTCTGTT TTCTCTTTT CTGTCTCTT CTGTCTTTT TTGTCTTTT TTTCTCTTA 480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAC CTTTATTTT TCAGGAAATC TGAAGAACTA 540
CAGTCTCCAT GCCTGCTCAG CCAAGAAGGA GCTCACTGTG GGCACCAAG ACAGGAGACC 600
AATGTGGAGA CCTGTGAGCC TGTGTCCGGC CCGTAATCT CAAGCACAGG GCAGGCTTCC 660
TGAGCATTTA AGAGAAATAT TGGGAGAAAC AAACAGAAAC TGAAGAAATA TGCAAGGTGT 720
CTTCTTTGGA TGTATTCCA TGATAGATAG TAGGGGAGG AGTGAGAGAG GCTGACTAGG 780
TCTGACATG GAGCTCGGAA GAGTCAGGCT GTGATTCGGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGCTGGAAT CTGAGGGTCA GTGTCCAG TCACTCAGAG ACAGAAATCA 900
AGCATAGCCC TTGCTGATGG CAA

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Seq ID NO: B44 DNA sequence  
Nucleic Acid Accession #: NM\_014421.1  
Coding sequence: 718..1497

65  
70  
75  
80

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1 11 21 31 41 51
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GGCTGCGCAG CGATTGCTG TCTCTGTGA GTCAGGGGAC AACGCTTCGG GGCACACTGTG 120
AGTGGCGGTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTCGGTC CGGGGACGTC 180
TCTGATCCC CTAATAAGC GCCTGCTAAC TTTGAAAAGG AGCACTGTGT CCTGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAGGA 300
GCTGATCGGG GCTCTCTGAT CAATTAAGAG GAGAGTTAAA CCGCCGAGAT CCGCGCGGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTCT 420
TGCACTTGG GTACAGCTTC CTGGGCGAGA AAGCGCTCG CATTTGATTG CTTCCAGTTA 480
TTGAGAACT TCTGTCTCTG GTGGAGAGC GGGTCTCGCT TGGGTTCGCG TAATTTCTGT 540
CCTGAGCGCT GAGACTGAGT TCATAGGGTC CTGGTCCCC GAACACAGGA GGGTGTAGGG 600
AACACATCT GCAAGCCCC GCAACCAAG TGAGGGGCCC CGTGTGGGG TCTCTCTCC 660
CTTGTCTTC CCACCCCTCC GGGCTTTGCG TCTTCTGGG GACCCCTCG CCGGAGATG 720
GCGCGTTGA TGGGAGCAA GGATTCGTCC TGCTGCTGCG TCCTACTGGC CGCGGTGCTG 780
ATGGTGGAGA GCTCACAGAT CGGCAGTTCG CGGGCCAAAC TCAACTCCAT CAAGTCTCT 840
CTGGGCGGGG AGACGCTCG TCAGGCGGCC AATCGATCTG CCGGCATGTA CCAAGGACTG 900
GCATTCCGGC GCAAGCGGCC GGGCAAAAAC CTGGGCGAGG CTAACCTCTG TAGCACTGAT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCAACC AAGGATCATC GGCCTGCATG 1020
GTGTGTCGGA GAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCC CAGTACCGCG 1080
TGCAATAATG GCATCTGTAT CCCAGTACT GAAAGCATCT TAACCCCTCA CATCCCGGCT 1140

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5 CTGGATGGTA CTCGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200  
 TGGCAGAATC TAGGAAGACC ACACACTAAG ATGTACATA TAAAGGGCA TGAAGGAGAC 1260  
 CCCTGCTAC GATCATCAGA CTGCATTGAA GGGTTTGTCT GTGCTCGTCA TTTCTGGACC 1320  
 AAAATCTGCA AACCAGTGCT CCATCAGGGG GAAGTCTGTA CCAACAACG CAAGAAGGGT 1380  
 TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAGTA 1440  
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGCAGAA AATTGTATCA 1500  
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560  
 GGTGGAAAAAT AAGGTTTCAGA TGCAGAAGAA TGGCTAAAAAT AAGAAACGTG ATAAGAATAT 1620  
 10 AGATGATCAC AAAAGGGAG AAAGAAAAACA TGAAGTGAAT AGATTAGAAT GGGTGACAAA 1680  
 TGCAGTGCGC CCAGTGTTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTTGT 1740  
 GGAAGATGCT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTACTGATGA GTAGCATGTG 1800  
 ACTTTCCAAG AGTTTAGGTT GTGCTGGAGG AGAGGTTTCC TTCAGATTGC TGATTGCTTA 1860  
 TACAAATAAC CTACATGCCA GATTCTTATT CAACGTTAGA GTTTAACAAA ATACTCCTAG 1920  
 AATAACTTGT TATACATAG GTTCTAAAAA TAAATTTGCT AAACAAGAAA TGAACATG 1980  
 15 GAGCATTTGT AATTATCAAC AGAAAAATTAC CTTTGTGATT GTAACTACTC TTCTGCTGTT 2040  
 CAATCAAGAG TCTTGGTAGA TAAGAAAAAA ATCAGTCAAT ATTTCCAAT AATTGCAAAA 2100  
 TAATGGCCAG TTGTTTAGGA AGGCCTTTAG GAAGACAAAT AATAACAAA CAAACAGCCA 2160  
 CAAATACTTT TTTTCAAAA TTTTAGTTT ACCTGTAAAT AATAAGAACT GATACAAGAC 2220  
 AAAAAAGATT CCTTCAGATT CTACGGAATG ACAGTATATC TCTCTTATC CTATGTGATT 2280  
 20 CCTGCTCTGA ATGCATTATA TTTTCCAAAG TATACCCATA AATTGTGACT AGTAAAAATAC 2340  
 TTACACAGAG CAGAAATTTT ACAGATGGCA AAAAAATTTA AAGATGTCCA ATATATGTGG 2400  
 GAAAAGAGCT AACAGAGAGA TCATTATTTT TTAAGATTG GCCATAACT GTATTTTGAT 2460  
 AGAATTAGAT TGGTAATAC ATGTATTAT ACATCTCTG TGGTAATAGA GACTTGAGCT 2520  
 25 GGATCTGTAC TGCACGTGAG TAAGCAAGAA AATTGGGAAA ACTTTTCGT TTGTTGAGT 2580  
 TTTGGCAACA CATAGATCAT ATGTCTGAGG CACAAGTTGG CTGTTCACT TTGAACCCAG 2640  
 GGGATGCACA GTCTAAATGA ATATCTGCAT GGGATTGCT ATCATAATNT TTCCTATGCT 2700  
 GNTGAATTCN GTGTGAGGCT CTGTGTCCTT CCTATCTCA AATTATTAT TTTATAGTGC 2760  
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 30 GAGTAGTGAG GTTTCTATGC CCTCTATAAG CTTCTGACTA GCCAATGGCA TCATCCAATT 2880  
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45 Seq ID NO: B45 Protein sequence  
 Protein Accession #: NP\_055236.1

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Seq ID NO: B47 Protein sequence  
 Protein Accession #: NP\_063938.1

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35 Seq ID NO: B49 Protein sequence  
 Protein Accession #: BAB33378.1; CAB66517.1

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55 Seq ID NO: B50 DNA sequence  
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Seq ID NO: B51 Protein sequence  
Protein Accession #: XP\_084965.1

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Seq ID NO: B52 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2016

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GGCGGGCATC GCGCGCGCGA GCGCGGGCCC GGGGAGGTCC GCACGCGAGA GGACGCTTCC 960
AGGAGCGGGG CGGTTCCCGT AAAGACGGTC CCGCTTGTGC ACTCCGAGG CGGCAGCGCG 1020
CGGGCGCCCG CGGCCCCAGA CCTTGCCTCT GTGATCCAC CCTCAGACC GTCGGCAGAT 1080
CGTATTGTT TGAATGTTTC TGACGTGACT TCACTGAAA GCTTTGACTC TCTTACAGGC 1140
TGTGAGATA TTATTGACGA CCAAGAGGAA GAGGAGGTC CCAGCTGTGA CAAGCATGTC 1200
CCCGGCCAG GCAAGCCCGG TCTGTCTAAA AAGAACCCCG CGGTGTGTGC CTACCAAGGA 1260
GGCGGGGAAG AGATGGCCAG CCGGACGAG GTGGACGACA CCTATCTACA GGAGTTCTCG 1320
GACATGCTCT CCCAGACCGA GGAGCAGGGA CCGGAGCCCC AGGAGGGGCG GGCTAAGGTG 1380
GCAGCTGCGC TGGAAACCAA GGTGGTGCCC GAGACCCCA AAGACCCAG GTGTGTGGA 1440
GCGGCCAAGG ACGCGTCTC GTCAAGCGC AGGAGGCTCA ACCGATTCC CATCGAGCCC 1500
CATCTAAGG AGGAGCCCAA GCACCCGAG AAGGAGCAG AGGAGGCGT CCCCAACAGC 1560
GACGAGGCTC ACTGGGACTC CACCAAGCCA GGGCCAGAGG AAGACAGCTC GAGCAGGGG 1620
AAGAGGCGCG GCATCCCCCG GGATAGCTAC AGCGGGGAG CGCTCTATGA TCTCTATGCT 1680
GACCCGAGCG GAAGTCCAG AACCCCTCTT GGAGGGAAG ACAACGAGGA GACGTCTCTC 1740
CTGTCCCGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACAGGC 1800
AGCTTGTCTA AGGACTCTAA GATCCCTATT AGCATCAAG ACCTGACCAA CCTTCCATCT 1860
AGCCATCCCG TGTGTGACCA GCAACCTCC AGGAGTGAGA TGCCCAAGAA AAAAATCCCG 1920
GTTTCCAAAG TGCTGTGTCG CAGAGTCAGC AACCGGGGCT TGGCTGGGAC CACCATCAGA 1980
GCAACGGCTC GCCACGACAG TGCCAAAAG TTGTGA

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Seq ID NO: B53 Protein sequence  
Protein Accession #: FGENESH predicted

80

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1      11      21      31      41      51
|      |      |      |      |      |
METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
GKINKAAPFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
EPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKKN GRSENGKGEP 180
VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE 240
TPRAAREPEE PSQDAPRDP A GEPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA 300

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5 AGHRRAPGP GEVRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VPPSPDPSAD 360  
 RICLMFSDVT SLKSFDSLGT CGDIIADQEE EAGPSCDKHV PGPGKPAISK KNPGVVAYQG 420  
 GGEEMASPE VDDTYLQEPW DMLSQTEBQG PEPQEGAAKV AAALETKVVP ETPKDTRCVE 480  
 AAKDASSVKR RRLNRIPIEP HPKEEPKHPE KEQQEGVPSN DEGYWDSTTP GPEEDSSSSG 540  
 KKAGIPRDSY SGDADLYDLYA DFDGSPATLP GGDNEETSS LSRLKPVSPG TITCPLRTPG 600  
 SLLKDSKIPI SIKHLTNLPS SHPVVHQQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660  
 ATACHDSAKK L

10 Seq ID NO: B54 DNA sequence  
 Nucleic Acid Accession #: NM\_014138.1  
 Coding sequence: 60..854

15 1 11 21 31 41 51  
 CTGCAGAGAC TTCCAGGAA GGTCCAGGCG CCTCTCAGCC TTCGTACTCA GAACAGCCGA 60  
 TGATGGGCTT CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCCAG 120  
 AGGGGCTGCT CCGCCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA 180  
 GGCTGGAGTT CCTTCAGAGG AAGAARAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240  
 ATCAGATGGC CCCCTATGCT GTTGGGAGGG AAGCCAGAAAT CTCCCCATTA GGTGACAGAA 300  
 20 GTCAAGATCG ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360  
 GGATCCCTGG GAGAGATAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGACGG 420  
 GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAGCC CGGGCCTCTG CCTGAAGCGG 480  
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540  
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCCATG 600  
 25 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC 660  
 CCATTTTGGG GACCAACACG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720  
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCCG AGGAAGGTCC TCATGTTTCG 780  
 TGCTGTCTAT TCTCGGATGG CTGTGAGGCA TTCCTTGGCA AGGACCGCTG CGTACCAGCG 840  
 GTCTCAACCG CATCTCACAT GGCTCCTGTG ATGCATGTTG TCGCTTCCCC ACCCGGGATC 900  
 30 TCCATCTCTC TCCCTCTCTC GCTGTCACTA AGAGATCACA TGTCTGTGTA GTGTGAATGC 960  
 CTGTGTGCTG TCCGTGCTTT TTGCACCATT GAGTTGACTG CCTCTGAGAA CGACGACTAG 1020  
 GCCTGTGTA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGATGGGC AGGTAAACGC 1080  
 AGTGTGGGAA AGGAATGTGG AATGAGAACT TGGTGGTTCA CCGCTGTACT ATTTGTGTAA 1140  
 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCCAG 1200  
 35 TAGTAGTCTC CCTTACAGGA ATTTTTCAGC GGGTTCCTCA TCATCAATAC CAAATAAATA 1260  
 TATGTAGVAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

40 Seq ID NO: B55 Protein sequence  
 Protein Accession #: NP\_054857.1

45 1 11 21 31 41 51  
 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA FLRHVRRRHR 60  
 DIMAPYAVGR EARIPLGDR SQNRFRCECR YCQSHRPNLS GIPGESNRAP HPSSWETLVQ 120  
 GLSGILTSLG TNQPGPLPEA ALQPOETEEK RQREERQESK IMFQRLKQW LEEN

50 Seq ID NO: B56 DNA sequence  
 Nucleic Acid Accession #: NM\_000025.1  
 Coding sequence: 198..1424

55 1 11 21 31 41 51  
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 TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTGGCTCTC ATGCCCTGCT 120  
 GTCCCTCCCC CTGAGCCAGG TGATTGGGA GACCCCTCC TCTCTCTT CCCTACCGCC 180  
 CCAAGCGGGA CCGGGGATG GCTCCGTGGC CTCACGAGAA CAGCTCTCTT GCCCATGGC 240  
 60 CGGACCTCCC CACCCTGGCG CCCAATACCG CCAACACCAG TGGGCTGCCA GGGGTTCCGT 300  
 GGGAGGCGGC CCTAGCCGGG GCCCTGCTGG CCGTGGCGGT GCTGGCCACC GTGGGAGGCA 360  
 ACCGTCTGGT CATCGTGGCC ATCCCTGGA CTCGAGACT CCAGACCATG ACCAAGCTGT 420  
 TCGTACTTC GCTGGCCGCA GCCGACCTGG TGATGGGACT CCTGGTGGT CCGCCGGCGG 480  
 CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGGAG CTGTGGACCT 540  
 CGGTGGAGCT GCTGTGTGTG ACCGCCAGCA TGGAAACCT GTGCCCGCTG GCCGTGGACC 600  
 65 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTCAACAG CGCTGGCCCC 660  
 GGACAGCTGT GGTCTGTGTG TGGGTCTGTG CGGCCGCGGT GTCGTTTGGC CCCATCATGA 720  
 GCCAGTGGTG GCGGTAGGG GCCGACCGCG AGGCGCAGCG CTGCCACTCC AACCGCGCT 780  
 GCTGTGCTT CGCCTCAAC ATGCCCTACG TGTGCTGTC CTCTCCGTC TCCTTCTACC 840  
 TTCTCTTCT CGTGATGCTC TTGCTTACG CGCGGTTTT CTGTGTGGCT ACGGCCAGC 900  
 70 TCGCTTGTCT GCGCGGGGAG CTGGGCCGCT TTCCGCCCGA GGAGTCTCCG CCGCGCGCT 960  
 CGGCTCTCT GCGCCCGGCC CCGGTGGGGA CGTGCGCTCC GCCCGAAGGG GTGCCCGCT 1020  
 GCGGCGCGCG GCCCGCGCGC CTCCTGCTC TCGGGAACA CCGGGCCCTG TGCACTTGG 1080  
 GTCTCATCAT GGGACCTTC ACTCTCTGCT GGTGCGCTT CTCTGCGC AACGTGCTGC 1140  
 GCGCCCTGGG GGGCCCTCT CTAGTCCCGG GCCCGGCTT CCTTCCCTG AACTGGCTAG 1200  
 75 GTTATGCCAA TTCTGCTTC AACCCGCTCA TCTACTGCG CAGCCCGAGC TTTCGACGG 1260  
 CCTTCCGCGT TCTCTGTGCG CGCTGCGGCC GTGCGCTGCC TCGGAGGCC TGCGCGCGCG 1320  
 CCGGCGCGCG CTTCTTCCCG TCGGGGCTTC CTGGGCGCG GAGCAGCCCA GCGCAGCCCA 1380  
 GGCTTTGCCA AGGCTCGAC GGGGCTTCTT GGGAGTTTC TTAGGCTGA AGGACAAGAA 1440  
 80 GCAACAACCT TGTGTATCAG AACCTCTGG CCTCTGTTC GAATGAGTCC 1500  
 CATGGGATTC CCGCGCTGTG ACACCTTACC CTCCAGAAC TGACGACTGG GCCATGTGAC 1560  
 CCAAGGAGG ATCTTACCA AGTGGGTTTT CACCATCTC TTGCTCTCTG TCTGAGAGAT 1620  
 GTTTTCTAAA CCCAGCCTT GAACCTTACT CCTCCCTCAG TGGTAGTGTG CAGGTGCGCT 1680  
 GGAGCAGCAG GCTGGCTTTG GTAGGGGCAC CCATCACCG GCTTGCCTGT GCAGTCAGTG 1740  
 AGTGCTTAGG GCAAGAGAG CTCCCTGGT TCCATTCCTT CTGCCACCCA AACCTGTAGT 1800



5  
10  
15

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTGGGG GTTTTATCTC TGGTTCCTTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTCGCCAGGG 1980
TTTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATTAG AACAGATCCC TTCTTTCTCT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTCGGCCCA CTTCCTCTCC 2100
GTTTGTITTC TTTTCATAAT CCACTTACTC CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAAAACAAA 2220
AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCTTCTCTG AAATCTTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400
GCAATTTGTC CCTCCATGCT ATAATCCAGT GGTGCCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGGGTGTGTG TGTGTGTGTG TGTGTGTGGA GGCACAGGCA CAAAGCATTG CTTGGGTGTG 2520
TCAAATGTCT TGTGTCTATA ATATATTCTG ATGTTTCCCA GCCTTTCCAC AACCTCTACC 2580
TTCCACTCA CCTTCCCCAG CTACAAAAAT CTGTATTATC CTCTAAAGT AAAACTGGAG 2640
TTAC

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Seq ID NO: B57 Protein sequence  
Protein Accession #: NP\_000016.1

20  
25  
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1 11 21 31 41 51
MAPWPHENSS LAPWPDLPFL APNTANTISGL PGVPWEAALA GALLALAVLA TVGNNLLVIV 60
AIAWTPRLQT MTNVFVTSIA AADLVMLGLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
VTASIELTCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VVVVSAVSVF APIMSQWNRV 180
GADAEARQCH SNPRCCAFAS NMPYVLLSSS VSFYLLPLVM LFVYARVVFV ATROLRLLRG 240
ELGRFPPEES PPAPSRSLAP APVGTCAPE GVPACGRRA RLLPLREHRA LCTGLIMGT 300
FTLCWLPFFL ANVLRALGGP SLVPGPAFLA LNWLYGANSF FNPLIYCRSP DFRSAFRRL 360
CRGRRLPPE PCAARPALF PSQVPAARSS PAQPRLCQRL DGASWGV

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Seq ID NO: B58 DNA sequence  
Nucleic Acid Accession #: NM\_032553.1  
Coding sequence: 37..1038

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40  
45  
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1 11 21 31 41 51
CACCATTAGG CAAAGATAGT TTCTCTAGAG AGAATCATGC CTGCTAATTA CACGTGTACC 60
AGGCCAGATG GAGACAATAC AGATTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC 120
ATTCTGTGTC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTATATG 180
AAAGAAACAA AACGAGCTGT GATATTTATG ATAAACTTAG CCATTGCTGA CTTACTACAA 240
GTTCTTCTCT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300
GGTCTCTGCA TGTCTCTGTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGGTCTGCA TCAGTGTGCG ACGATTTTGG TTCTCATGT ACCCTTTTCC CTTCCTGAC 420
TGCAACAGAG AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCCTGCC 480
TGTGTACTCT TTCCACTCCT CAGAACCACT GATGATACCT CTGGCAATAG GACCAATGTC 540
TTTGTGGATC TTCCACTCAG GAATGTCAAC CTGGCCCACT CCGTTGTTAT GATGACCAT 600
GGGAGATTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660
GTTTTATCAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TTGAAGATGA TTCTAACCTG TGCAGGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780
AGTTTTCTCT TAGATTTCCT GGTGAAGTCC AATGAAATTA AAAGCTGCCT AGCCAGAAGG 840
GTGATTCTAA TATTTTCTTC TGTGGCATG TGTCTTGCTA GTCTGAATTC ATGCTCTGAC 900
CAGATCATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAAG ACAAGATTG 960
CATGACAGCA TCCAATCCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
ACACCTGAAT TATGCTAAAA CAAAAACCA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080
CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAAC ACAGCTTTTC 1140
AGTTCTGCTC TATCTTACTG CTATGGGGAA TTCACTTCTT CAAAGCAGGA CCTATTTGGA 1200
GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTT CTTCAGT

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Seq ID NO: B59 Protein sequence  
Protein Accession #: NP\_115942.1

60  
65  
70

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1 11 21 31 41 51
MPANYTCTRP DGDNTDFRYF IYAVTYTVIL VPGLIGNILA LNVFYGYMKE TKRAVIFMIN 60
LAIADLLQVL SLPLRIFYFL NHDWPFPGPL CMFCFYLYKV NMYASIVFLV CISVRRFNFL 120
MYPFRPHDCK QKYDLYISIA GWLIICLACV LPPLRLTSD TSGNRTKCFV DLPTNRNVLA 180
QSVVMTIGE LIGFVTEPLI VLYCTWKTIV SLQDKYPMQA DLGEKQKALK MLTTCAGVFL 240
ICFAPYHFSF PLDFLVKSNE IKSCLARRVI LIFHSVALCL ASLNSCLDPV IYFSTNEFR 300
RRLSRQDLHD SIQLHAKSFV SNHTASTMTP ELC

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Seq ID NO: B60 DNA sequence  
Nucleic Acid Accession #: CAT cluster

75  
80

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1 11 21 31 41 51
GATTCGGATT TTAATCCGAC TCACTATAGG GAATTTTGGC CTCGAGGCC AAGAATTCCG 60
CCCGAGGGTT AGACATTATA CTGAGTCTTT TTCAATCAC GGTATGCTTT TATTTTACCC 120
TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTCTTTTCA 180
TACATTTTAA GGAATTTATA CATTTCATC TGAATTTGTA TTCAATATCT TCTAGAAACC 240
AAGAGTGGAC TTGGTATCCG TCTGATTATA TTTTCTTTGT TGGTAAAGAG CCTCTTTT 300
CCCTTTTAT TTTTCTCTTC TCTTCTCTTA GTGTTTATA TCTTATTTT ATGAATGTAG 360
TCTAATATT TAGAACACTG TCTCCGAGTA TGTGTTTATT TGGGTTTGTG TTTTGAACAT 420
TGCCCTCAGG TCGAGTTTAA TGTGTGTTTA TGTTCCTAT TTGAGGTGG ACACCTAGAA 480
AATTTTCTCA ATTCGAAAC TATTTTCTTT CAGCACTCAG AAATTTTAT CAAAGATTAT 540
TTCCAGGATT ATTTCTCTGC CTGTTTCTTT CGTGTCTCTA ACCTAGAATT CAATTGTTTA 600

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ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATTGTC 660  
 ATATCTTTTG GACTATTGTC TGAAGCAAT AAATGTATAT TACTTTAAAA AAAAAAAAAA 720  
 AAAAACHCAT TTTCAAATTT AATACACACA AATTGTGCAT ACCACACAC ATATACCACA 780  
 GATATATTCA TTTCAGGAT TTCTTTAAGT GTTATTTTAA AAATAATCAT ATTCTTATTT 840  
 TGTGAACCTG GGGATTTCCT GAAACTTTTT GAAAACTCTC ATTAGTCTGT GTTTGTGTGG 900  
 TTCTTTTAAA TTATCTCTTC CTTCAGAATT ACTTTTGTGT TTTGAATTG AGTCTTTGCC 960  
 ATTCATAAGG CGGCTTTCC TTGAATACCA GATAACTCTG AGTTCTCTGT TCATATTTAA 1020  
 GAATAAATAA CCTAATTGTA AAAAAAAAAA AAAAA

10 Seq ID NO: B61 DNA sequence  
 Nucleic Acid Accession #: NM\_014522.1  
 Coding sequence: 846..3911

15 1 11 21 31 41 51  
 CTGGTGGTCC AGTACCTCCA AAGATATGGA ATACACTCCT GAAATATCCT GAAAACTTTT 60  
 TTTTTTCAGA ATCCCTTAAT AAGCAGTTAT GTCAATCTGA AAGTTGCTTA CTGTGACTTT 120  
 ATATTAATAG CTATTCTTGT TTTTCTTATC CAAAGAAAAA TCCTCTAATC CCCTTTTCAC 180  
 ATGATAGTTG TTACCATGTT TAGGCATTAG TCACATCAAC CCCTCTCCTC TCCCAAACTT 240  
 CTCTCTCTCA AATCAAACTT TATTAGTCCC TCCTTTATAA TGATTCCTTG CCTCGTTTAA 300  
 TCCGATCAAA TTTTTTTCCA CTTTGATGCC CAGAGCTGAA GAAATGGACT ACTGTATAAA 360  
 TTATTCATTG CCAAGAGAAT AATTGCATT TAAACCCATA TTATAACAA GAATAATGAT 420  
 TATATTTTGT GATTGTGAAC AAATACCCCT TATTTTCCCT TAACATTGA ATTAATATTT 480  
 TTAATTATTT GTATTCTCTT TAACTATCTT GGTATATTAA AGTATTATCT TTTATATATT 540  
 TATCAATGGT GGACACTTTT ATAGGTACTC TGTGTCAATT TGTACTCTGT AGGTATCTTA 600  
 TTTCAATTAT CTTTATCTCT AATGTACGAA TTCATAATAT TGTATTGAGA ACAAATTTAT 660  
 CACTAATTAA CAGAGTGTC AATTATGCTAA CATCTCAATT ACTGATTTTA ATTTAAACAA 720  
 GTTTTGTGTA ACATGCACTG TTAGGGTTGG CTCTCTAATA ATTTCTTCTT CCTCTCTCT 780  
 CTCTCTCTCT CTTTGGTCA GTGTGTGTGG GGTTAATACA ACAAACCTGA ACAAGTGTAC 840  
 CTGGTATGGA CTGTGTGTCC GGGACGTACA TTTTCCGGT CCTGCTAGCA TGGCTGGTGT 900  
 TCCACTCTGG CGCCAGGAG AAAAAGTACA CCATCCGAGA AGAAATGCCA GAAACGTCC 960  
 TGATAGGGCA CTGTGTGAAA GACCTTAACT TGTGCTGAT TCCAAACAAG TCCTTGACAA 1020  
 CTGCTATGCA GTTCAAGCTA GTGTACAAGA CCGGAGATGT GCCACTGATT CGAATTGAAG 1080  
 AGGATACTGG TGAGATCTTC ACTACTGGCG CTGCAATTGA TCGTGAGAAA TTATGTGCTG 1140  
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 TATTTAGACT GGTTAAGATA CGTTTTCTGA TAGAAGATAT AAATGATAAT GCACCATTTG 1260  
 TCCAGCAAC AGTTATCAAC ATATCAATTC CAGAGAATCT GGCTATAAAC TCTAAATATA 1320  
 CTCTCCACGC GGCTGTGTAT CCTGACGTAG GAATAAACCG AGTTCAAAAC TACGAACATA 1380  
 TTAAGAGTCA AAACATTTT GGCCTCGATG TCATTGAAAC ACCAGAAGGA GACAGATGTC 1440  
 CACACTGAT TGTTCAAAAG GAGTTAGATA GGGAAAGGAA GGATACCTAC GTGATGAAAG 1500  
 TAAAGGTTGA AGATGTTGAC TTTCTCAA GATCCAGTAC TGCTATTTTG CAAGTGAGTG 1560  
 TTACTGATAC AAATGACAAC CACCCAGTCT TTAAGGAGAC AGAGATTGAA GTGAGTATAC 1620  
 CAGAAAATGC TCCGTGATGG ACTTCAGTGA CACAGCTCCA TGCCACAGAT CTGACATAG 1680  
 GTGAAAATGC CAAGATCCAC TTCTCTTCA GCAATCTAGT CTCCACATT GCCAGGAGAT 1740  
 TATTTCACTT CAATGCCACC ACTGGACTTA TCACAACTCA AGAACCACTG GATAGGGAAG 1800  
 AAACACCAA CCACAAGTTA CTGGTTTGG CAAGTGTGAG TGGATTGATG CCAGCAAGAG 1860  
 CAATGGTGTCT CAATGATGTT ACAGATGTCA ATGATAATGT CCAATCCATT GACATAAGAT 1920  
 ACATCGTCAA TCCTGTCAAT GACACAGTTG TTTCTTCAGA AAATATTCCA CTCAACACCA 1980  
 AAATTGTCTCT CATAACTGTG ACGGATAAGG ATGOGGACCA TAATGGCAGG GTGACATGCT 2040  
 TCACAGATCA TGAATCCCTT TACAGATTAA GGCAGTATT CAGTAATCAG TTCTCTCTGG 2100  
 AGACTGCAGC ATATCTTGAC TATGAGTCCA CAAAGAATA TGCCATTAAA TTACTGGCTG 2160  
 CAGATGCTGG CAAACCTCTT TTGAATCAGT CAGCAATGCT CTTCATCAAA GTGAAAGATG 2220  
 AAAATGCTGG TGCTCCAGTT TTTCCACAGT CTTTCTTAAC TGTTCATATT CCTGAGAATA 2280  
 ACTCTCTCGG CATCCAGTTG ACGAAGTAA GTGCAATGGA TGCAGACAGT GGGCCTAATG 2340  
 CTAAGATCAA TTACTGTCTA GGCCCTGATG CTCCACCTGA ATTCAGCCTG GATTGTCTGA 2400  
 CAGGCATGCT GACTGTAGTG AAGAACTAG ATAGAGAAAA AGAGGATAAA TATTATTCCA 2460  
 CAATTCTGGC AAAAGATAAC GGGGTACCAC CCTTAACCAAG CAATGTCAAC GTCTTTGTAA 2520  
 GCATTATTGA TCAAGATGAC AATAGCCGAG TTTTCACTCA CAATGAATAC AACTTCTATG 2580  
 TCCAGAAAAA CCTTCCAAGG CATGGTACAG TAGGACTAAT CACTGTAACT GATCCTGATT 2640  
 ATGGAGACAA TTCTGCAGTT ACGCTCTCCA TTTTAGATGA GAATGATGAC TTCACCATG 2700  
 ATTACAAAC TGGTGTCTAT CGACCAAATA TTTCAATTGA TAGAGAAAAA CAAGAATCTT 2760  
 ACACCTTTCTA TGTAAAGGCT GAGGATGGTG GTAGAGTATC ACGTTCTTCA AGTGCCAAAG 2820  
 TAACCATAAA TGTGGTTGAT GTCAATGACA ACAACCACT TTTCAATTGTC CCTCCTTCCA 2880  
 ACTGTTCTTA TGAATTGGTT CTACOGTCCA CTAATCCAGG CACAGTGGTC TTTCAAGTAA 2940  
 TTGCTGTGTA CAATGACACT GGCATGAATG CAGAGGTTGG TTACAGCATT GTAGGAGGAA 3000  
 ACACAAGAGA TCTGTTTGCA ATCGAACCAAG AAACAGGCAA CATAACATTG ATGGAGAAAT 3060  
 GTGATGTTAC AGACCTTGGT TTACACAGAG TGTGGTCAA AGCTAATGAC TTAGGACAGC 3120  
 CTGATTCTCT CTTCAGTGTG GTAATTGTCA ATCTGTTCTG GAATGAGTGG GTGACCAATG 3180  
 CTACACTGAT TAATGAACCT GTGCGCAAAA GCACCTGAAGC ACCAGTGACC CCAATACTG 3240  
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 CTGGCACCAT AACTGTGTTT GTAGTTATTT TCATCACTGC TGTAGTAAGA TGTGCGCAGG 3360  
 CACCACACCT TAAGGCTGCT CAGAAAAACA AGCAGAATTC TGAATGGGCT ACCCCAAACC 3420  
 CAGAAAACAG GCAGATGATA ATGATGAAGA AAAAGAAAAA GAAGAAGAAG CATTCCCTTA 3480  
 AGAACTTGCT GCTTAATTTT GTCATATTG AAGAACTAA GGCAGATGAT GTTGACAGTG 3540  
 ATGGAAACAG AGTCACACTA GACCTTCTTA TTGATCTAGA AGAGCAAAAC ATGGGAAAGT 3600  
 ACAATTGGGT AACTACACCT ACTACTTTCA AGCCCGACAG CCCTGATTGG GCCCGACACT 3660  
 ACAAACTCTG CTCTCCACAG CCGCTCTTCC AAATTCAGCC TGAACCTCCC CTGAATTCTGA 3720  
 AGCACCATAT CATCCAAGAA CTGCTCTCTG ATAACACCTT TGTGGCTGTG GACTCTATCT 3780  
 CCAAGTGTTC CTCAAGCAGT TCAGATCCCT ACAGCGTTTC TGACTGTGGC TATCCAGTGA 3840  
 CGACCTTCGA GGTACCTGTT TCGGTACACA CCAGACCGGT AGGTATCCAA GTTTCTAACA 3900  
 CAACCTTCTA ACTATTGTTT TATTATTATT TTCAGTTGAT GTAGAACTTT ACAAATCTA 3960  
 TTGACTTCAA AGAGGGATCA AAACATCAT ATTCTACAGA TGTACCAAT AGATATATGG 4020  
 ATTCATTAA GTTTGGTAGA AGATGAGAAC AAAATAACTA CTGATTAGG AAAATTGGAT 4080  
 GCAGAATAAT AATTATAGTA GGGGCAATTT TGTCTGTAGA TGGCAGTATG ACAATTCTTG 4140

5 CTAGAGAATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCACTGTC CTCAGTACCA 4200  
 TTGTGTGCAT GAGGATCAGA ATAGTCTGGG CTAGATACAT CACATTAAG CTTTTCAGAA 4260  
 TCTGATAAAT AGCTCTAAAT ACTAATGATA TTGAGAAGCC TAGCTTCACT TGGGAAAAATC 4320  
 TGTGGCTGTT CACAGAAATT CAGCACCAAG TTATTCCCCC CATACTCTAC CAGGCCCTTCA 4380  
 GGTCCTCATA AAGAAAAAGT TCGTTTTTTCAG ATTAGGAAC CAAATATTAT TTGGTGCATC 4440  
 AAATCTACAG TCACACAATA TAACAAGAAAT GGGATTAGAA AAATGAAAGC CTACTCATTG 4500  
 TCATCTTTAA GCCAGAGAAT GAAATATATA TGAGGTCTCT GGATAGCTAT TTAAATATT 4560  
 GCATATTAT GCAAGGTATT TTGAGCCCTT CAGAAGACAT TCT

10 Seq ID NO: B62 Protein sequence  
 Protein Accession #: NP\_055337.1

15 1 11 21 31 41 51  
 MDLLSGTYIF AVLLACVVFH SGAQEKNTYI REEMPENVLI GDLLKDLNLS LIPNKSLLTA 60  
 MQPKLVYKTG DVPLIRIEED TGEIPTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF 120  
 RLVKIRFLIE DINDNAPLEP ATVINISIEP NSAINSKYTL PAAVDPDVGI NGVQNYELIK 180  
 SQNIFGLDVI ETEPGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT 240  
 DTNDNHPVPI ETEIEVSIPE NAPVGTSTVQ LHATDADIGE NAKIHPSFSN LVSNIARRLF 300  
 20 HLNATTGLIT IKEPLDREET FNHKLVLAS DGGLMPARAM VLVNVTVDND NVPSIDIRYI 360  
 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCT DHEIPFRLRP VFSNQFLLET 420  
 AAYLDYESTK EYAIKLLAAD AGKPLNQSA MLFIKVKDEN DNAPVFTQSF VTSIPENNNS 480  
 PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKKLDR EKEDKYLFTI 540  
 LAKDNGVPEL TSNVTVFVSI IDQNDNSPVE THNEYNFYVE ENLPRHGTG LITVTDPDYG 600  
 25 DNSAVTSLIL DEMDDPTIDS QTGVIRPNIS PDREKQESYT FYVKAEDGGR VSRSSSAKVT 660  
 INVVDVNDNK PVFIVPPSNC SYELVLPSTN PGTVVVFQVIA VNDNTGMNAE VRSIVGGNT 720  
 RDLFAIDQET GNITLMEKCD VTDLGLHRLV VKANDLGQPD SLFSVVIINL FVNESVTNAT 780  
 LINELVKST EAPVTPNTEI ADVSSPTSDY VKILVAAVAG TITVVVIFI TAVVRCRQAP 840  
 30 HLKAAQKNQK NSEWATNPPE NRQMIMMKKK KKKKKGSPKN LLLNFVTIEE TKADDVDSOG 900  
 NRVTLDLPID LEEQTMGKYN WVTPTTFKP DSPDLARHYK SASQPAFQI QPETPLNSKH 960  
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 F

35 Seq ID NO: B63 DNA sequence  
 Nucleic Acid Accession #: XM\_059180.2  
 Coding sequence: 276..3740

40 1 11 21 31 41 51  
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 GCGGCGCTAGC GAGCCTCGCG GTCCGACCCA GCCAGCGCAG CGACGGGGCG CTGCTTGGCC 180  
 CAGGCGCACA CGGAAGTGCG CTCTCTGAA GTAGCTTTGG AAAGTAGAGA AGAAATCCA 240  
 45 GTTTGCTTCT TGGAGAACAC TGGACAGCTG AATAAATGCA GTATCTAAAT ATAAAGAGG 300  
 ACTGCAATGC CATGGCTTTC TGTGCTAAAA TGAGGAGCTC CAAGAAGACT GAGGTGAACC 360  
 TTGAGGCCCC TGAGCCAGGG GTGGAAGTGA TCTTCTATCT GTCGGACAGG GAGCCCTTCC 420  
 GGCTGGCGAG TGGACAGTAC ACAGCAGAGG AACTGTGCTC CAGGGCTGCA CAGGCATGCC 480  
 GTATCTCTCC TCTTTGTGAC AACCTCTTTG CCTGTATGCA CGAGAACACC AAGCTCTGGT 540  
 50 ATGCTCCAAA TCGACCAATC ACOGTTGATG ACAAGATGTC CCTCGGCTC CACTACCGGA 600  
 TGAGGTTCTA TTTCACCAAT TGGCATGGAA CCAACGACAA TGAGCAGTCA GTGTGGCGTC 660  
 ATTCTCCAAA GAGACGAGAA AATGGCTACG AGAAAAAATA GATTCCAGAT GCACCCCTC 720  
 TCCTTGATGC CAGCTCACTG GAGTATCTGT TTGCTCAGGG ACAGTATGAT TTGGTGAAAT 780  
 GCCTGGCTCC TATTCGAGAC CCCAAGACCG AGCAGGATGG ACATGATATT GAGAAGCAGT 840  
 55 GTCTAGGGAT GGCTGTCTCTG GCCATCTCAC ACTATGCCAT GATGAAGAAG ATGCAGTTGC 900  
 CAGAACTGCC CAGAGCATCT AGCTACAAGC GATATATCCC AGAAACATTG AATAAGTCCA 960  
 TCAGACGAGC GAACCTTCTC ACCAGGATGC GGATAAATAA TGTTTTCAAG GATTCTCTAA 1020  
 AGGAATTTAA CACACAGACC ATTTGTGACA GCAGCGTGTG CAGCATGAC CTGAAGGTGA 1080  
 AATACTTGGC TACCTTGGAA ACTTTGACAA AACATTACGG TGCTGAAATA TTTGAGACTT 1140  
 60 CCATGTTACT GATTTCATCA GAAAATGAGA TGAATTGGTT TCATTGCAAT GACCGTGGAA 1200  
 ACCTTCTCTA CTACGAAGTG ATGTGACTG GGAATCTTGG AATCCAGTGG AGGCATAAAC 1260  
 CAAATGTTGT TTCTGTGAAA AAGGAAAAAA ATAAACTGAA GCGGAAAAAA CTGGAATAA 1320  
 AACACAGAAA GGATGAGGAG AAAAAACAAGA TCCGGGAAGA GTGGAACAAT TTTTCTTACT 1380  
 TCCTGAAAT CACTCACATT GTAATAAAGG AGTCTGTGGT CAGCATTAAAC AAGCAGGACA 1440  
 65 ACAAGAAAAAT GGAAGTGAAG CTCTCTTCCC ACGAGGAGGC CTGTCTCTTT GTGTCCCTGG 1500  
 TAGATGGCTA CTTCGGGCTC ACAGCAGATG CCCATCATTA CCTCTGCACC GACGTGGCCC 1560  
 CCGCGTTGAT CGTCCACAAC ATACAGAATG GCTGTCTATG TCCAATCTGT ACAGAATAAG 1620  
 CCATCAATAA ATTGCGGCAA GAAGGAAGCG AGGAGGGGAT GTACGTGCTG AGGTGGAGCT 1680  
 GCACCGACTT TGACAACATC CTCATGACCG TCACTGTCTT TGAGAAGTCT GAGCAGGTGC 1740  
 70 AGGGTGCCCA GAAGCAGTTC AAGAACTTTC AGATCGAGGT GCAGAAGGCG CCGTACAGTC 1800  
 TGCAACGGTTC GGACCGCAGC TTCCCCAGCT TGGGAGACCT CATGAGCCAC CTCAGGAAGC 1860  
 AGATCTCTGG CACGGATAAC ATCAGCTTCA TGCTAAAAAG CTGCTGCCAG CCAAGGCCCC 1920  
 GAGAATCTCT CAACCTGCTG GTGGCTACTA AGAAGGCCCA GAGATGGCAG CCGGTCTACC 1980  
 CCATGAGCCA GCTGAGTTTC GATCGGATCC TCAAGAAGGA TCTGGTGCAG GCGAGCACC 2040  
 75 TTGGGAGAGG CACGAGAACCA CACATCTATT CTGGGACCCT GATGGATTAC AAGGATGACG 2100  
 AAGGAACCTC TGAAGAGAAG AAGATAAAGG TGATCCTCAA AGTCTTAGAC CCCAGCCACA 2160  
 GGGATATTTC CTGCGCTTTC TTGAGGCGAG CCAGCATGAT GAGACAGGTC TCCACAAAC 2220  
 ACATCGTGTA CCTCTATGGC GTCTGTGTCC GCGACGTGGA GAATATCATG GTGGAAGAGT 2280  
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 80 CATGGAAATC CAAAGTTGCC AAACAGCTGG CCAAGTCCCT GAGCTACTTG GAGGATAAAG 2400  
 ACCTGGTCCA TGGAAATGTG TGTACTAAAA ACCTCCTCCT GGCCCGTGAG GGCATCGACA 2460  
 GTGAGTGTGG CCCATTCATC AAGCTCAGTG ACCCGGCAT CCCCATTACG GTGCTGTCTA 2520  
 GGCAGGAATG CATTGAACGA ATCCCATGGA TTGCTCCTGA GTGTGTTGAG GACTCCAAGA 2580  
 ACCTGAGTGT GGCTGCTGAC AAGTGGAGCT TTGGAACAC GCTCTGGGAA ATCTGCTACA 2640  
 ATGGCGAGAT CCCCTTGAAA GACAAGACGC TGATTGAGAA AGAGAGATTG TATGAAGCC 2700

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GGTGCAGGCC AGTGACACCA TCATGTAAGG AGCTGGCTGA CCTCATGACC CGCTGCATGA 2760
ACTATGACCC CAATCAGAGG CCTTCTCTCC GAGCCATCAT GAGAGACATT AATAAGCTTG 2820
AAGAGCAGAA TCCAGATATT GTTTCAGAAA AAAAACCAGC AACTGAAGTG GACCCACAC 2880
ATTTTGAAAA GCGCTTCTTA AAGAGGATCC GTGACTTGGG AGAGGGCCAC TTGCGGAAGG 2940
TTGAGCTCTG CAGGTATGAC CCCGAAGGGG ACAATACAGG GGAGCAGGTG GCTGTTAAAT 3000
CTCTGAAGCC TGAGAGTGGA GGTAACCACA TAGCTGATCT GAAAAAGGAA ATCGAGATCT 3060
TAAGGAACCT CTATCATGAG AACATTGTGA AGTACAAAGG AATCTGCACA GAAGACGGAG 3120
GAAATGGTAT TAAGCTCATC ATGGAATTTC TGCCTTGGG AAGCCTTAAG GAATATCTTC 3180
CAAGAATAAA GAACAAAATA AACCTCAAAC AGCAGCTAAA ATATGCCGTT CAGATTGTGA 3240
AGGGGATGGA CTATTGGGT TCTCGGCAAT ACGTTTCCCG GGACTTGGCA GCAAGAAATG 3300
TCCTTGTTGA GAGTGAACAC CAAGTGAAAA TTGGAGACTT CGGTTTAAAC AAAGCAATTG 3360
AAACCGATAA GGAGTATTAC ACOGTCAAGG ATGACCGGGA CAGCCCTGTG TTTTGGTATG 3420
CTCCAGAATG TTTAATGCAA TCTAAATTTT ATATTGCCTC TGACGCTGG TCTTTTGGAG 3480
TCACCTGCGA TGAGCTGCTG ACTTACTGTG ATTACAGATC TAGTCCCATG GCTTTGTGCC 3540
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CTTCTCCTGC AACAAATGCC CAAGTCATTT TTTAAAAATT TCTAATGAAA GAAGTTTGTG 3840
TTCTGTCCAA AAGTCACTG AACTCATACT TCAGTACATA TACATGTATA AGGCACACTG 3900
TAGTGCTTAA GAGTGTAAAG GACTTCTCT TTAATTTGG TACCAGTAAC TTAGTGACAC 3960
ATAATGACAA CCAAAATATT TGAAAGCACT TAAGCACTCC TCCTGTGGA AAGAATATAC 4020
CACCATTCA TCIGGCTAGT TCACCATCAC AACTGCATTA CCAAAAGGGG ATTTTGAAG 4080
ACGAGGAGTT GACCAAAATA ATATCTGAAG ATGATTGCTT TTCCCTGCTG CCAGCTGATC 4140
TGAAATGTTT TGCTGGCACA TTAATCATAG ATAAAGAAAG ATTGATGGAC TTAGCCCTCA 4200
AATTTCAGTA TCTATACAGT ACTAGACCAT GCATTCTTAA AATATTAGAT ACCAGGTAGT 4260
ATATATTGTT TCTGTACAAA AATGACTGTA TTCTCTCACC AGTAGGACTT AAACCTTTGT 4320
TCTCCAGTGG CTTAGCTCTT GTTCTTTGG GTGATCACTA GCACCATTT TTGAGAAAGC 4380
TGGTTCTACA TGGGGGGATA GCTGTGGAAT AGATAATTG CTGCATGTTA ATTCTCAAGA 4440
ACTAAGCCTG TGCCAGTCTT TTCCTAAGCA GTATACCTTT AATCAGAACT CATTCCACAG 4500
ACCTGGATGC TATTACACAT GCTTTAAGA AACGTCAATG TATATCCTTT TATAACTCTA 4560
CCACTTTGGG GCAAGCTATT CCAGCACTGG TTTTGAATGC TGTATGCAAC CAGTCTGAAT 4620
ACCAATACG CTGCACTGTT CTTAGAGGGT TTCATACCT ACCACCGATC TACAGGGTT 4680
GATCCCTGTT TTTACCATCA ATCATCACCC TGTGGTGCAA CACTTGAAAG ACCCGGCTAG 4740
AGGCACATAT GACTTCAGGA TCCACTAGAC AGTTTTCAGT TTGCTTGGAG GTAGCTGGGT 4800
AATCAAAAT GTTTAGTCAT TGATTCAATG TGAACGATTA CGGTCTTAT GACCAAGAGT 4860
CTGAAATCT TTTTGTATG CTGTTAGTA TCTGTTTGT ATTGTTACTT TTCACCTGTT 4920
GAGCCCAAT TCAGGATTGG TTCAGTGGCA GCAATGAAGT TGCCATTATA ATTGTTTAT 4980
AGCCTACATC ACCAAGGTCT CTGTGTCAA CCTGTGGCCA CTCTATATGC ACTTGTGTTA 5040
CTCTTATAC AATAAATAT ACTAAAGACT TT

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Seq ID NO: B64 Protein sequence  
Protein Accession #: A39577

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1 11 21 31 41 51
| | | | |
MQYLNIEDC NAMAFCAKMR SSKKTEVNLE APEPGVEVIF YLSDREPLRL GSGEYTAEEEL 60
CIRAAQACRI SPLCHNLPAL YDENTKLWYA PNRTITVDDK MSLRLHYMR FYFTNWHGTN 120
DNEQSVWRHS PKQKQNGYEK KKIIPDATPLL DASSLEYLFA QGQYDLVKCL APIRDPKTEQ 180
DGHDIENECL GMAVLALSHY AMMKQMQLPE LPKDISYKRY IPETLNKSIR QRNLLTRMRI 240
NNVFDFLKE PNKLTICDSS VSTHDLKVKY LATLETLTKH YGAEIFETSM LLISSENNEM 300
WHSNDGNGV LLYEVMVTGN LGIQWRHKPN VVSVEKEKNK LKRRKLENDK KDBEENKIR 360
BEWNFSFPP EITHIVIKES VVSINKQDNK KMELKLSHE EALSFSVLVD GYFRLTADAH 420
HYLCTDVAPP LIVHNIQNC HGPICTEYAI NKLREQGSEE GMYVLWVSCD DFDNIMLVT 480
CFEKSEQVQG AQRQKFNQI EVQKGRYSIH GSDRSFPLG DLMHLKKQI LRTDNISFML 540
KRCCQPKRE ISNLIIVATK AQEWQPVYPM SQLSPDRILK KDLVQGEHLG RGRTRHIYSG 600
TLADYKDEB TSEEKKIKVI LKVLDPSHRD ISLAPFEAAS MMRQVSHKHI VYLYGVCVRD 660
VENIMVEEFV EGGPLDLFPH RKSDVLTTPW KFKVAKQLAS ALSYLEDKDL VHGNVCTKNL 720
LLAREGIDSE CGPFIKLSDP GIPITVLSRQ ECIERIPWIA PECVEDSKNL SVAADKNSFG 780
TTLWEICYNQ EIPLKDKTLI EKERFYESSR RVPVPSCKEL ADLMTRCMY DPNQRPFFRA 840
IMRDINKLEE QNPDIIVSRKK NQPTVEDPTH FEKRFLKRIR DLGEGHFGKV ELCRYDPEDN 900
TGEQVAVKSL KPESGNNHIA DLKKEIEILR NLYHENIVKY KGICTEDGDN GIKLIMEFLP 960
SGSLKEYLPK NKNKINLKQQ LKYAVQICKG MDYLSRQYV HRDLAARNVL VESEHQVKIG 1020
DFGLTKALET KTEYYTVKDD RDSFVFWYAP ECLMQSKFYI ASDVWSFGVT LHELLTYCDS 1080
DSSPMALFLK MIGPTHGQMT VTRLVNTLKE GKRLPCFPNC PDEYVQLMRK CWEPQPSNRT 1140
SFQNLIEGFE ALLK

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Seq ID NO: B65 DNA sequence  
Nucleic Acid Accession #: NM\_004867.1  
Coding sequence: 140..931

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80

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1 11 21 31 41 51
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GATCCAGAC CTCGGCTTGC AGTAGTGTTA GACTGAAGAT AAAGTAAGTG CTGTTTGGGC 60
TAACAGGATC TCCTCTTGCA GTCTGCAGCC CAGGACGCTG ATTCCAGCAG CGCCTTACCG 120
CGCAGCCCGA AGATTCACTA TGGTGAAAAA CGCCTTCAAT ACCCTTACCG CGGTGCAAAA 180
GGAGGAGGGG CGGCAAGACG TGGAGGCCCT CCTGAGCCGC ACGGTCAAG CTCAGATACT 240
GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGAAGAAAGG GGCTCCTCTG GGAGATGTAT 300
GCTTACTCTC TTAGGCCCTTT CATTTCATCT GGCAGGACTT ATTGTTGGTG GAGCCTGCAT 360
TTACAAGTAT TTCAATGCCA AGAGCACCAT TTACCGTGGG GAGATGTGCT TTTTGTATTC 420
TGAGGATCCT CCAAAATCCC TTCGTGGAGG AGAGCCTAAC TTCTGCCTCT TGACTGAGGA 480
GGCTGACATT CGTGAGGATG ACAACATGTC AATCATTGAT GTGCCCTGCC CCAGTTTCTC 540
TGATAGTGAC CCGTCAGCAA TTATTCATGA CTTTGAAAAG GGAATGACTG CTTACCTGGA 600
CTTGTTGCTG GGGAACTGCT ATCTGATGCC CCTCAATACT TCTATTGTGA TGCCCTCCAA 660

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AAATCTGGTA GAGCTCTTTG GCAAACTGGC GAGTGGCAGA TATCTGCCTC AAACCTTATGT 720  
GGTTGAGAAA GACCTAGTTG CTGTGGAGGA AATTCGTGAT GTTAGTAACC TTGGCATCTT 780  
TATTTACCAA CTTTGCAATA ACAGAAAGTC CTTCGCCTT CGTCGCAGAG ACCTCTTGCT 840  
GGGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAACGAATT 900  
TATTGTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAAT 960  
AAGAAGTCAG AGATTTACAA TATGACTTTA ACATTAAGGT TTATGGGATA CTCAAGATAT 1020  
TTACTCATGC ATTTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080  
AA

Seq ID NO: B66 Protein sequence  
Protein Accession #: NP\_004858.1

1 11 21 31 41 51  
MVKIAFNTPT AVQKEEARQD VEALLSRTVR TQILTQKELR VATQEKEGSS GRCMLTLGL 60  
SFILAGLIVG GACIYKYFMP KSTIYRGEMC PFDSEDPANS LRGGEPNPLP VTEEDADIRE 120  
DNIAIIDVPV PSFSDSDPAA ITHDFEKGMT AYLDLLLGNC YLMLPLNTSIV MPPKMLVELF 180  
GKLASGRYLP QTYVVRDLV AVEBIRDVS N LGIPYQLCN NRKSPRLRRR DLLLGFNKRA 240  
IDKCWKIRHF PNEFIVETKI CQE

Seq ID NO: B67 DNA sequence  
Nucleic Acid Accession #: XM\_083862.1  
Coding sequence: 121..813

1 11 21 31 41 51  
ACGCGGGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGCGATG 60  
CCTTGAACCT GGGAAACTAT GTGAAGCAAC ACTCTGGATT TTGAAGACA TCCTTTCATC 120  
ATGGGACAGC AATATTGGGA TCAGACACAG TTGGTTATTA ACAAGTTACC AGAAAAAGTA 180  
GCAAAACATG TTACCTGGGT TCGAGAGAGT GGCTCCTTAA CTTATGAAGA ATTTCTCGGG 240  
AGAGTAGCTG AGCTTAATGA TGTAAACGGCT AAAGTGGCTT CTGGCCAGGA AAAACATCTT 300  
CTCTTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTT GGAAGTGGT TGTACGGGTG 360  
GTCTGTACCA AGATTAACAA AAGCAGTGGC ATTGTGGAGG CATCACGGAT CATGAATTTA 420  
TACCACTTTA TTCAACTTTA TAAAGATATC ACAAGTCAAG CAGCAGGAGT ATCGGCACAG 480  
AGCTCCACCT CTGAAGAACC TGATGAAAC TCATCTCTG TAACATCTTG TCAGGCTAGT 540  
CTTTGGATGG GAAGGTGAA GCAGCTGACC GATGAGGAGG AGTGTGTAT CTGTATGGAT 600  
GGGCGGGCTG ACCTCATCTT GCCTTGTGCT CACAGCTTTT GTCAGAAAGT TATTGATAAA 660  
TGGAGTGATC GACACAGGAA TTGCCCTATT TGTGCGCTAC AGATGACTGG AGCAAATGAA 720  
TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACATAT TCTTAACATG 780  
CTGTATGAGG GACGCCAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTGTCTA 840  
TTGTGGGCTC AATATTTGG TCATGGGGGA AGAATGTAGG GTTGTGGCAC TGGCACAGAC 900  
ACAGGAAAT CCATTTTCCC CACTCTTTA TTTTGTCTAT TCTGATCAT TGTCCCCCTT 960  
TTAAAAATAA ACTTCCCATG TCTTCCAAAA AAAAAAAAAA AAAAA

Seq ID NO: B68 Protein sequence  
Protein Accession #: XP\_083862.1

1 11 21 31 41 51  
MGQIQSDQIQ LVINKLPEKV AKHVLVRES GSLTYEEFLG RVARLNDVTA KVASGQEKHL 60  
LFEVQPGSDS SAFKVVVVR VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120  
SSTSEEPDEN SSVTSQAS LWMGRVKQLT DEEECCICMD GRADLILPCA HSFCQKCIDK 180  
WSDRHRNCPI CRLQMTGANE SWVVSADPTE DDMANYILNM ADEAGQPHRP

Seq ID NO: B69 DNA sequence  
Nucleic Acid Accession #: NM\_002975.1  
Coding sequence: 180..1151

1 11 21 31 41 51  
GACCAACCG ACCGACAGA GACGAGGAGA GGAACAGGAA GAGAGAAGCT GGGAGAATCG 60  
GGAACCTGGG GGCTAGTGAC CTGCACACAG GGCAGGGGCA CTGGCAGTT CCCAGAGGCC 120  
ACCCCTCCCA CCCAGACAT CCAGACATCT GGAACCTTGG GTGCCAAGAG TCCAGCTTAA 180  
TGCAGGCAGC CTGGCTTTTG GGGGCTTTGG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG 240  
GGGCTCGGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCAG GAGGAGGAGC 300  
GGGAGAGGGA GGCCCTGATG CTGAAGCATC TGCAGGAAGC CCTAGGACTG CTGCTGGGA 360  
GGGGGATGA GAATCTTGC GGAACCTGTG AGGGAAGAGA GGAAGTGGG ATGAGGAGG 420  
ACCAGGGGGA GGAAGAGGAG GAGGAAGCAA CCCCCACCC ATCCTCGGC CCCAGCCCT 480  
CTCCACCCCT TGAGGACATC GTCACTTACA TCCTGGGCGG CCTGGCCGGC CTGGACGAG 540  
GCTGCACCA GCTGCACGTC CGTCTGCAG CGTTGGACAC CCGGCTGGTC GAGCTGACCC 600  
AGGGGCTGGG GCAGCTGGGG AACGCGGCAG GGCACACCCG CGATGCCGTG CAGCCCTGC 660  
AGGAGGCGCA GGGTGGCGCC GAGCGCGAGC ACGGCGGCTT GAGGGGCTGC CTGAAGGGGC 720  
TGCGCTGGG CCACAAGTGC TTCTGTCTCT CGCGGACTT GGAAGCTCAG GCGGCGGCGC 780  
AGGCGCGGTG CAGGCGCGGG GCGGCGAGCC TGGCGCAGCC GGCAGACCGC CAGCAGATGG 840  
AGGCGCTCAC TCGGTACCTG CGCGCGGCGC TCGCTCCCTA CAACCTGGCC GTGTGGCTGG 900  
GCGTGCAGGA TCGGCGCGCC GAGGCGCTCT ACCTCTTGA AAAACGCCAG CGCGTGTCT 960  
TCTTCCGCTG GCATCGCTCA CCGCGCCCG AGCTGGCGGC CCAGCCGAGC GCCTGCGCGC 1020  
ATCCGCTCAG CCGGACAGG CCCAACGGTG GCAAGCTGGA GAACTGCGTG GCGCAGGCT 1080  
CTGACGAGG CTCTGGTGG GACCACGACT GCCAGCGGG TCTCTACTAC GTCTGCGAGT 1140  
TCCCTTCTA GCGGGCGCGG TACCCCGCTT CCTTGCCCAT CCCACACCC GGCCTTTCCC 1200  
TGCGGCGTGC CCACCTCTCT CCGGAATGCG CCTTCCCTTC CTGGCCACGA ATGGCAGCGT 1260  
CCTCCCGGAC CCGCAGTCTG GCGCTTCTG GAGGGGCTCT TCGGCTGCGC GCATCTCTCC 1320  
TGTGTAGTGT CTTTCTTTGA AGGGGCGGGC ACCAGGCTAG GTCCGCTGCC AATAAATCCT 1380  
TGTGAATCT GAAAAAATAA AAAAAA

Seq ID NO: B70 Protein sequence  
Protein Accession #: NP\_002966.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MQAANLLGAL VVPQLLGFGH GARGAEREWE GGWGGAEQEE REREALMLKH LQELGLPAG 60
RGDENPAGTV EGKEDWEMEE DQEEEEEEEA TPTPSSGPSP SPTPEDIVTY ILGRLAGLDA 120
GLHQLHVRHL ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGLCKG 180
10    LRLGHKCFLL SRDFAQAAA QARCTARGGS LAQPADRQOM EALTRYLRAA LAPYNWPVWL 240
GVHDDRRAEGL YLFENGQRVS FFAWHRSPRP ELGAQPSASP HPLSPDQPNG GTLENCVAQA 300
SDDGSSWDHHD CQRRLYYVCE PPF
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Seq ID NO: B71 DNA sequence  
Nucleic Acid Accession #: BC000839.1

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15      1      11      21      31      41      51
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CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG 60
20    TGGGGCTTTG TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGSTCCCCC TTCCTATGAT 120
GAGGACCTTT TCACGACCTT GTACTGAGCT CCGTGAGGAT AAGTAACCTC GAGGAGATGG 180
GCCCTGCAAG CCTCCTCTCT AGCGTCTGTG TCAGAAAATA GCGTTTTCGA AATGCCCTGA 240
GTTGACCTAA TGCTCTATTG GGCTCCTGTC TSCAGGATTI ACGGCAAGT TGGAAACGAA 300
GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA 360
25    GACCCATCTT TATGCAAAAG CAGCGTTACA GTAATGTTC AGCATCTCAT AATCTATCCT 420
GGGGAATTCG GCTGCCTCCC AGGGTGAATA CAGTATTCC TGATGACAGT CTGCCTCTAT 480
CTTACAGAGC AGCTTGTTCG TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC 540
TAACCAATAA CCTGCTTGGC TCAAAGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
TTGAGGAAAA CTAGGTGTCT GTGTTCACTC CAGGCTGAAG TTACAGGTCT GAGCAATAAA 660
30    GGTGTATAAA AATGGAATC TGTCTGGAG GACATCAGAA GGTGAATTTT CCAAGTCTCT 720
GGACAACCTA GCTGTTGAAA AGCTTCTCGG GTTTGGGGGG TATTTCAGAT GTACCTTAAA 780
GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT 840
GTGTATCACA TTCTGTATT TTATCACCCC CTTCCTGCAA CATTATTAT CTGGAATCTA 900
CCTGCCCTTT TGTTTTITAG ATACAAGGGC TTGGTTTTGT TACCCAGGCT GGTTTCAAGG 960
35    CCATAGCTTT AAGAGATCCT CTCACCACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
TTCATGSCAC CGCAGCTTTG CTGCCTTTCT TACATGATCC AGGCCAGAA CCCAACTCA 1080
GGCACTGTAT AGATGACCAC TTCTGTAAAC TACTGACCTA GCTTGTGCC AATTGTTGAT 1140
TGAATCTCCC ATAACCTCAC TTCGTGCTCG TTCTCTGTA TACAGCCACC TTCTGTTCCC 1200
40    GTCATGAGCC TTATGCTCTC CATTGTCATA TTGCAATAC TATGTTCCAT GTAGGTAGCT 1260
CAITCAGGGC CTTGCTCTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCATTTG 1320
TGTGCTGTG TTGTTGTTG ATGAAAAATA TAAATGATT GATTACATA AAAAAAATA 1380
AAAAAA
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Seq ID NO: B72 DNA sequence  
Nucleic Acid Accession #: CAT cluster

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45      1      11      21      31      41      51
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50    CTTTGTACTT GTCTTTTCTT TTTATTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA 120
CGCACTATGG CACGAGGCTC GTGCTGCTCG GCCAGGGCGA CTGGCGGATA AGGTCTTGTG 180
CGTGGCCTCG AGGCTTAAAA GTAGCAGTGG GCTTTGTGA AGGACAAAAT GGCAGTGGCG 240
GGCGGTGTAG GTCCCCCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG 300
TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTCTA 360
55    GAAAATAGCG TTTTCCAAAT GCCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC 420
AGGAATTACG CGCAGCTTGG AACCGAAGAG AGCTCTGTG TTGCAATGTT CAGCCCAACA 480
GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCAAGCCAG CGTTACAGTA 540
ATGTTCCAGC ATCTCATAAT CTATCCTGGG GAATTACGCT GCCTCCAGG GTGAATACAG 600
GTATTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGCTGTG TTCACTCCAG 660
60    AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC 720
ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGCTGTG TTCACTCCAG 780
GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAAATCTGT CTTGGAGGAC 840
ATCAGAAGGT GAATTTTCCA AGTCTTGGG CAACCTAGCT GTTGAAAGC TTTCTGGGTT 900
TGGGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTANGA CACTGGGAGC 960
65    CAATGAAACA GCAGTTGAGG GTTGTCTGTG TATCACATTT CTGTATTTTA TCACCCCTTT 1020
CCTGCAACAT TATTATCTG GAATCTACCT GCGCTTTTGT TTTTATGATA CAAGGGCTTG 1080
GTTTGTGTAC CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
TCCAAAGTGC TGGGATTGCA GGTGTGATTG ATGGCACCAC GACTTGTCTG CCTTCTTAC 1200
70    ATGATCCAGG CCCAGAACCC AAAGCTCAGG ACTGTATAGA TGACCACTTT CGTAAACTAC 1260
TGACCTAGCT TGTGTCGAAT TGTGTATGTA ACTTCCATA ACTCCACTTC GTGTCTGTTT 1320
CTCTGTATAC AGCCACCTTC TGTCCCGTTC ATGAGCCTTT AGGTCTCCAT TTGCATATTG 1380
CAATATCTAT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG 1440
TTCCCTTGAG GACTGSGCTGT CAATTTGTGT TGCTGTGTG GTGTGTGATG AAAATAATAA 1500
75    AATGATTGAT TACATAAAAA AAAAAAATAA AAAAAAATAA CAAAAAATAA 1560
CGCGGCGCTT TTCCCGGGG GCACAAAGTT ATAAACGCC GTCCATC
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Seq ID NO: B73 sequence  
Nucleic Acid Accession #: NM\_000222.1  
Coding sequence: 22..2952

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CTGCTCTTAC TGCTTCGCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120
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	CCGTCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGCACCTGA	TCCGGGCTTT	GTCAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACACGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCGAAGC	TTTTCTTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCACAGA	CCCAGAACTG	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGGCAT	CATGATCAAA	540
	AGTGTGAAC	GCGCTACCA	TGGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTCTG	CGGAAAAATT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAAGC	TGTGCTCTGT	660
	GTGTCTGTGT	CCAAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTAC	AGTGACGTGC	720
	ACAATAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAAAGTGGG	AAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGCTGACT	TCAATTATGA	ACGTACAGGA	840
	ACGTTGACTA	TCAGTTCAGC	GAGAGTTAAT	GATTCTGGAG	TGTTTATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACAACA	ACCTTGAAG	TAGTAGATAA	AGGATTCAAT	960
	AAATATCTCC	CCATGATAAA	CACATACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTG	1020
	ATTGTTGAAT	CAATGATTTG	CCCCAACCT	GAACACCAGC	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAGTAA	TATCAGATAC	1140
	GTAAGTGAAC	TTTATCTAAC	GAGATTAAAA	GGCACCAGAG	GAGGCACTTA	CACATTCTTA	1200
20	GTGTCCAATT	CTGACGTCAA	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAATCTCTGA	CTTACGACAG	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTG	1320
	CCAGAGCCCA	CAATGATTTG	GTATTTTGT	CCAGGAACTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGGATGTGCA	GACACTAAAC	TCACTGTGGC	CACGTTTGG	AAAGCTAGTG	1440
	GTTCAGAGTT	CTATAGATTG	TAGTGCATTG	AAGCACAATG	GCACGGTTGA	ATGTAAGGCT	1500
25	TACAACGATG	TGGGCAAGAC	TTCTGCCTAT	TTTAACCTTG	CATTAAAGG	TAACACACAA	1560
	GAGCAATCC	ATCCCCACAC	CCTGTTCACT	CCTTTGCTGA	TGTTTTCGT	AATCGTAGCT	1620
	GGCATGATGT	GCATTATTGT	GATGATTCTG	ACCTACAAAT	ATTTACAGAA	ACCCATGTAT	1680
	GAAGTACAGT	GGAGGTTTGT	TGAGGAGATA	AATGGAAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAACCTC	CTTATGATCA	CAATGGGAG	TTTCCAGAA	ACAGGCTGAG	TTTTGGGAAA	1800
30	ACCTGGGTG	CTGGAGCTTT	CGGGAAGGTT	GTTGAGGCAA	CTGCTTATGG	CTTAATTAAAG	1860
	TCAGATGCGG	CCATGACTGT	CGCTGTAAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGAAGCCG	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TTGTAATCA	CATGAATATT	1980
	GTGAATCTAC	TTGAGGCTG	CACCATTTGA	GGGCCACCC	TGTCATTAC	AGAATATTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTGAGA	AGAAAACGTG	ATTCATTIAT	TGTTTCAAAG	2100
35	CAGGAAGATC	ATGCAGAAGC	TGCACCTTAT	AGAAATCTTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGCCG	ACAAAGGAGC	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCCGCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAGGTGG	CAAGGGGCAT	GGCTTTCCTC	GCCTCCAAGA	ATTGTATTCA	CAGAGACTTG	2400
40	GCAGCCAGAA	ATATCCTCCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTTGGTCTA	2460
	CGCAGACACA	TCAAGAATGA	TTCTAATTAT	GTGGTTAAAG	GAAACGCTCG	ACTACCTGTG	2520
	AAGTGACCTG	CACCTGAAAG	CATTTTCAAC	TGTGTATACA	CGTTTGAAG	TGACGCTGGG	2580
	TCCTATGGGA	TTTTTCTTTG	GGAGCTGTTC	TCITTAGGAA	GCAGCCCTTA	TCTTGGAAATG	2640
	COGTTGGAAT	CTAAGTTCTA	CAAGATGATC	AAGGAAGGCT	TCCGATGCT	CAGCCTGAA	2700
45	CACGCACTG	CTGAATGTGA	TGACATAATG	AAGACTTGCT	GGGATGCAGA	TCCCCTAAAA	2760
	AGACCAACAT	TCAAGCAAAAT	TGTTTCACTA	ATTGAGAAGC	AGATTTCAGA	GAGCACCAAT	2820
	CATATTACT	CCAACCTTAG	AAACTGCAGC	CCCAACCGAC	AGAAGCCCGT	GGTAGACCAT	2880
	TCTGTGCGGA	TCAATTCTGT	CGGCAGCACC	GCTTCTCCT	CCGACCTCT	GCTTGTGCAC	2940
	GACGATGCT	GAGCAGAATC	AGTGTTTGGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCTTCCATGA	TGGTTATTTT	CTTTTCTTTC	AACTTGCATC	CAACTCCAGG	ATAGTGGGCA	3060
	CCCCACTGCA	ATCCTGTCTT	TCTGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTCATCAGC	3120
	CACCATCTGA	TTGCAAGGTT	TCCAACCTGA	TATATTCCCA	ATAGCAACGT	AGCTTCTACC	3180
	ATGAACAGAA	AACATTCTGA	TTTGGAAAAA	GAGAGGGAGG	TATGACTGGG	GGGCCAGAGT	3240
	CCTTTCCAAG	GCTTCTCCAA	TTCTGCCCAA	AAATATGGTT	GATAGTTTAC	CTGAATAAAT	3300
55	GSTAGTAATC	ACAGTTGGCC	TTCAGAACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
	AGCTGAAAC	CTAAGTCCCT	TATGTGGAAA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACT	GGCCTTAGA	AATCTAGTAT	TTTATGCTGG	GAATGAGACA	TAGGCCATGA	3480
	AAAAATGAT	CCCCAAGTGT	GAACAAAGAA	TGCTCTTCTG	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGGTTTT	TAAATAGAGT	TTGCTATTAG	AGCATTGAAT	TGGAGAGAAG	3600
60	GCCTCCCTAG	CCAGCACTTG	TATATACGCA	TCTATAAATT	GTCCGTGTTT	ATACATTGTA	3660
	GGGGAACAA	CCATAAGGTT	TGTTTCTGT	ATACAACCTT	GGCATTATGT	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACAG	TTAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAGCA	CAGTTGAAC	AAAATCTCCT	CTTTAGCTG	ATGAACCTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAATG	GCATTGTACT	CAATGGATT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCAGT	GCATGGCTCC	CACAGGAGTG	GGMAAACACT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAAATAAAGT	ATAGGTTTAG	CCTCCTTCGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTACGTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGTCCC	TGAGTCCAAG	AGGGTCTTCT	AGTACCTGAA	4140
	AAGTAACTTG	GCTTTCATTA	TTAGTACTGC	TCTTGTCTCT	TTTCACATAG	CTGTCTAGAG	4200
70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCACTTC	ACCTGCACTT	AAGGCACCTT	GTTATTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTACGACT	4380
	GTAGCCTGGA	TATTATTCTT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
	AACTCCCCCT	CCTCAGTCCC	CAATATAAAA	GGCAAAATGT	TACATGGCAG	AGTTTGTGTG	4500
75	TGTCCTTGAA	AGATTTCAGG	ATGTTGCCTT	TATGGTTTCC	CCCTTCTACA	TTTCTTAGAC	4560
	TACATTATAGA	GAACGTGTGC	CGTTATCTGG	AAGTAACCAT	TTGCACTGGA	GTTCTATGCT	4620
	CTCGCACTT	TCCAAAGTTA	ACAGATTTTG	GGGTTGTGTT	GTCAACCAAG	AGATTGTTGT	4680
	TGCGCACTACT	TGTCCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4800
80	TTGCCATACT	TTGTCGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4920
	AATGCTTTT	GAATATTCCC	AAGCCCATGA	GTCCCTGAAA	ATATTTTATA	TATATACAGT	4980
	AACTTTATGT	GTAAATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
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Seq ID NO: B74 protein sequence  
Protein Accession #: NP\_000213.1

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PGFVKWTFEI LDETENKNQN EWITEKAEAT NTGKYCTCNK HGLSNSIYVF VRDPKLLFLV 120
DRSLYKEDND DTLVRCPLTD PEVTNYSLKG CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAPKA VPVSVSKAS YLLREGEFT VTCTIKDVSS 240
SVYSTWKREN SQTKLQEKYN SWHHGDFNFE RQATLTISSA RVNDSGVFMC YANNTFGSAN 300
VTITLLEVVDK GFNIFPMIN TTVFVNDGEN VDLIVEYFAF PKPEHQWIY MNRTFTDKWE 360
DYPKSENESE IRYVSELHLT RLKGTGEGTY TFLVNSDVN AALAFNVYVN TKPEILTYDR 420
LVNGLQCQVA AGFPEPTIDW YFCPGTEQRC SASVLVVDVQ TLNSSGPPFG KLVVQSSIDS 480
SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG MNKEQIHPHT LFTPLLIGFV IVAGMMCIIV 540
MILTYKYLQK PMYEVQWKVV EEINGNNTYV IDPTQLPYDH KWEFFRNRLS FGKTLGAGAP 600
GKVVEATATG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLSYLGNH MNIVNLLGAC 660
TIGGPTLVIT EYCCYGDLIN FLRRKRDSPI CSKQEDHAEA ALYKMLLHSH ESSCSDSTNE 720
YMDMKPGVSY VVPTKADKRR SVRIGSYIER DVTPAIMEDD ELALDLEDDL SPSYQVAKGM 780
AFLASKNCHL RDLAARNILL THGRITKICD PGLARDIKND SNYVVKGNAR LPVKWMAPE 840
IFNCVYTFES DVWSYGIWLF ELFSLGSSPY PCMPVDSKPY KMIKEGFRML SPEHAPAE 900
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Seq ID NO: B75 DNA sequence  
Nucleic Acid Accession #: NM\_004456  
Coding sequence: 58..2298

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GAGTACATGC GACTGAGACA GCTCAGAGC TTCAAGCAG CTGATGAAGT AAAGAGTATG 180
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CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 300
GAGTGTTCGG TGACAGTGA CTGTGATTTT CCAACACAAG TCATCCCATT AAAGACTCTG 360
AATGCAGTTG CTTCACTACC CATAATGTAT TCTTGGTCTC CCCTACAGCA GAATTTTATG 420
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GATGTACTCT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAGTACA CGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAATTTTGT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
CATCTGGAGG ATCAGCAGGA TGATAAGAA AGCCGCCAC CTCGGAAT TCCTCTGTAT 720
AAAAATTTGG AGGCCATTTT CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAATAAAG 780
GAAAAATATA AAGAACTCAC CGAAGCAGC CTCCAGGCG CACTTCTCTC TGAATGTACC 840
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CGGATAAAGA CCCACACAAA ACGTCCAGGA GGGCGCAGAA GAGGACGGCT TCCCAATAAC 1140
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CCTGACTCT GTCTTACTTG TGGAGCCGCT GACCAATGGG ACAGTAAAAA TGTGCTCTG 1860
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AACAAAATTC GTTTTGCAAA TCATTGCGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCACAGGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTGCG CATCGAAGA 2280
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CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
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GCCTCTCAC CAGCTGCAAA GTGTTTGTGA CAGTGAATT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAATTTGAA AAAAAAATA AAAAAA

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Seq ID NO: B76 Protein sequence  
Protein Accession #: NP\_004447

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80      1      11      21      31      41      51
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KQRIQPVHII LTVSVSLRGT RECSVTSDDL PPTQVPLKLT LNAVASVPII YSWSPQLQNF 120
MVEDETVLHN IPYMGDEVID QDGTFFIEELI KNYDGKVVHD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDPEEREKQK KLEDRHDDK ESRPPRKFPK DKILEALISM FPDKGTAEL 240
KEKYKELTEQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRFC KYDCFLHPH 300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFPAALTA ERIKTPPKRP GRRRRRLPN 360

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NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEEEK KDETSSSSEA NSRCQTPIMM 420  
 KNPTEPPENV ENSGAEMSMF RVLIGTYIDN FCAIARLIGT KTCRQVYEFR VKESSIIAPA 480  
 PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPROPQ DSSPCVIAQ 540  
 NPCEKFCQCS SEQNRFPFGC RCKAQCNKQ CPCYLAVREC DPDLCLTCCA ADHWDKSNVS 600  
 CNKCSIQRGS KKHLLLPSPD VAGWGIFIKD PVQKNEFISE YCGEIIISQDE ADRRGKVYDK 660  
 YMCSEFLFNLN NDFVVDATRK GNKIRFANHNS VNPNCYAKVM MVNGDHRIGI FAKRAIQTCE 720  
 ELFVDYRYSQ ADALXYVGIE REMEIP

Seq ID NO: B77 DNA sequence  
 Nucleic Acid Accession #: NM\_007015  
 Coding sequence: 1..1005

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 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240  
 20 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300  
 TTTAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC 360  
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 ATTCTGTAGG TGGGCGCCCT GACCAACAG AGCATCTCCT CCAACTGGA AGGCAAGATC 480  
 ATGCCAGTCA AATATGAAGA AAATCTCTCT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540  
 GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAACCTCTGC GTGACCTTCC TATTTTCTGG 600  
 25 CTTAACCAA CCTATCCAAA AGAAATCCAG AGGGAAAGAA GAGAAGTGGT AAGAAAAATT 660  
 GTTCCAACCTA CCACAAAAG ACCACACAGT GGACCAAGGA GCAACCCAGG CGCTGGAAGA 720  
 CTGAATAATG AAACAGAGCC CAGTGTTCAA GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780  
 CCTTATCATC AGCAGGAAGG GGAAGCATG ACATTGAGC CTAGACTGGA TCACGAAGGA 840  
 30 ATCTGTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGACTCG TGAACCCCTG 900  
 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960  
 ATCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT 1020  
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTG 1080  
 ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGTTTATTC TTGCACTCT 1140  
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 AGTTTGCC

Seq ID NO: B78 Protein sequence  
 Protein Accession #: NP\_008946

1 11 21 31 41 51  
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 45 MTENSDKVP I ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60  
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 TGIKFAAGEK CYIKAKVKAR IPEVGAVTKQ SISKLEGGI MPVKYEENSL IWVAVDQPVK 180  
 DNSFLSSKVL ELCDGLPIFW LKPTYPEIKI RERREVRRI VPTTTRKPHS GPRSNPGAGR 240  
 LNNETRPSVQ EDSQAFNPDN FYHQEGESM TFDPRLDHEG ICCIECRSY THQKICEPL 300  
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Seq ID NO: B79 DNA sequence  
 Nucleic Acid Accession #: NM\_012449.1  
 Coding sequence: 66..1085

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 | | | | |  
 55 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60  
 AATTAATGGA AAGCAGAAA GACATCACAA ACCAAGAAGA ACTTTGAAA ATGAAGCCTA 120  
 60 GGAGAAATTT AGAAGAAGAC GATTATTGCG ATAAGGACAC GGGAGAGACC AGCATGCTAA 180  
 AAGACCTGT GCTTTTGCAT TTGCACAAA CAGCCCATGC TGATGAATT GACTGCCCTT 240  
 CAGAAGTTCA GCACACACAG GAATCTTTC CACAGTGCCA CTTGCCAATT AAAATAGCTG 300  
 CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTCTGAG GGAAGTAATT CACCTTTAG 360  
 CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAG AAAGTCTTGC 420  
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTACCTGCC AGGTGTGATA GCAGCAATTG 480  
 65 TCCAACCTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540  
 TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTTCG TGTACTGCAT GCAATTTATA 600  
 GTCTGTCTTA CCCAATGAGG CGATCCCTGA GATACAAGTT GCTAACTGG GCATATCAAC 660  
 AGGTCCAACA AAATAAGAA GATGCCCTGA TTGACATGA TGTTTGGAGA ATGGAGATT 720  
 ATGTGTCTCT GGAATTGTG GGATGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780  
 70 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTAGAGC AAGCTAGGAA 840  
 TTGTTCCCTC TCTACTGGGC ACAATACACG CATTGATTTT TGCCCTGGAAT AAGTGGATAG 900  
 ATATAAACA ATTTGTATGG TATACACCTC CACTTTTAT GATAGCTGTT TTCCTTCAA 960  
 TTGTTGCTCT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA 1020  
 75 AGATTAGACA TGGTTGGGAA GACGTACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080  
 TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTITAT CACCAACATT 1140  
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence  
 Protein Accession #: NP\_036581.1

1 11 21 31 41 51  
 | | | | |  
 80 MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLEQTA HADEFDCPSE 60  
 LQHTQELFPQ WHPPIKIAAI IASLTFLYTL LREVIHPLAT SHQYFYKIP ILVINKVLPM 120

VSITLLALVY LPGVIAAIVQ LHNQTKYKKF PHWLDKWLMT RKQFGLLSFF FAVLHAIYSL 180  
 SYPMRRSYRY KLLNWAYQQV QONKEDAWIE HDVVRMEIVV SLGIVGLAIL ALLAVTSIPS 240  
 VSDSLTWREF HYIQSKLGIV SLLGTIHAL IFANNKWIDI KQFVWYTPPT FMAVFLPIV 300  
 VLIFKSILEF PCLRKILKI RHGWEDVTIKI NKTEICSQL

Seq ID NO: B81 DNA sequence  
 Nucleic Acid Accession #: NM\_000684  
 Coding sequence: 87..1520

1 11 21 31 41 51  
 TGCTACCCCG GCCCGGCTT CTGGGGTGT CCCCAACCAC GGCCACAGCC TGCCACACCC 60  
 CCCGCCCCCG GCCTCCGAG CTGCGCATGG GCGCGGGGT GCTCGTCTG GGCGCCTCG 120  
 AGCCCGGTAA CCTGTCTCG GCGGCACCG TCCCGACCG GCGCGCCAC GGCGCGCGC 180  
 TGCTGGTGCC CGCGTCGCG CCGCTCTCT TGCTGCTCC GCGCAGGAA AGCCCGGAG 240  
 CGCTGTCTCA CAGTGGACA GCGGCGATGG GTCTGCTGAT GGCGCTCATC GTGCTGCTCA 300  
 TGTGGCGGG CAATGTCTG GTGATCGTGG CCATCGCCAA GACCGCGCG CTGCAGACGC 360  
 TCACCAACCT CTTTCATATG TCCCTGGCCA GCGCGACCT GGTCTGGGG CTGCTGGTGG 420  
 TGCCGTTCCG GGCCACCATC GTGGTGTGG GCGCTGGGA GTACGGCTCC TTCTTCTCG 480  
 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAC CATCGAGACC CTGTGTGTCA 540  
 TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCAAGAC GTGCTGACGC 600  
 GCGCGCGGC GCGGGGCTC GTGTGACCG TGTGGCCAT CTGCGCCCTG GTGTCTCTCC 660  
 TGCCCATCTT CATGCACTG TGGCGGCGG AGAGCGACGA GCGCGCGCG TGCTACAACG 720  
 ACCCAAGTG CTGCGACTTC GTACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT 780  
 CCTTCTACGT GCCCTGTGC ATCATGCGCT TCGTGTACCT GCGGGTGTTC CGCGAGGCCC 840  
 AGAAGCAGTC GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCTCGGCGCG CCAGCGCGCG 900  
 CGCCCTCGCC CTGCGCTCG CCGTCTCCG CGCCCGGCG GCGCGCGCG CCGCGCGCG 960  
 CGCGCGCGCG CGCGCCACC GCGCGCTGG CCAACGGGCG TGGGGTAAAG CGCGCGCCT 1020  
 CGCGCTCTGT GGCCCTACGC GAGCAGAAG CGCTCAAGAC GCTGGGCATC ATCATGGCG 1080  
 TCTTCAACGT CTGCTGGCTG CCTTCTTCT TGGCCAACGT GGTGAAGGCC TTCCACCGCG 1140  
 AGCTGGTGGC CGACCGCTC TCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCT 1200  
 TCAACCCAT CATCTACTG CCGAGCCCG ACTTCCGCA GGCCTCCAG GACTGTCTCT 1260  
 GCTGCGCGCG CAGGGCTGCC CGCGGCGCC ACGGACCCA CGGAGACCG CCGCGCGCT 1320  
 CGGGCTGTCT GCGCGGCGC GGACCCCGC CATCGCCCG GCGCGCTCG GACGACGAG 1380  
 ACGAGCATGT CGTGGGGCC ACGCGCCCG CGCGCTGCT GGAGCCCTG GCGCGCTGCA 1440  
 ACGCGGGGCG GCGCGGAGC AGCGACTCGA GCCTGGACGA GCGGTGCGC CCGGCTCG 1500  
 CCTCGGAATC CAAGGTGTAG GCGCGGCGC GGGCGCGGA CTCGCGCAC GGTCTCCAG 1560  
 GGGAAAGAG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAATCGA AGCCCAAT 1620  
 CTCGTCTGA ATCATCGAG GCAAAGAGAA AAGCCACGA CGTTGCACA AAAAGGAAAG 1680  
 TTTGGGAGG GATGGAGAG TGGCTTGTG ATGTTCCTG TTG

Seq ID NO: B82 Protein sequence  
 Protein Accession #: NP\_000675.1

1 11 21 31 41 51  
 MGAGVLVLGA SEPNLSSAA PLEDGAATAA RLLVPASPPA SLLPPASESP EPLSQWNTAG 60  
 MGLMALIVL LIVAGNLVLI VAIKTPRLQ TLNLFIMSL ASADLVMGLL VVPFGATIVV 120  
 WGRWEYGSFP CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSL TRARAGLVC 180  
 TVWALSALVS FLPLMHWRW AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240  
 AEVYLRVFER AQKQVKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPPPP RPAAAAATAP 300  
 LANGRACKRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF PLANVVKAFH RELVPRDLFV 360  
 PFNWLGYANS AFNPIIYCRS PFERKAFQGL LCCARRAARR RHATHGDRPR ASGLARPGP 420  
 PPSPGAASDD DDDVVGATP PARLLEPWAG CNGGAADSD SSLDEPCRFG FASESKV

Seq ID NO: B83 DNA sequence  
 Nucleic Acid Accession #: NM\_000729.2  
 Coding sequence: 2..421

1 11 21 31 41 51  
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 AGCCATGAAC AGCGCGTGT GCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCT 120  
 GACGAGCGCG GTGCTCCCG CAGATCCCG GGGCTCGGG CTGCAGCGG CAGAGGAGC 180  
 GCGCCGTAGG CAGCTGAGG TATGCGAGAG AACGGATGG GAGTCCCGAG CGCACCTGGG 240  
 CGCCCTGCTG GCAAGATACA TCCAGCAGG CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300  
 CGTTAAGAAC CTGCAGAAC TGGACCCAG CCACAGGATA AGTGACCGGG ACTACATGGG 360  
 CTGGATGGAT TTTGGCGCTC GCAGTGCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420  
 GCGCCATCA GCGCAACGGA AGCAACCTCC CAACCCAGAG GAGGAGAAAT AAGACAACAA 480  
 TCACACTCAT AACTCATTTG CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540  
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CAGTGCACAC CACACAGCT CACCAGAAGT 600  
 TGTGCAAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660  
 TATGCTATTA AAGGATTTC ATTCGTC

Seq ID NO: B84 Protein sequence  
 Protein Accession #: NP\_000720.1

1 11 21 31 41 51  
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEEAP RRLRVQSRT DGESEHLAGA 60  
 LLARYIQQAR KAPSGRMSIV KNLQNLDP SH RISDRYMGW MDFGRSSAE YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	<b>A1 DNA SEQUENCE</b>	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Gene name:	Hs.154210
	Unigene number:	M31210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	251-1396
	Coding sequence:	
15	TCTAAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG	60
	AACGCAACTT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA	120
	AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT	180
	CTCGCTCGC CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CGGCTTCTCT GGGGACACAG	240
	GGTTGGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCAGCGCA GCTCGGTCTC	300
	TGACTAGCTC AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT	360
	CAGGCGGAC AAGGAGAACA GCATTAAACT GACCTCGGTG GTGTTTCATT TCATCTGCTG	420
20	CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCOA	480
	CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTGTG CAGGAGTAGC	540
	CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CCGCCCACTG	600
	GTTTCTCGCG GAAGGGAGTA TGTTTGTGGC CCTGTCAAGC TCCGTGTTCG GTCTCTCTGC	660
	CATCGCCATT GAGCGTATA TCACAATGCT GAAATGAAA CTCACAACG GGAGCAATAA	720
25	CTTCGGCTCT TGTCTGTAA TCAGCGCTG CTGGGTCTAT TCCCTCATCC TGGGTGGCCT	780
	GCCTATCATG GGCTGGAAT GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCCGCT	840
	CTACCACAAG CACTATATCC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT	900
	CGTCACTCTG TACTCGAGAA TCTACTCCTT GGTCAAGACT CGGAGCGGCC GCCTGACGTT	960
30	CCGCAAGAAC ATTTCCAAG CCAGCGCAG CTCTGAGAAT GTGGCGCTCG TCAAGACCGT	1020
	AATTATCGTC CTGAGCGTCT TCATCGCCTG CTGGGCACCG CTCTTCATCC TGCTCTCTGT	1080
	GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCCTCTTC AGAGCGGAGT ACTTCTCTGT	1140
	GTAGCTGTG CTCAACTCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT	1200
	GGCTCGGGCC TTCACTCGGA TCATGTCTTG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG	1260
	CAAAITCAAG CGACCCATCA TCGCGGCGAT GGAATTGAGC GCGAGCAAT CCGACAATTC	1320
35	CTCCACCCCC CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAACCGT	1380
	CAACTCTTCT TCCTAGAACT GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTCG	1440
	CTGGCCACCC CAGTGTGTTG AAAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT	1500
	GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGCTGGTGT CGGCTGTGTT	1560
	TGGGTAGAGT TAGTTCTCTG GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCTC	1620
40	GGAATATATA TTCTACCCCC CTGGAGCTTT GATTTTGCA TGAGCCAAAG GTCTAGCATT	1680
	GTCAAGCTCC TAAAGGTTTC ATTTGGCCCC TCCTCAAGA CTAATGTCCC CATGTGAAAG	1740
	CGTCTCTTTG TCTGGAGCTT TGAGGAGATG TTTTCTCTCA CTTTAGTTTC AAACCCAGT	1800
	GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCCCTGTACA TCCACACCC CACCTCTCTC	1860
	TCCTTCTATA CCCTCTCTCA AGTTCCTTT ACTTTATACT TTAACCTACT GAGAGTTATC	1920
45	AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAT AGGCTATGTT GAGTACGTAG	1980
	GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAACAAT GTCCTTCCCT GAGGCCAAAG	2040
	TTTCCATGTA AGCGGGATCC GTTTTGTGGA ATTTGGTTGA AGTCACTTTG ATTCTTTAA	2100
	AAAACATCTT TCAATGAAA TGTGTTACCA TTTCATATCC ATTGAAGCCG AAATCTGCAT	2160
50	AAGGAAGCCC ACTTATCTA AATGATATTA GCCAGGATCC TTGTTGTCCT AGGAGAAACA	2220
	GACAAGCAAA ACAAGTGAA AACCGAATGG ATTAACTTTT GCAACCAAG GGAGATTCTT	2280
	TAGCAATGA GTCTAACAAA TATGACATCC GTCTTTOCCA CTTTGTGTA TGTATTTC	2340
	AGAATCTTGT GTGATTCAIT TCAAGCAACA ACATGTTGTA TTTTGTGTG TTAAGAGTAC	2400
	TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTTATGGA TTTTCTAAC	2460
	CCGTGTTTAA TTTTCTAGAA TCCACCTCT TGTGCCCTTA AGCATTACTT TAACGGGTAG	2520
55	GGAAACGCCG AACTTTTAAG TCCAGCTATT CATTAGATAG TAATTGAAGA TATGTATAAA	2580
	TATTACAAG AATAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC	2640
	CGAGAGATGT CTTGTTTTT TAAAAAGAAT AGTATTTAAT AGGTTTCTGA CTTTGTGGA	2700
	TCATTTTGCA CATAGCTTTA TCAACTTTA AACATTAATA AACTGATTTT TTTAAAG	
60	<b>A2 Protein sequence:</b>	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Gene name:	Hs.154210
	Unigene number:	M31210
	Probeset Accession #:	AAA52336
65	Protein Accession #:	none found
	Signal sequence:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Transmembrane domains:	plasma membrane
	Cellular Localization:	
70	1 11 21 31 41 51	
	MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSV VFILICCFII	60
	LENIFVLITI WKTKFHRPM YFIGNLALS DLLAGVAYTA NLLLSGATTY KLTQAQWFLR	120
75	EGSMFVALSA SVFSLIAIAI ERYITMLQMK LHNGSNPNRL PLLISACWVI SLILGGLPIM	180
	GWNCISALSS CSTVLPVLYHK HYILFCTTVF TLLLLSIVIL YCRIYSLVRT RSRRLTFRKN	240
	ISKASRSSEN VALLKTVIIV LSVFIACWAP LPFILLLDVG CKVKTCIDILF RAELYFLVLAV	300
	LNSGTNPPIY TLNKMERRA FIRIMSCCKC PSGDSAGKFK RPIIAGMEFS RSKSDNSSHP	360
	QKDEGDNPET IMSSGNVNSS S	
80	<b>A3 DNA SEQUENCE</b>	G protein-coupled receptor 51
	Gene name:	Hs.198612
	Unigene number:	AA452928
	Probeset Accession #:	NM_004624.1
	Nucleic Acid Accession #:	

Coding sequence:

1-2826 (underlined sequences correspond to start and stop codons)

```

5      1      11      21      31      41      51
|      |      |      |      |      |
ATGGCTTCCC CGCGGAGGTC CGGGCAGCCA GGGCGGCCGC CGCCGCGGCC ACCGCGGCCC 60
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GGCTGGGGGCG GGGGCGCCCC CGGCGCGCCG CCGAGCAGCC CGCGCTCTC CATCATGGGC 180
CTCATGCGCG TCACCAAGGA GGTGGCCAAG GGCAGCATCG GCGCGGTGT GCTCCCGCC 240
GTGGAATCGG CATCGAGCA GATCGGCAAC GAGTCACTCC TGCGCCCTTA CTTCCTCGAC 300
CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAAGGGT TGAAGCCTT CTACGATGCA 360
ATAAATACG GGCAGAACCA CTGATGGTG TTTGAGGCGC TCTGTCCATC CGTCACATCC 420
ATCATTCGAG AGTCCCTCCA AGGCTGGAAT CTGGTGACG TTTCTTTGCG TCAACCAAG 480
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CTGACGCAAG ACCTTCAGAG GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCTGTAT 660
GGCGAGGACA TTGAGATTTC AGACCCGAG AGCTTCTCCA ACGATCCCTG TACCAAGTGT 720
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GCAAAAGTGT TCTGTTGTGC ATACGAGGAG AACATGTATG GTAGTAAATA TCAGTGGATC 840
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CCCTGAGCT CCAAGCAGAT CAAGACCATC TCAGGAAAGA CTCACAGCA GTATGAGAGA 1020
GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGTA CGCTACGAT 1080
GGCATCTGGG TCATGCGCAA GACACTGCAG AGGGCCATGG AGACACTGCA TGCCAGCAGC 1140
CGGCACGAGC GGATCCAGGA CTCAACTAC ACGGACCACA CGCTGGGCG GATCATCTCT 1200
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GAGAGAATGG GGACCATTA ATTTACTCAA TTCAAGACA GCAGGAGGT GAAGTGGGA 1320
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TCCGAACCA CAAAGACAA GACCATCATC CTGGAGCAGC TGCAGAGAT CTCCCTACCT 1440
CTCTACAGCA TCCTCTCTGC CCTCACCATC CTCGGGATGA TCATGGCCAG TGCTTTTCTC 1500
TTCTTCAACA TCAAGAACCG GAATCAGAAG CTCATAAGA TGTGAGTCC ATACATGAAC 1560
AACCTTATCA TCCTTGGAGG GATGCTCTCC TATGCTTCCA TATTTCTCTT TGGCCTTGAT 1620
GGATCCTTTG TCTCTGAAA GACCTTTGAA ACACCTTGCA CGTCAAGAC CTGGATTCTC 1680
ACCGTGGGCT ACAGACGCGC TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCAAGCC 1740
ATCTTCAAAA ATGTGAAAT GAAGAAGAAG ATCATCAAGG ACCAGAACT GCTTGTGATC 1800
GTGGGGGCGA TGCTGCTGAT CGACCTGTGT ATCTGATCT GCTGGCAGCG TGTGGACCCC 1860
CTGCGAAGGA CAGTGGAGAA GTACAGCATG GAGCGGAGC CAGCAGGAGC GGATATCTCC 1920
ATCCGCCCCC TCCTGGAGCA CTGTGAGAAC ACCATATGA CCATCTGGCT TGGCATGCTC 1980
TATGCTTACA AGGACTTCT CATGTTGTTT GGTGTTTCT TAGCTTGGGA GACCCGCAAC 2040
GTCAGCATCC CCGCACTCAA CGACAGCAAG TACATCGGGA TGAGTGTCTA CAACGTGGGG 2100
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CAGCCTACC TCCATCCAT GAGAGGCGTG GACGCCAGCT GTGTCAAGCC CTGGTCAAG 2760
CCCACGCCCA GCCCGGCCA CAGACATGTG CCACCTCTCT TCCGAGTCAT GGTCTCGGGC 2820
CTGTAA

```

**A4 Protein sequence:**

Gene name: G protein-coupled receptor 51  
 Unigene number: Hs.198612  
 Probeset Accession #: AA452928  
 Protein Accession #: NP\_005449.1  
 Signal sequence: 1-42  
 Pfam domains: 7tm\_3 [481-754], ANF\_receptor [130-204]  
 Transmembrane domains: 22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744  
 Cellular Localization: plasma membrane

```

65      1      11      21      31      41      51
|      |      |      |      |      |
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IMPLTKEVAK GSGRGVLPV VELAIEQIRN ESLLRPYPLD LRLYDTECDN AKGLKAFYDA 120
IKYGNHLMV FGVCPSVTS IIAESLQGNV LVQLSFAATT PVLADKKKYP YPFRTVPSDN 180
AVNPAILKLL KHYQKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV 240
KKLKNQVRI ILQQDQDMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS 300
RCLRNKLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQOYER EYNNKRSVGW PSKFHGYAYD 360
GIWVIKTLQ RAMETHLASS RHQRIQDFNY TDHTLGRIL NAMNETNFFG VTQGVVFRNG 420
ERMGTIKFTQ FQDSREVRVG EYNNAVATLE IINDTIRPQG SEPPKDKTII LEQLRKISLP 480
LYSILSALT I LQMIMASAFI PFNIKRNQK LKMSPPYMN NLIIIGMML YASIFLFGLD 540
GSFVSEKFFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKIVKMKKK IIKDQKLLVI 600
VGGMLLDLC ILICWQAVDP LRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660
YAYKGLMLF GCLAWETRNV VSIPALNDSK YIGMSVYNVG IMCIIGAAS FLTRDQFNQ 720
FCIVALVII F CSTITLCLVF VPKLITLRN PDAATQNRFF QFTQNKQKED SKTSTSVTSV 780
NQASTSRLEG LQSENERLRM KITELDKLE EVTMLQDTP EKTITYIKQNH YQELNDILNL 840
GNFTSTGGG KALLKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLFILH 900
HAYLPSIGGV DASCVSFCVS PTASPRHRHV PPSFRVWVSG L

```

A5 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 ProbeSet Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCG GGGAACTACT TCACCAATGA 120
GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCAATCCCG GCGCCTGGCA 180
GTGTGAOCGG CTGCTGACTG GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
15 GTGCAAAATGT GGCCTCAACT TCTTCCCTGT TGCCAGCGCG ATCCATTGCA TCATTGGTGG 300
CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
AAACCTCTCT CTTCGTCTCA CCGCCCGCTA CCACTGCAAG AACGGCTCTT GTATTGACAA 420
GAGCTTCATC TGCATGTGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
AAGTTCTCAA GAACCCGCGA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
20 TTACCCAGCG ATCACCATTG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
CTGCTGGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGTGCCTGGT 660
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AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140
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AACTATCTCT GCATTCTCTT CCTCCCCAGT ACTTCAGAGA TGTTTTCTG CGCTCTCAGT 1260
TGACATGATC TGTGTGCGGT CTTTCTGTCT AGGTCACTCT TCCCTGGGA CCCGAGATCA 1320
CACCCCTCAT TTTACATTA TTCTGTCTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
AAATAGGCTG GAAGTAGGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
35 CGCTGGACCC AATTCCTCTT GCTGGGTAGT TACCTTAGAG CATTGGGGA TTGGGTTAG 1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTACCCCCCC CAAAAAATT CCATTGAGC 1560
ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAGT TTCAGCAGAG TCAGTGGCCA 1620
AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTTATTT TGGTTTGTG 1680
AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTG CCAAGAAATG 1740
40 CTCAATTCTA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCACTCTAA AATAGGCAGG 1800
GAGCCTCTCC CATGATTTTA TCCAGTTCT CAGCTCCTAA AATGCAAGCT GCCAAGACCC 1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTCTG GACTGTCAAC CTCCAGCTG 1920
ACCTGCCCTG AGCCAAGGA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
GTATGTCCTG GTGGCCCAAC CCGAGCCTGT CTGCTCAATT CATGCAGCCT CAACACTGGC 2040
45 CTCCAAAGTT CCCTTAACAC TTGCAAAATC CTTTTCCTCT GTGCATTGG ACTTGAGGAC 2100
ACTGGTTTCT TGGCAGGTTA TCCAGTTCT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
CTGCACGTG CAGCTCTCTC TTCCCAAGGT CCAATACCA GCACTCTAG TTAGAGTTAG 2220
GGTCAGGGTC AGGCTCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
50 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
TGAAACAGTG TGTGTGTTTT TTCCCTCTTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400
AGCTGTCTCT TTTTGTGTTT TTCCCTTAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460
ACACCTCTGC CCGCTGAGC CCGCTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
ACATTGTGTC ATTGTGTCAC TTTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580
55 AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700
AGGTGTGTTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760
CCACTCCGGG CAGCTGTGAC CCATTGAGG CTTCTTTCCG CAGCTGAAGA AATGTTAGT 2820
AACCTGTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGCTAAAG TGCATTTCAG 2880
TGATCCCTGT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTACAGAA 2940
60 AAGCTAGCCA CTGGTATTTT GTTTGTTTAA AAAAAAATAA GAAAGAAAGA AAGAAAGAAA 3000
AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
CTGAGTAATC CAATAAGGAA CTTTGTATGA CAGCCAGAA GTGTTAGAAC TCTGGCTGAA 3120
CATTTCATCT CCGTGTGATC AGAAGGCTT TATTTCTCCC TTTGATGGGG CCGCTTCTC 3180
TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
65 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT 3300
AGATAAGGGA TGCTTAATAA TGCTTTTAA AAACAAACAG GGACATTTT ATTATAGATT 3360
TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGGC GGCAGGGTTT 3420
TTTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
70 TTTTAACTC ATTTCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCA 3540
AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600
AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
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GAAAGGTTGT GTGTCGTGTC TTTTGTGTTT TTGGTTAGGC TTGCTTTTGT TTTTAAAT 3780
75 TTATACCTTC TAATAAATTT GCAGTTTCAT TCTTCTGTTT TGTGCAAAWG GWMCTAMARM 3840
AAMMAAAAC ANWTTGGGG GGGCTGGGC CTCGGAAAAA GTTTTTAAAC CCATCTCGGG 3900
TGGGGCGCGG GGGCCCAAGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAA 3960
GAAACCTGG CCAAGAAAAA GGTGGCGAGA ATTTCTCCAC CCAGAAAAAA ACGCGCGGG 4020
GGAACCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGC 4080
80 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

```

A6 Protein sequence:

Gene name: ESTs

Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51  
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECPKAKSK CGPTFFPCAS GIHCIIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSP ICDGQNNQD NSDEESSCESS QEPGSGQVVF TSENQLVYVP SITYAIIGSS 180  
 15 VIFVLVALL ALVLHQKRR NMLMTLPVHR LQHPVLLSRL VLDHPHHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

20 A7 DNA SEQUENCE  
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Nucleic Acid Accession #: NM\_002205  
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51  
 ATGGGGAGCC GGACGCCAGA GTCCCTCTC CACGCCGTGC AGCTGGCGTG GGGCCCCCGG 60  
 CGCGACCCC CGCTSSSTGCC GCTGCTGTG CTGCTSSSTG CGCCGCCACC CAGGCTCGGG 120  
 GGCTTCAACT TAGACGCGGA GGCCCCAGCA GTACTCTCGG GGCCCCCGGG CTCCTCTTC 180  
 GGATTCTCAG TGGAGTTTAA CCGCCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240  
 CCCAAGGCTA ATACCAAGCA GCCAGGAGTG CTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCCTCGGCT 300  
 35 TGGGGTGCCA GCCCCACACA GTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCCTCGGCT 360  
 CTGGAGTCTC CACTGTCCAG CTCAGAGGGA GAGGAGCCGT TGGAGTACAA GTCCCTTGCA 420  
 TGGTTCCGGG CAACAGTTCC AGCCCATGGC TCCTCCATCT TGGCATGGC TCCACTGTAC 480  
 AGCTGGGCGA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540  
 GATAACTTCA CCCGAATTCG GGAGTATGCA CCTGCGCGCT CAGATTTTCA CTGGGAGCA 600  
 40 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGGAGTTCA CCAAGACTGG CCGTGTGGT 660  
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720  
 ATTGCAGAA CTATTATCCC GGAGTACAGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 840  
 CGCCAGGCCA GTTCCATCTA TGTATGACAG TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 900  
 45 TTCACTGTCA CCATCCTTAA TGGCTCAGAC ATTGCATCCC TCTACAATCT CTCAGGGGAA 960  
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGCATCCC TCTACAATCT CTCAGGGGAA 1020  
 CAGATGGCTC CCTACTTTGG CTATGCAAGT GCGGCCACAG ACCTCAATGG GGACGGGCTG 1080  
 GATGACTTGC TGGTGGGGGC ACCCTGTGTC ATGGATCGGA CCCCTGAAGG GCGGGCTCAG 1140  
 GAGGTGGGCA GGGTCTACGT CTACCTGAGC CACCCAGCCG GCATAGAGCC CAGCCGCCAC 1200  
 50 CTTACCTTCA CTGGCCATGA TGAGTTTGGC GGCATCGGGG CTCCCTTTGG TGGGAGAGCC 1260  
 GACCTGGACC AGGATGGCTA CAATGATGTG GGCATCGGGG CTCCCTTTGG TGGGAGAGCC 1320  
 CAGCAGGGAG TAGTGTGTGT ATTTCTGGGG GGCAGGAGAG GGCTGGGCTC TAAGCCTTCC 1380  
 CAGGTTCTGC AGCCCTCTGT GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1440  
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCCTTTGG 1500  
 55 GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CCGTAGTGGG GAACCTGTG 1560  
 ATCTTCCCGC CCATGTTCAA CCGAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1620  
 GCGTGCATCA ACCTTAGCTT CTGCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1680  
 GGTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1740  
 CTGTCTCTGG CCTCCAGGCA GGCAACCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1800  
 60 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAAGG AGTCAGAATT TCGAGACAAA 1860  
 CTCTCGCCGA TTCACTCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1920  
 CACGGCCTCA GSCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1980  
 ATCTGTCTGG ACTGTGGAGA AGACAACATC TGTGTGCTTG ACCTGCAGCT GGAAGTGT 2040  
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC 2100  
 65 CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCAACCG CCCTCCAGAG 2160  
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2220  
 TTTGCGGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGAGGA 2280  
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGACAC TAAGAAACC 2340  
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2400  
 70 TCCTTTGGCC TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCGAAGCCT 2460  
 GAGGCACTGC TATTCCTCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2520  
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCC CAGCTCTAT 2580  
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 GTGACCAGAG TTAACGGACT CAATGTCACC ACCAATCACC CCATTAAACC AAGGGGCTG 2700  
 75 GAGTTGGATC CCGAGGGTTC CCTGCAACAC CAGCAAAAAC GGAAGCTCC AAGCGCAGC 2760  
 TCTGCTTCTT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2820  
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTGTG TTTCCAGTGT 2880  
 TGGGCCAAGA CTTTCTGTGA GCGGGAGCAC CAGCCATTTA GCTGCAAGT TGAGGCTGTG 2940  
 TACAAGGCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCCA AAAAGAGCGT 3000  
 80 CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGGCT CCACTGTGG 3060  
 ATCATCATCC TAGCCATCCT GTTGGGCTC CTGCTCTAG GTCTACTCAT CTACATCCTC 3120  
 TACAAGCTTG GATTCTTCAA ACCTCCCTC CCATATGGCA CCGCATGGA AAAAGCTCAG 3180  
 CTCAGGCTC CAGCCACCTC TGATGCTGA

**A8 Protein sequence:**

5 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Protein Accession #: NP\_002196  
 Signal sequence: 1-42  
 10 Transmembrane domains: 998-1020  
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036  
 Cellular Localization: plasma membrane

15 1 11 21 31 41 51  
 MGSRTPESEL HAVQLRWGPR RRPPLLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGGSFF 60  
 GPSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120  
 20 LESSLSSSSG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVTCTYLSL 180  
 DNPTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ QQILSATQEQ 240  
 IAESYYPEVL INLVQQLQQT RQASSIYDSS YLGYSVAVGE FSGDDTDEFV AGVPKGNLTY 300  
 GYVITLNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DLLLVGAPLL MDRTPDGRPQ 360  
 EVGRVYVYIQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420  
 25 QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGDRDLGNG YPDILVGSFG 480  
 VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540  
 GFTVELQLDW QKQKGGVRRR LFLASRQATL TQTLLEIONGA REDCREMKIY LRNESEFRDK 600  
 LSPHIALNLF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAP ILLDCGEDNI CVPDLQLEVF 660  
 GEQNHVYLGQ KNALNLTFAH QNVGEGGAYE AELRVTPAPE AEYSGLVHRP GNFSLSLCDY 720  
 30 FAVNQSRLLV CDLGNPMKAG ASLWGGRLPT VPHLRDTKKT IQDFQILSK NLNNSQSDV 780  
 SFRLSVEAQA QVTLLNGVSKP EAVLFPVSDW HPRDQPKQEE DLGPAVHHVY ELINQGPSSI 840  
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QQKREAPSR 900  
 SASSGPGILK CPEAECFRLR CELGPLHQE SQSLQLHFRV WAKTELQREH QPFSLQCEAV 960  
 YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020  
 35 YKLGFFKRSL PYGTAMEKAQ LKPPATSDA

**A9 DNA SEQUENCE**

40 Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Nucleic Acid Accession #: NM\_002211.1  
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 ATGAATTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT 60  
 CAACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120  
 50 CAGGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180  
 TCTGCACGAT GTGATGATT AGAAGCCTTA AAAAAGAAAG GTTGCCCTCC AGATGACATA 240  
 GAAATCCCA CAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAAACCA CCGTAGCAAA 300  
 GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCA CAAGTTGGTT 360  
 TTGCGATTAA GATCAGGGGA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC 420  
 55 TATCCCATG ACCCTTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTGGAG 480  
 AATGTAAGAA GTCTTGAAG AGATCTGATG AATGAAATGA GGAGGATTAC TTCGGACTTC 540  
 AGAATTGAT TTGCTCTATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600  
 GCTAAGCTCA GGAACCTTG CACAAGTGAA CAGAACTGCA CCAGCCCAT TAGCTACAAA 660  
 AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGG AAAACAGCGC 720  
 60 ATATCTGAA ATTGGATTG TCCAGAAGGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780  
 TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840  
 GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATG TTTTACCAAA TGAATGGACAA 900  
 TGTCACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960  
 CACCTTGTCC AGAAACTGAG TGAAAATAAT ATTACAGCAA TTTTGCAGT TACTGAAGAA 1020  
 65 TTTACAGCTG TTTACAGGA GCTGAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080  
 TCTGCAAAAT CTAGCAATGT AATTCAGTTG ATCATTGATG CATACAATTC CCTTTCCTCA 1140  
 GAAGTCATT TCGAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200  
 TCGAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCCATT 1260  
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 70 GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGTTTAT TCTTCAGTAC 1380  
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 GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560  
 AGTTCAGAAA TCTGCAGTAA CAATGGAGAG TGCCTCTGCG GACAGTGTGT TTGTAGGAAG 1620  
 75 AGGGATAATA CAAATGAAAT TTATTCTGGC AAATCTCGG AGTGTGATAA TTTCAACTGT 1680  
 GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGTTGTTT GCAAGTGTG TGTGTGTGAG 1740  
 TGCAACCCCA ACTACATCGG CAGTGCATGT GACTGTTCTT TGGATACTAG TACTGTGAA 1800  
 GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTCGG AGTGTGTGT CTGTAAGTGT 1860  
 ACAGATCCGA AGTTTCAAGG GCAAACGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920  
 80 GCTGAGCATA AAGAAATGTT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980  
 TGCAACAGG AATGTTCTTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTAACC 2040  
 CAGCGGTGCC AACCTGATCC TGTGTCCCAT TGTAAAGGAGA AGGATGTTGA CGACTGTTGG 2100  
 TTCTATTTTA CGTATTCACT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAA 2160  
 CCAGAGTGTC CCACTGGTCC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220

GTTCTTATTG GCCTTGCAAT ACTGCTGATA TGAAGCTTT TAATGATAAT TCATGACAGA 2280  
 AGGGAGTTTG CTAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT 2340  
 CCTATTATA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGG AAAATGA

# **A10 Protein sequence:**

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Protein Accession #: NP\_002202.1  
 Signal sequence: 1-21  
 Transmembrane domains: 732-754  
 INB domain: 34-464  
 PSI domain: 26-76  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MNLQPIFWIG	LISSVCCVFA	QTDENRCLKA	NAKSCGECIQ	AGPNCGWCTN	STFLQEGMPT	60
SARCDLEAL	KKKGCPDDI	ENPRGSKDIK	KKNVNTNRSK	GTAELKPED	ITQIQPQQLV	120
LRLRSGEPT	FTLKPKRAED	YPIDLYYIMD	LSYSMKDDLE	NVKSIGTDLIM	NEMRRITSDF	180
RIGFGSFVEK	TVMPIYSTTP	AKLRNPCTSE	QNCTSPFSYK	NVLSLTNKGE	VFNELVKGQR	240
ISGNLDSPEG	GFDAIMQVAV	CGSLIGWRNV	TRLRVFSTDA	GFHFAGDGKL	GGIVLPNDGQ	300
CHLENNMYTM	SHYVDYPSIA	HLVQKLSENN	IQTIFAVTEE	FQPVYKELKN	LIPKSAVGTL	360
SANSSNVQL	IIDAVNSLSS	EVILENGKLS	EGVTISYKSY	CKNGVNGTGE	NGRKSNSISI	420
GDEVQFEISI	TSNCKPKKDS	DSFKIRPLGF	TEEVEVILQY	ICECECQSEG	IPESPKCHEG	480
NGTFECGACR	CNEGRVGRHC	ECSTDENVSE	DMDAYCRKEN	SSEICSNNGE	CVCQCVCVRK	540
RDNTEIYISG	KFCECDNFNC	DRSNGLICGG	NGVCRCRCE	CNPNYTGSAK	DCSLDTSTCE	600
ASNGQICNGR	GICEGVCCKR	TDPKFQGGTC	EMCQTCGLVC	AEHKECVQCR	AFNKGEKKDT	660
CTQECSEYFNI	TKVESRDKLP	QPVQPDVSH	CKEKDVDDCW	FYFTYSVNGN	NEVMVHVVEN	720
PECPTGPDII	PIVAGVVGAI	VLIGLALLLI	WKLLMIHNR	REFAKFEKEK	MNAKWDVTGEN	780
PIYKSAVTTV	VNPKYEGK					

## **All DNA SEQUENCE**

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGATTGCTT	CACAGTTTCT	CTCAGCTCTC	ACTTTGGTGC	TTCTCATTAA	AGAGAGTGGA	60
GCTCGGTCTT	ACAACACCTC	CACGGAAGCT	ATGACTTATG	ATGAGGCCAG	TGCTTATTGT	120
CAGCAAAAGT	ACACACACCT	GGTTGCAATT	CAAAACAAG	AAGAGATTGA	GTACCTAAAC	180
TCCATATTGA	GCTATTCAAC	AAGTTATTAC	TGGATTGGAA	TCAGAAAAGT	CAACAATGTG	240
TGGGTCTGGG	TAGGAACCCA	GAAACCTCTG	ACAGAAGAAG	CCAAGAAGTG	GGCTCCAGGT	300
GAAACCAACA	ATAGGCAAAA	AGATGAGGAC	TGCGTGGAGA	TCTACATCAA	GAGAGAAAAA	360
GATGTGGGGA	TGTGGAATGA	TGAGAGGTGC	AGCAAGAAGA	AGCTTGCCCT	ATGCTACACA	420
GCTGCCTGTA	CCAATACATC	CTGCAGTGGC	CACGGTGAAT	GTGTAGAGAC	CATCAATAAT	480
TACACTTGCA	AGTGTGACCC	TGGCTTCAGT	GGACTCAAGT	GTGAGCAAAT	TGTGAAGTGT	540
ACAGCCCTGG	AATCCCTCTG	GCATGGAAGC	CTGGTTTGCA	GTACCCCACT	GGGAAACTTC	600
AGCTACAATT	CTTCCTGCTC	TATCAGCTGT	GATAGGGGTT	ACCTGCCAAG	CAGCATGGAG	660
ACCATGCACT	GTATGTCTCT	TGGAGAATGG	AGTGTCTCTA	TTCCAGCCTG	CAATGTGGTT	720
GAGTGTGATG	CTGTGACAAA	TCCAGCCAAT	GGGTTCGTGG	AATGTTTCCA	AAACCTGGGA	780
AGCTTCCCAT	GGAAACACAC	CTGTACATTT	GACTGTGAAG	AAGGATTGTA	ACTAATGGGA	840
GCCAGAGGCC	TTCACTGTAC	CTCATCTGGG	AATTGGGACA	ACGAGAAGCC	AACGTGTAAA	900
GCTGTGACAT	GCAGGGCCGT	CCGCCAGCCT	CAGAAATGGT	CTGTGAGGTG	CAGCCATTCC	960
CCTGCTGGAG	AGTTCAACCT	CAAAATCATC	TGCAACTTCA	CCTGTGAGGA	AGGCTTCATG	1020
TTGCAGGGAC	CAGCCAGGT	TGAATGCACC	ACTCAAGGGC	AGTGGACACA	GCAAAATCCCA	1080
GTTTGTGAAG	CTTTCCAGTG	CACAGCCTTG	TCCAACCCCG	AGCGAGGCTA	CATGAATTGT	1140
CTTCCTAGTG	CTTCTGGCAG	TTTCOGTTAT	GGGTCCAGCT	GTGAGTTCTC	CTGTGAGCAG	1200
GGTTTGTGT	TGAAGGGATC	CAAAAGGCTC	CAATGTGGCC	CCACAGGGGA	GTGGGACAA	1260
GAGAAGCCCA	CATGTGAAGC	TGTGAGATGC	GATGCTGTCC	ACCAGCCCCC	GAAGGGTTTG	1320
GTGAGGTGTG	CTCATTCCCC	TATTGGAGAA	TTCACTTACA	AGTCTCTCTG	TGCTTTCAGC	1380
TGTGAGGAGG	GATTTGAATT	ATATGGATCA	ACTCAACTTG	AGTGACATC	TCAGGGACAA	1440
TGGACAGAAG	AGGTTCTCTC	CTGCCAAGTG	GTAATAATGT	CAAGCCTGSC	AGTTCGCGGA	1500
AAGATCAACA	TGAGCTCTCAG	TGGGGAGCCC	GTGTTTGCCA	CTGTGTGCAA	GTTCGCTGTG	1560
CCTGAAGGAT	GGAGCTCTCA	TGGCTCTGCA	GCTCGGACAT	GTGAGGCCAC	AGGACACTGG	1620
TCTGGCCTGC	TACCTACCTG	TGAAGCTCCC	ACTGAGTCCA	ACATTCCTCT	GGTAGCTGGA	1680
CTTCTGCTG	CTGACTCTC	CCTCTGACA	TTAGCACCAT	TTCTCTCTG	GCTTCGGAAA	1740
TGCTTACGGA	AAGCAAGAAA	ATTTGTTCTT	GCCAGCAGCT	GCCAAAGCCT	TGAATCAGAC	1800
GGAAGCTACC	AAAAGCCTTC	TTACATCCTT	TAA			

## **A12 Protein sequence:**

Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 Transmembrane domains: 555-573  
 C-lectin domain: 23-139



Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKEEIEYLN 60  
 SILSYSPSY WIGIRKVVNV WVVGTQKPL TEEAKNWAPG EPNRQKDED CVEIYIKREK 120  
 DVGMMNDERC SKKLALCYT AACTNTSCSG HGEVETINN YTCKDPGFS GLKCEQIVNC 180  
 10 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
 ECDVATNPAN GFVECFQNPQ SFPWNTTCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNFTCEEGFM LQGPQVVECT TQGGWTQIIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GPVLKGSKRL QCGPTGEWDN 420  
 EKPTCEAVRC DAVHQPPLGL VRCASPIGE FTYKSSCAPS CEEGFELYGS TOLECTSQGQ 480  
 15 WTEVPVSCQV VKCSSLAVPG KIMMSCSGEP VFGTVCKFAC PBGWTNLGSA ARTCGATGHW 540  
 SGLLPTCEAP TESNIPLVAG LSAAGLSLIT LAPFLWLRLK CLRRAKKFVP ASSCQSLESD 600  
 GSYQKFSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60  
 CCGAGTTTG AGGTGGGCAC CTGGATCAAA ATCACCTTA TTCTGGTGA CTGATCATC 120  
 30 TTCGTGATGG GCCTTCTGGG GAACAGCGCC ACCATTCCGG TCACCCAGGT GCTGAGAAG 180  
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGACATC 240  
 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC 300  
 ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360  
 GCTACGCTGC TGCACTGTCT GACACTCAGC TTGAGCGCT ACATCGCCAT CTGTACACCC 420  
 35 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480  
 GTCACCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540  
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGG CCACCCAGAG 600  
 CAGCCCGAGA CCTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660  
 CAGTCCAGCA TCTTCGGGCG CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720  
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780  
 ACGCGGCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGCGAG 840  
 ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG 900  
 ATTGAGGAGA TCATGGCTGC GGCCAAACCC AAGCAGACT GGACGAGTTC CTACTTCCGG 960  
 CGGTACATGA TCTCTCTCCC CTTCGCGAG AGTTTTCT ACCTCAGTTC GGTCAACAAC 1020  
 45 CGCTCTCTGT ACACGGTGTCT CTGCGAGCAG TTTGCGGGG TGTTCTGTGA GGTGCTGTGC 1080  
 TGCCGCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGGTGACA TGCGCACTCC 1140  
 ACCACCGACA GCGCCCGCTT TGTGAGCGC CGTTGCTCT TCGCGTCCG GCGCCAGTCC 1200  
 TCTGCAAGGA GAACGTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260  
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCGACC 1320  
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm 1 [72-172, 224-344]  
 60 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 Cellular Localization: plasma membrane

65 1 11 21 31 41 51  
 MASPSLPDSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTOVLQK 60  
 KGYLQKEVTD HNVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLCKL HTFLFEACSY 120  
 ATLLHLVTL FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTBYPL 180  
 VNVPSHRLT CNRSSTRHHE QPETSNNMSIC TNLSSRWTVF QSSIFGAFV YLVVLLSVAF 240  
 70 MCMNMQVLM KSQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIV TLAVCWMPNQ 300  
 IRRIMAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVTVQLC 360  
 CRLSLQIANE EKRLRVHAHS TDSARFVQR PLLFASRRQS SARTEKIPL STPQSEAEPO 420  
 SKSQSLSLSE LEPNSGAKPA NSAAENGFOE HEV

A1 ProstateA15 DNA sequence

80 Gene name: CBGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGGTCGCGG	CACACCTCCC	CGGCGCGCG	CGGCCACGCG	CGGCACTCCG	CGGCTCTGCG	60
	CCGCAACCGC	TGAGCCATCC	ATGGGGGTCC	CGGGCCGCAA	CGGTCCCGGG	CGGGCTCGGG	120
5	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCGCG	CACTGCTGCT	GCTGGCGGGG	CGCGTCCGCG	180
	CGGGTCGGGG	CGGTGCGCGG	GGGCGCGCAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCGAGCGCC	CTGTGTGAGA	ACACACCCAC	CTCCTACAAG	TGCTCCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTTTGA	ATATTCCAGG	CAATTATGCT	TGCACTTGTT	420
10	TGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCCTGG	480
	AGAACAATGG	CGGCTGCCAG	CATACCTGTG	TCAACGTGAT	GGGGAGCTAT	GAGTGTCTGT	540
	GCAAGGAGGG	GTGTTTCTCT	AGTGACAATC	AGCACACCTG	CATTCAACCG	TCCGAAGAGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCACAT	CTGCAAGGAG	GCCCAAGGGG	660
	GCAGCGTCGC	CTGTGAGTGC	AGGCTGCGTT	TTGAGCTGGC	CAAGAACCAG	AGAGACTGCA	720
15	TCCTGACCTG	TAAACATGGG	AACGGTGGGT	GCCAGCAGTC	CTGTGACGAT	ACAGCCGATG	780
	GCCAGAGCTG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCTTG	840
	AGCGAGAGGA	CAGTGTCTGT	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAAACCGGT	GAACCGCGGG	CTGCTCATGG	AAACGTGTGC	TGTCAACAA	GGAGGCTGTG	960
	ACCGCACCTG	TAAAGTACTT	TGACAGGTTG	TCCACTGCGG	TTGTCTCTGT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAGAGCA	TGTAAAGATA	TTGATGAGTG	CCAGACCCCG	AATGGAGGTT	1080
	GTGATCATTT	CTGCAAAAAC	ATCGTGGGCA	GTGTTGACTG	CGGCTGCAAG	AAAGGATTTA	1140
	AATTATTAA	AGATGAGAAG	TCTTGCCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCAAG	CTGCATCAAC	CACCTGCGCA	CATTGCTTTG	TGCTTGCAAC	CGAGGGTACA	1260
25	CCCTGTATGG	CTTCACCCAC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
	GTGACGAGGT	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGCCAC	CCTGGGTACA	1380
	AGCTCCACTG	GAATGAAAAA	GACTGTGTGG	AAGTGAAGGG	GCTCTGCGCC	ACAAGTGTGT	1440
	CACCCCGTGT	GTCCCTGACG	TGCGGTGAAG	GTGGTGGAGG	AGAGCGGTGC	TTCCTCAGAT	1500
	GTCACTCTGG	CATTCACTTC	TCTTCAGATG	TCACCACCAT	CAGGACAAGT	GTAACCTTTA	1560
30	AGCTAAATGA	AGGCAAGTGT	AGTTTGAATA	ATGCTGAGCT	GTGTCGCGAG	GGTCTGCGAC	1620
	CAGCACTACC	AGAGAGAGCAC	AGCTCAGTAA	AAGAGAGCTT	CGCTACGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAATCAAGTC	CCAGGAGGCC	CTGGCCGACC	AAGCACCCTT	AAGGAATATG	1740
	TTATCACTGT	TGAGTTTGAG	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGCGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
35	AGGCCGTCGA	CAGGGAGCAG	TTTCACCTCC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
	AAAAGCCTCC	CAGAACATCT	GAAGCCGAGG	CAGAGTCTGT	TGGAGTGGGC	CAGGGTCATG	1980
	CAGAAAACCA	ATGTGTCACT	TGCAAGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAACGCT	2040
	GCATTTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATCTT	GGGGCCCTGA	AGACCCGAGA	AGCTTGGAAT	ATGCTGAAAT	2160
40	GTGGAGGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCACTT	TGCCAGCTCT	2220
	GTGCCCTGGG	CAGGTTCCAG	CCTGAAGCTG	GTGCAACTTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAACATCACT	GGAGCTACTT	CCTTTTCAGGA	CTGTGAAACC	AGAGTTCAAT	2340
	GTTCACCTGG	ACATTTCTAC	AACACCACCA	CTCACOGATG	TATTCGTGTC	CCAGTGGGAA	2400
	CATACCAGCC	TGAATTTGGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAT	ACTACGACTG	2460
45	ACTTTGATGG	CTCCACAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
	GAGATTTTAC	TGGGTACATT	GAATCCCCAA	ACTACCCAGG	CAATTACCCA	GCCAACACCG	2580
	AGGTACCTGG	GACCATCAAC	CCACCCGCCA	AGCGCCGCGT	CCTGATCGTG	GTCCCTGAGA	2640
	TCCTCTGCGC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAAT	2700
	CCATTTCTGT	GACAACATAT	GAACCTGCGC	AGACCTACGA	ACGCCCCATC	GCCTTCACCT	2760
50	CCAGGTCAAA	GAAGCTGTGG	ATTCAAGTCA	AGTCCAATGA	AGGGAACAGC	GCTAGAGGGT	2820
	TCCAGGTCCC	ATACGTGACA	TATGATGAGG	ACTACAGGGA	ACTCATTGAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAACC	ATCAGGAAT	ACTTAAGGAT	AAGAACTTTA	2940
	TCAAGGCTCT	GTGTTGATGC	CTGGCCCATC	CCCAGAACTA	TTTCAAGTAC	ACAGCCGAGG	3000
	AGTCCCGAGA	GATGTTTCCA	AGATGTTTCA	TCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
55	TTTTGAGACC	TTACAATGTA	CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
	GGTGTGGTGG	ACAGAGCTGT	CTTCTCTCTG	CATGTGAGCA	CAGTGGGATA	TTGCTGCCTC	3180
	CGTATCAGT	GACTCATGAT	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GAACCTGGTT	TTTCTTTCCC	AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGCTCT	GGATAGATCA	CGGCTGGCTG	GAGCTGGACT	3360
60	TTGGTCAGCC	TAGGTGAGAC	TCACCTGTCC	TTCTGGGGTC	TTACTCTCTC	TCAAGGAGTC	3420
	TGTAGTCCAA	AGGAGGCCAC	AGAATAAGCT	GCTTATTCTG	AAACTTCAGC	TTCTCTAGC	3480
	COGGCCCTCT	CTAAGGGGAGC	CCTCTGCAGT	OGTGTGCAGG	CTCTGACCAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCTGCGAGG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGATCC	CAGGAACCTG	3660
65	AGTTCTAAGC	AGTGTCTGCT	AAAAAATAAA	GCAGAAAGAA	TTAGAAATAA	ATAAAAACTA	3720
	AGCACTTCTG	GAGACAT					

## A16 Protein sequence

Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like\_domains [49-84,132-167,177-213,286-321,407-442]  
 CUB\_domain [809-918]  
 Cellular Localization: may be secreted

	1	11	21	31	41	51	
80	MGVAGNRNRP	AAWAVLLLLL	LLPPLLLLLL	AVPPGRGRAA	GPQEDVDECA	QGLDDCHADA	60
	LCQNTPTSYK	CSCKPGYQGE	GRQCEDIDEC	GNELNGGCVH	DCLNIPGNIR	CTCPDGFMLA	120
	HDGHNCLDWD	ECLNNGGQ	HTCVNVMGYS	ECCCKEGFPL	SDNQHTCIHR	SEEGLSGMNK	180
	DHGCSHICKE	APRGSVACBC	RPGFELAKNQ	RDCILTCNHG	NGGQHSQSD	TADGPECSCH	240
	PQYKMHDTGR	SCLEREDTVL	EVTESNITTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300

STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGPTH CGDTNECSIN NGGCOQVCVN 420  
 TVGSYEQCH PGYKLHNKK DCVEVKGLLP TSVSPRVLH CGSGGGGDC FLRCHSGIHL 480  
 SSDVTITRTS VTFKLNKGK SLKNAELFPE GLRPAPEKH SSVKESFRYV NLTCSSGKQV 540  
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLKPAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKPPRPTS ERQAESCQVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660  
 TFQNEEGQMT CEPCEPRPGNS GALKTPEAWN MSECGLCQP GEYSADGFAP COLCALGTFQ 720  
 PEAGRTSCFP CGGGLATKHQ GATSPQDCET RVQCSPGHFY NTTTHRCIRC PVGTYPPEFG 780  
 KNNCVSCPGN TTDFDGTSTN ITQCKNRRCG GELGDFGTGI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRLIV VPEIFLPIED DCGDYLVMRK TSSNSVTTY ETCQTYERFI APTSRSKLW 900  
 IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960  
 LAHPQNYPKY TAQESREMF RSPFIRLLRSK VSRFLRPYK

**A17 DNA sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

1 11 21 31 41 51  
 | | | | |  
 CAAAAGAAA TAGATAAAAT AAATGGAATA TTAGAAGAGT CTCTGTGATA TGATGGTTTT 60  
 CTGAAGGCTC CTGCAGAAAT GAAAGTTTCT ATTCCAACCTA AAGCCTTAGA ATTGATGGAC 120  
 ATGCAAACTT TCAAAGCAGA GCTCCCGAG AAGCCATCTG CTTTCGAGCC TGCCATTGAA 180  
 ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240  
 GATCAGATGT TCCTTTCAGA ATCAAAACAA AAGAASGTTG AAGAAAATTC TTGGGATTCT 300  
 GAGAGTCTCC GTGAGACTGT TTCACAGAAG GATGTGTGTG TACCCAAAGC TACACATCAA 360  
 AAAGAAATGG ATAAATAAAG TGGAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420  
 GATACAGTTC ATTCTTGTGA AAGAACAAGG GAACCTCAAA AAGACCCCTG TGACCCACGT 480  
 TCAGAAAA

**A18 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Protein Accession #: none found  
 Signal sequence: none  
 Transmembrane domains: none  
 Cellular Localization: nuclear

1 11 21 31 41 51  
 | | | | |  
 QKEIDKINGK LEESPDNDGF LKAPCRMVVS IPTKALELMD MQTFKAEPPE KPSAFEPALIE 60  
 MQKSVENKAL ELKNEQTLRA DQMFPSKQ KXVEENSWDS ESLRETVSQK DVCVPKATHQ 120  
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPDPR SGK

**Breast****A19 DNA SEQUENCE**

Gene name: TMPSR33a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ACCGGGCACC GGACGGCTCG GGTACTTTGG TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180  
 AGAGGTCCCT AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCGCCCTC 240  
 TCATTCCGAT CGCTTTTGG CCTGTGATGAT TTGAAATAAA GTCCCTGTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTICC AATCATGCTC 360  
 ATTGGGATCA TTGCATGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCGGTGC TCCAGGTGTT CACAGCTGCT TGGTGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGT TGCCTGTGCC CACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAAECTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGGT TACCTTGACG TGCACAGCCT GTGCTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTGAGTTCC AGGCTACCA CCTGTGCGGG GGCTCTGTCA TCAAGCCCTG GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTA TGACTGTGAC CTCCCAAGT CATGGACCAT CCAGTGGGT 1020  
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080  
 AGCAAGTACA AGCAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGT GCCCGGGCCA 1140  
 CTCACGTCA ATGAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGAAAGG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTCC TGAACCAAGC GGCCTGCTCT TTGATTTCCT ACAAGATCTG CAACCAAGG 1320  
 GAGGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380

5 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACAGC CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCGGTG TCACCTCTCT CTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG 1680  
 TTCOOGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGT CCCAGGCTGG 1800  
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 10 TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT 1920  
 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCTGCT TCAGCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040  
 ACGCTAGCC TCAGCTCTCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTCG AAAATTCTCT 2160  
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 15 AGCCAGGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAAGAA 2280  
 CCAAACCCAC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCTTAT TTTTCATGAT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400  
 20 TTGTCCTTG ATTCCAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAAAA

**A20 Protein sequence:**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 25 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SpC domain: 216-444  
 30 Cellular Localization: not determined

35 1 11 21 31 41 51  
 MGENDPFAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFPF IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVILQVF 120  
 TAASWKTMCS DDWKGHYANR ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180  
 VTAHHHSYVV RECCASGHV VTLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240  
 40 LCGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCMT SGWGATEDGA GDASPVLNHA 360  
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQQGD SGGPLVCQER RLWLKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEHQMER DLKT

**A21 DNA SEQUENCE**

45 Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Nucleic Acid Accession #: AA428090  
 Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG 60  
 CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAATC 120  
 55 TTTTCAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT 180  
 GATCTCTGTT GGCCTTCTCG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240  
 GGAAAAACAA CTAACTCAG CCATTGCCCC AATTTCACC TTGCTAGTTA TCAGAGTTCA 300  
 CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGAATTT TATCTGAGC 360  
 60 AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAC ATTGCCTCCA GCTGCAAGC 420  
 AAGGGCATTG CCATTATGAA AGCCCCCTCA AGACTCTCTG CTATTTTCAA AACATGGAAA 480  
 GAAAAAGGGA AAAAAAGAAA AAAAAATAA ATTAGAAGGA TTTGTTCTCT AATTGGGGCT 540  
 CCCAAAAATG AGAAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATATT TTAACCTCTC 600  
 CAAGCAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTATT 660  
 65 TTTCTTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCTTCTCT ATCTGGATCT 720  
 GTTCTGCTCT ATTTCTCTTT CAAAGTCATC TTTCAAGGAA CTGCGCCTGA TTAATTGAT 780  
 TTTAACCAAC CAAATAAGAT ATTTGATATA TTAATTTAAA CTTTGTGAGA TGATTGATTA 840  
 GGAATTGCAT CATGTTTACA TGAGTATACC GAATTCAAAG TTAACCTTCA TAAGCAGGAG 900  
 TTTTACACA TCGTAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA 960  
 70 CTGAATGTTT TTGAAATAAA CACATTTTTA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020  
 CTTTTCACAC AAAATATATC AGTGAGAGAG TGTGTTGTTA AGAAAAAATA TCAAAGCACA 1080  
 ACAGATTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTGTAGA ATGGTGATT 1140  
 GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200  
 TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCCTATTGC TAGAAGGATG 1260  
 75 AAAGTGAATC CATATAAAC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAACTTTAT 1320  
 TATTCAGATT TAGATGTAAAC AGACATCTTT GCTGCGCTGA GATGTTTGC ATAGAAATA 1380  
 CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAAAAACAA ATAAATATA 1440  
 ACCAAAAAAT TTCATGTGTT GTAAGAACAG AACTATTATA GCCAATTC TAGTATTCAA 1500  
 ATCAGGACTA CAAATTGAAT TCTTTTCTT AGCAACATGA AATCATTCCA TATGAAGAC 1560  
 80 ATTTTCTGCT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTTT GAGATGTTCC 1620  
 CCCCTCATGC CTCCCCCAA GTTTTCATG TGGTTGTCAA ATAGTCCGC

**A22 Protein sequence:**

Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 113-129  
 Cellular Localization: not determined

10 1 11 21 31 41 51  
 MKPSLKHWD IKMFSEIDQR QVVGEEIHLQ VVSVSYLVEN PSDTDDLMSI VEESDSCYNR 60  
 DSVGLPGRAG DRLQPKTKPR GKTTNLSHLP NFHLASYQSS LLFKLQSSYY GNLLVEFELS 120  
 KCFVQLAVLK QKHCLQLQS KGIAIMKAPQ RLSAIFKTKW EKGKKEKKII IRRICSLIWA 180  
 PKNEK

#### A23 DNA SEQUENCE

20 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Nucleic Acid Accession #: AL133619  
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 ATGAGCGGTG CCGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCCGGGCTCT 60  
 CGCGCCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCCGCA GAGCCCGCAG 120  
 CTCAGGCAGA GCGAGCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCTCCCA GGCACACTCA 300  
 ACACTGCCGC TCCCGCAGCA CAGAACACA GCCATCACT CCAGCACAGC CCTGGGCTCA 360  
 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTG CCCACCTGGC TGCACTGGCC 420  
 CTTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGTACCTCT 480  
 AGCCGTGGCT GGAAGATGTT ATGCAGCCAA GCACAGCAGC TGCTGTCTCT GGGGAAGCCA 540  
 GGGCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGCT GCTCCCCAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAATGGG AAGGAACCCC TGGGACAGCC CTTGCCCTCT TAGATCTTTG 660  
 CCTCAGATTG CTTGCTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCGAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGTT TTCTTGCCA CTGTGCCAAG 840  
 GCACTTCCCC ATCTCTACAG CGGCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATTATCTTT GGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960  
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCAGGGA 1020  
 GACATGGAGA AGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCAGTGC TGGGGAGCCT 1140  
 GACAGGACAC GGAAGAGGCG CATGCTTCC CTGCGGACCT GCTGTTCCAT GTGTCCCAAG 1200  
 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTTG 1260  
 GCGCTCTGCT GGGTCTGCAT CAACGAGTG TGGGTAGAGC CGGAGGACC CAGCCCTGCC 1320  
 AGGCTGAAGG AGGGCTCTC ACGGACACAC AGGCAGGAG GCAAGCGTGG GCGCTCTTGG 1380  
 GCGGCTAGCG CCGACACTGT CGCTCTCTCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCTCTCTAA TTCAAGCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCTTCAACA AGCAAGATTG AAGAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560  
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGCA GGCAGAAAG 1620  
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC 1680  
 AGGCAGATGG GGGCGGGGCA ACACCCCCCA ATGATCTTGC CCCTTCCCTC GCGAAAGCCC 1740  
 ACCACACTTA ATCCAGTGCA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCG 1800  
 ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCGACC 1860  
 CCGGAGGAAG CTAGCTTTCC CAGGAGCCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920  
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGGG AGCGTGCCAT CCTGCCCGCA 1980  
 CTGAAGCAGA CCCGGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCATGCGAG 2040  
 AAACGGCGCC TGCATCGCTC AGTGCTTTGA

#### A24 Protein sequence:

65 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Protein Accession #: T43457  
 Signal sequence: none found  
 Transmembrane domains: 303-322  
 Cellular Localization: not determined

75 1 11 21 31 41 51  
 MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60  
 QQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALFPQAH S TLPLPQHRNT AINSSTRLGS 120  
 GGTQDGEPLQ TVLAHLAALA FVCPQSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAGROV ATGCSPDLPP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH 240  
 MLGAQGIWTH SIQGSPLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300  
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGEGP FPSRCGNSSE 360  
 LFwakCGFSR QPQPCSAADA DRTRBEAMLS LGTCCSMCPK PSCFPDGPSP NHLRSASAPL 420  
 GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPKGKRGRLA GGSADTVRSP ADSLSMSSFO 480  
 SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQQQARK 540

EKAEASNAGA ACMGNSQHQG ROMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600  
 TQELRHLKSL LEGSQRPOAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTPKNIFA ERQKRLQAMQ KRRLHRSVL

**A25 DNA SEQUENCE**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Nucleic Acid Accession #: NM\_000949  
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 15 GGAGGCTGAA ATCCCCAGAC GCGGGTTTTC TGGGCTGGGC TTCTGCTTA CTCACCTCTT 60  
 CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTCCACACA ATGGAGCTTC 120  
 ATGTCTCGT GCAGGAAGTA CTATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180  
 TAAAGAACTC TCCTATTCTT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCTGTAA 240  
 GTGAACCTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAAATGTGG 300  
 20 CATCTGCAAC CGTTTTCAC CTGCTACTTT TTCTCAACAC CTGCTTCTG AATGGACAGT 360  
 TACCTCTCGG AAAACCTGAG ATCTTTAAAT GTCGTCTCC CAATAAGGAA ACATTCACT 420  
 GCTGTGGAG GCCTGGGACA GATGGAGGAC TTCTACCAA TTATTCAGT ACTTACCACA 480  
 GGGAGGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCAACTCTCT 540  
 25 GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600  
 CTAACCAAT GGGAGCAGT TTCTCGGATG AACTTTATGT GGAGTGAAT TACATAGTTC 660  
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACA GCCAGAAGC AGAAAAACCT 720  
 ACCGTGTGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAATCTGT TGGTTTCAAGC 780  
 TCCTGTATGA TAATCGATT TAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG 840  
 30 GGCAGCAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900  
 TTGCTGAGAC ACCAGACCAT GGATACCTGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960  
 TACCTAGTGA CTTCAACATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCTTTCTG 1020  
 CTGTCTCTG TTTGATTATT GTCTGGGAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080  
 GCATCTTTCC GCAGATTCTT GGGCCAAAAA TAAAGGATT TGATGCTCAT CTGTGGGAGA 1140  
 35 AGGCGAAGTC TGAAGAATA CTGAGTGCC CTGGATGCCA AGACTTTCTT CCCACTTCTG 1200  
 ACTATGAGGA CTTGCTGGTG GAGTATTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260  
 TGTCAGTCCA TTCAAAAGAA CACCCAGTC AAGGTATGAA ACCCACTAC CTGGATCCTG 1320  
 ACATGACTC AGGCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380  
 AACCCAGGAC CAATCCCTCC ACATTCTATG ATCTGTAGGT CATTGAGAAG CCAGAGAATC 1440  
 40 CTGAACAAC CCACACCTGG GACCCCAAGT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500  
 TTGATGCTGG TGGATCCAA TGTTCACAT GGCCTTACC ACAGCCGAGC CAGCACAAAC 1560  
 CCAGATCCTC TTACCACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGG CCTGCAGGTG 1620  
 CACCGGCCAC TCTGTTGAAT GAAGCAGTA AAGATGCTTT AAAATCTCT CAAACCATTA 1680  
 AGTCTAGAGA AGAGGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA 1740  
 45 CTGACCAAGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800  
 CCTGTGATTA TGTGGAGATT CACAAGTCA ACAAGATGG TGCATTATCA TTGCTACCAA 1860  
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGAGC TCCTGAGAAC AATAAGGAGT 1920  
 ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGTGCGCA GATCCACATG 1980  
 CTAAAAAGT GGCTTGCTTT GAAGAATCAG CCAAGAGGC CCCACATCA CTTGAACAGA 2040  
 50 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100  
 TGGGTGGTTT TGGATTCTCT GATCCGCAAT GTTTTACACA CTCCCTTACC TGATAGCTTG 2160  
 ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTAGCTGA 2220  
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGGCTC CCAGCTCCTT TCATGCTCCA 2280  
 TTTTAAACCA CTTGCCCTCT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCTT 2340  
 55 AACTGTGATT TGTAGATTTA CTTTGTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400  
 AAAAGCACAC TCTTGTAGTAT TCTTGGGGA CAATGCCAAT AGGTATATCC TCTGGAAAG 2460  
 GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA 2520  
 AAGATGACAA AAGAAAATT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAAC 2580  
 AACTGCATAA CCTTTACACT CCTGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640  
 60 AAAGAAAGAA TGCATTCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700  
 TGTCTGATAT GCAAGTAAAG AAT

**A26 Protein sequence:**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Protein Accession #: NP\_000940  
 Signal sequence: 1-23  
 Transmembrane domains: 237-253  
 FN3 domains: 28-112, 127-215  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 75 MKENVASATV FTLLFLNLT LINGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGLPTNY 60  
 SLTYHREGT LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVNATNQMG SSPSDELYVD 120  
 80 VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW 180  
 EIHFAQQOTE FKLLSLHPGQ KYLVQVRCKP DHGYSWAWSP ATFIQIPSDF TMDTTVWIS 240  
 VAVLSVICL IIVVAVALKG YSMVTCIPFP VPGPKIKGFD AHLLEKKGSE ELLSALGCQD 300  
 FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDEPTDSG RGSQDSPLS 360  
 SERKEEPQAN PSTFYDEPEI EKPEPETH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420

PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQOREVE 480  
 SFHSETDQDT PWLLPQEKTP FGSAPKLDYV EIHKNVDGA LSLLPKQREN SGKPKKPGTP 540  
 ENNKEYAKVS GVMDDNLLVL VDPHAKNVA CFEESEAKEAP PSLEQNAQAEK ALANFTATSS 600  
 KCRLQLGGLD YLDPACTHFS FH

**A27 DNA SEQUENCE**

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)

Unigene number: Hs.169266

Probeset Accession #: L07615

Nucleic Acid Accession #: NM\_000909.1

Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60  
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTGGT AAATGGATT CAAATACGGG 120  
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180  
 ATAATCTATA ACAACCAAAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTGAAAA 240  
 TCATTAGTC CACTCTAATT TCTCAGAGAA GAATGCCAGC CTTCGGCTT TTGAAAATGA 300  
 TGATTGTCTAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTTCGCTATG GAGCTGTGAT 360  
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420  
 GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTGGCAT 480  
 CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540  
 GATGTGTAAAG TTGAATCCCT TTGTGCAATG TGTTCATC ACTGTGTCCA TTTTCTCTCT 600  
 GGTTCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660  
 TAATAGACAT GCTTATGTAG GTATTGCTGT GATTGGGCT CTTCGTGTGG CTTCCTCTTT 720  
 GCCTTTCTCTG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGATGC 780  
 GTACAAAGAC AAATACGCTG GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTCTA 840  
 TACCACTCTC CTCTTGGTGC TGCAGTATTT TGGTCCACTT TGTTTTATAT TTATTTGCTA 900  
 CTTCAAGATA TATATACGCC TAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960  
 TAAGTACAGG TCCAGTGAAG CCAAAGAAT CAATATCATG CTGCTCTCCA TTGTGTAGC 1020  
 ATTTGACATC TGCTGGCTCC CTCTTACCAT CTTTAACACT GTGTTGATG GGAATCATCA 1080  
 GATCATTTGT ACCTGCAACC ACAATCTGTT ATTCCTGCTC TGCCACCTCA CAGCAATGAT 1140  
 ATCCACTTGT GTCAACCCCA TATTTATGG GTTCCTGAAC AAAAACTTCC AGAGAGACTT 1200  
 GCAGTCTTTC TTCACTTTT GTGATTTCCG GTCTCGGGAT GATGATTATG AAACAATAGC 1260  
 CATGTCCAGG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCAGTCCG 1320  
 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380  
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACTACTCTT GATTACCTGT 1440  
 TCTCCCAAGG AATGGGCTTG AAATCATTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500  
 TTAAGTCTTT TGTGTAGTGT GTCAATAATTA CATTGTGAAC AAAAGGTGTG GGCTTTGGGG 1560  
 TCTTCTGGAA ATAGTTTGA CCAGACATCT TTGAAGTGCT TTTTGTGAAT TTATGCATAT 1620  
 AATATAAAGA CTTTATACT GTACTTATTG GAATGAAAT TCTTTAAAGT ATTACGATGC 1680  
 GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCAATTG ATTGGGTCAT CTTGATTAGA 1740  
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800  
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860  
 GAAGTCCATC AGAAGTGGTT TGAGGTTTCT GTTTTTTGGT GGTTTTTGGT TGTTTTTTTT 1920  
 TTTTTTCACC TTAAGGGAGG CTTTCATTTC CTCCCGACTG ATTGTCACTT AAATCAAAAT 1980  
 TTAATAATGA ATAAAAAGAC ATACTTCTCA GCTGCAATA TTATGGAGAA TTGGGCACCC 2040  
 ACAGGAATGA AGAGAGAAAG CAGCTCCCCA ACTTCAAAAC CATTTTGGA CCGACAAACA 2100  
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAAGT ATTGCTGCAA ATAGCTAAAT 2160  
 TATATTATT TGAATTGAT GTCAAGAGAT TTTCCATTT TTTTACAGAC TGTTCAGTGT 2220  
 TTGTCAAGCT TCTGGTCTAA TATGACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280  
 ACAAATATCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTTCAATGTC 2340  
 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTACCTAGC 2400  
 AGGMAAAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT 2460  
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TACTGTAAATA GTTGTGTAT 2520  
 GTTAATGTGC CTAATTTAT GTATCTTGT ATCATGATTG AGCCTCAGAA TCATTGAGG 2580  
 AAATATATT TTAAGAACA AGACATATT CAATGTATTA TACAGATAAA GTATTACATG 2640  
 TGTTTGATTT TAAAGGGCG GACATTTTAT TAAATCAAT ATTGTTTTT CTTTTCTGA 2700  
 GGAGTCTCTT TCAATTCAT TTTTCTCAT CCCATGACTT CCCTCCGATG GT

**A28 Protein sequence:**

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds

Unigene number: Hs.169266

Probeset Accession #: L07615

Protein Accession #: NP\_000900.1

Signal sequence: none found

Pfam domains: 7tm\_1 [57-91]

Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322

Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MNSTLFSQVE NHSVSNFSE KNAQLLAFEN DDCHLPLAMI FTILALAYGAV IILGVSGNLA 60  
 LIIIIILKQKE MRNVNITLV NLSFSDLLVA IMCLPPTFVY TLMDEWVFE AMCKLAPFVQ 120  
 CVSTTVSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180  
 DEFPQNVTL D AYKQKYVCFD QPPSDSHRLS YTTLLVLQY FGPLCFIFIC YPKIYIRLKR 240  
 RNNMDQMRD NKYRSSETR INIMLLSIVV AFVAVCWPLPT IFNTVFDWNH QIIATCNHNL 300  
 LFLLCILHTAM ISTCVNPIFY GFLNKNFQRD LQFFNFNCFD RSRDDDYETI AMSTMHTDVS 360

KTSLKQASPV AFKINNND NEKI

A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC 60
GGCTGCCCGG GCTGTGGCGC CAACGCCTCG GACGCGCCAG TCCCTTCGCC GCGGGCCGTG 120
GAGCCTGGGC TCSTGCGCGT CTCTTCGCGG GCGCTGATGC TGCTGGGCGT GGTGGGGAAC 180
TCGCTGGTGA TCTACGTCAT CTGCGGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
ATCGCCAACC TGGCGGCCAC GGACGTGACC TTCCTCCTGT GCTGCGTCCC CTTCACGGCC 300
CTGCTGTACC CGTGCGCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT GGTCAACTAC 360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCATAGAG TGTGGACCGC 420
TGGTAGGTGA CGGTGTTCCC GTTGGCGGCC CTGCACCGCC GCACGCCCGG CCTGGCGCTG 480
GCTGTAGCCG TCAGCATCTG GTTAGGCTCT GCGGCGGTGT CTGCGCGCGT GCTGCGCCTG 540
CAGCGCCTGT CAGCGGGGCC GCGCGCCTAC TGCAGTGAGG CCTTCCCGAG CCGGCGCCTG 600
GAGCGGCGCT CGTCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCGGCT GCTGCGCAAC 660
TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGTGGCG CCGCGCGCCC 720
GCGGATAGCG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAAG 780
GTCTCGCGCC TGTGGCGCGC CGTGGTCTCT CTCTTCGCGG CCTGCTGGGG GCGGCATCCG 840
CTGTTCTGCG TGTGTCAGCG GCTGGGCCCC GCGGGCTCCT GGCACCCACG CAGTACGCC 900
GCCTAGCGCG TTAAGACCTG GGCTCACTGC ATGTCTCTACA GCAACTCCGC GCTGAACCGG 960
CTGCTCTAGC CCTTCTGCGG CTGCACTTTC CGACAGGCGT TCCGCGCGGT CTGCCCTTGC 1020
GCGCGCGCGC GCGCGCGCGG CCGCGCGCGG CCGGAGCCCT CGGACCCCGC AGCCCCACAC 1080
GCGGAGCTGC ACGCCCTGGG GTCCACCCCG GCGCGCAGAA GCGAGGGAGC 1140
AGTGGGCTCG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAAACGCCC TCTCTGA

```

A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

Pfam domains: 7tm\_1 [59-323]

Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA ALMLLGLVGN 60
SLVIYVICRH KPMRTVINFY IANLAATDVT FLCCVFPFTA LLYPLPGNVL GDFMCKFVNY 120
IQQVSQVQAT ATLITAMSVD R WYTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAL 240
ADSLAQGVQL AERAGAVRAK VSRLLVAAVVL LFAACWGIQ LFLVLQALGP AGSWHFRSPA 300
AYALKTNWAC MSYSNSALNP LLYAFLGSHF RQAFRRVCPC APRRRPRRPR PGPSDFAAPF 360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL

```

A31 DNA SEQUENCE

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM\_014246

Nucleic Acid Accession #: NM\_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGCGCGCG CGCGCGCGCC CGTGTGTCGC GTGCTGCTGC TCCTGGCGCG CGCGCGCGCC 60
CTGCGCGCGA TGGGGCTGCG AGCGGCGCGC TGGGAGCCGC GCGTACCGCG CGGGACCGCG 120
GCCTTGGCCC TCAGCGCGCG CTGTACTTAC GCGGTGGGCG CCGCTTGACG GCGCGGGGCG 180
CGCGGGGAGC TGCTGGACGT GGGCGCGGAT GGGCGGCTGG CAGGACGTGG GCGGCTCTCG 240
GGCGCGGGGG GCGCGTGCCT GCTGCAAGTC CGCTTGGTGG CCGCAGTGTG CCGGACGGCG 300
CTGAGCGCGC GCGTGGCGCG GCGCACGACAC CTTCGCGGCT GCGGAGCCCG TGCGCGGCTC 360
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### 5 A32 Protein Sequence

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo  
 (Drosophila) homolog (CELSR1),  
 Hs.252387  
 Unigene number:  
 Protein Accession #: NP\_055061  
 Signal sequence: 1-20  
 Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,  
 1110-1199  
 Pfam domains: Laminin\_EGF [2003-2048], 7cm\_2 [2465-2708]  
 Latrophilin/GPS domains: 2407-2460  
 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704  
 Cellular Localization: plasma membrane

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 50 GKNCEQAMPH PQLPFGESV SWSDLNIIIS VPHYGLMFR TRKEDSVLME ATSGGPTSPR 1740  
 LQILNNYLQF EYSHGFSVDE SVMLSGLRVT DGEWHLLIE LKNVKEDSEM KHLVTMTLDY 1800  
 GMDQKNADIG GMLPLGLTVRS VVVGASEDK VSVRRGFRGC MQGVRMGGTP TNVATLNMNN 1860  
 ALKVRVKDGC DVDDPCTSSP CPFNRSCHDA WEDYSCVCDK GYLGINCVDA CHLNPCENMG 1920  
 ACVRSPGSPQ GYVCEGSPSH YGPYCENKLD LPCPRGWMGN PVOCPCHCAV SKGFDPDCNK 1980  
 55 TNGQCQCKEN YYKLLAQDTC LPDCPPPHGS HSRTCDDMAT QCACKPGVIG RQCNRCNDNF 2040  
 AEVTLGCEV IYNGCPKAFE AGIWWQTKF GQPAAVPCPK GSVGNVVRHC SGEKGNLPP 2100  
 LFNTTISFV DLRAMNEKLS RNETQVDGAR ALQLVRLRS ATQHTGLFPG NDVRTAYQLL 2160  
 GHVLQHSWQ QGFDLAATQD ADFHEDVIHS GSALLAPATR AAEQIQRSB GGTAQLRLRL 2220  
 EGYFSNVARN VRTYLRPFV IVTANMILAV DIFDKFNFTG ARVERFDTH EEPRELESS 2280  
 60 VSFPADFFRP PEEKSGPLL R PAGRRITPQT TRPGPCTERE APISRRRRHP DDAGQFAVAL 2340  
 VIYRTLGLQL LPERYDPDR SLRLPHRP II NTPMVSTLVY SEGAPLPRPL ERPVLVEFAL 2400  
 LEVEERTKPV CVPMNHS LAV GGTGWSARG CELLSRNTH VACQCSHTAS FAVLMDISRR 2460  
 ENGEVLPKI VTYAAVLSL AALLVAFVLL SILVRMLRSNL HSIKHLAVA LFLSQLVFI 2520  
 GINQTNPFPL CTVAAILLHY IYMTFAWTL VESLHVYRML TEVRNIDTGP MRFYVVGWG 2580  
 65 IPAIVTGLAV GLDPQGYGNP DFCWLSLQDT LIWSPAGPIG AVIIINTVTS VLSAKVSCQR 2640  
 KHHYKKGKI VSLRLTAFL LLLISATWLL GLLAVNRDAL SPHYLFAIPS GLQGPVLLF 2700  
 HCVLNQEVK HLKGLVGGK LHLSDSATR ATLLTRSLNC NTTFGDGPDM LRTDLGESTA 2760  
 SLDIVRDEG IQKLGVSSGL VRGSHGEPDA SLMPRSCKDP PGHSDSDSSE LSLDEQSSSY 2820  
 ASSHSSDSED DGVGAEEKWD PARGAVHSTP KGDAVANHVP AGWPDQLAE SDESPPSGKP 2880  
 70 RLKVTKVS ELHREBQGS RGEYPPDQES GGAARLASSQ PFEQRKGIK NKVTYPPPLT 2940  
 LTEQTLKRL REKLADCEQS FTSSTSSSLG SGGPDCAITV KSPGREGRD HLGAVAMNVR 3000  
 TGSQAQDGS SEKP

### 75 A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Probeset Accession #: X95876  
 Nucleic Acid Accession #: X95876  
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 CCAACCAAA GCACCAAGC AGAGGGGCG AGAGCACACC ACCAGCAGC CAGAGCACCA 60  
 GCCACGCCAT GGTCTTGAG GTGAGTGACC ACCAAGTGCT AAATGAGGCC GAGGTTGCCG 120

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CCCTCCTGGA  GAACCTCAGC  TCTTCCTATG  ACTATGGAGA  AAACGAGAGT  GACTCGTGCT  180
GTACCTCCCC  GCCCTGCCCA  CAGGACTTCA  GCCTGAACCT  CGACCGGGCC  TTCTTGCCAG  240
CCCTCTACAG  CCTCTCTTTT  CTGCTGGGGC  TGCTGGGCAA  CGCGCGGGTG  GCAGCCGTGC  300
TGCTGAGCCG  GCGGACAGCC  CTGAGCAGCA  CCGACACCTT  CTTGCTCCAC  CTAGCTGTAG  360
CAGACACGCT  GCTGGTGTGC  AACTTGCCGC  TCTGGGCAGT  GGACGCTGCC  GTCCAGTGGG  420
TCTTTGGCTC  TGGCCTCTGC  AAAGTGGCAG  GTGCCCTCTT  CAACATCAAC  TTCTACGCAG  480
GAGCCCTCCT  GCTGGCCTGC  ATCAGCTTTG  ACCGCTACCT  GAACATAGTT  CATGCCACCC  540
AGCTCTACCG  CCGGGGGCCC  CCGGCCCGCG  TGACCCCTAC  CTGCCTGGCT  GTCTGGGGGC  600
TCTGCCTGCT  TTTGCCCCCT  CCAGACTTCA  TCTTCCTGTC  GGGCCACCAC  GACGAGCGCC  660
TCAACGCCAC  CCACTGCCAA  TACAACCTCC  CACAGGTGGG  CCGCACGGCT  CTGCGGGTGC  720
TGCAGCTGGT  GGCCTGCTTT  CTGCTGCCCC  TGCTGGTCAT  GGCCTACTGC  TATGCCACA  780
TCTTGGCCGT  GCTGCTGGTT  TCCAGGGGCC  AGCGGGCGCT  GCGGGCCATG  CGGCTGGTGG  840
TGGTGGTCTG  GGTGGCTTTT  GCCCTCTGCT  GGACCCCTTA  TCACCTGGTG  GTGCTGGTGG  900
ACATCCTCAT  GGACCTGGGC  GCTTTGGCCC  GCAACTGTGG  CCGAGAAAGC  AGGGTAGAGC  960
TGGCCAACTC  GGTCACTTCA  GGCTGGGGCT  ACATGCAGTG  CTGCCTCAAC  CGGCTGCTCT  1020
ATGCTTTTGT  AGGGGTCAAG  TTCCGGGAGC  GAGTGTGGAT  GCTGCTCTTG  CGCTGGGGCT  1080
GCCCCAACCA  GAGAGGGGCT  CAGAGGCAGC  CATCGTCTTC  CGCGCGGGAT  TCATCTGGGT  1140
CTGAGACCTC  AGAGGCTCTC  TACTCGGGCT  TGTGAGGCGG  GAATCGGGGC  TCCCTTTTCG  1200
CCCACAGTCT  GACTTCCCCG  CATTCACGGC  TCCTCCTCTC  CTCTGCGGCG  TCTGGTCTCT  1260
CCCAATATCC  TGCTCCCCGG  GACTCACTGG  CAGCCCCAGC  ACCACCAAGT  CTCCCGGGAA  1320
GCCACCTGCT  CAGCTCTGAG  GACTGCACCA  TTGCTGCTCC  TTAGCTGCCA  AGCCCCATCC  1380
TGCCGCCCGA  GGTGGCTGCC  TGGAGCCCCA  CTGCCCTTCT  CATTTGGAAA  CTAAACTTTC  1440
ATCTTCCCA  AGTGGCGGGA  GTACAAGGCA  TGGCGTAGAG  GGTGCTGCC  CATGAAGCCA  1500
CAGCCCCAGC  CTCCAGCTCA  GCAGTGACTG  TGGCCATGGT  CCCCAGAGCC  TCTATATTTC  1560
CTCTTTTATT  TTTATGTCTA  AAATCTGTCT  TAAACTTTT  CAATAACAA  GATCGTCAGG  1620
ACCAAAAAAA  AAAAAAAAAA  AAAAAAAAAA  AAAAAAAAAA  AAAAAAAAAA  BHCLITERAT  1680
UREBHCBLAS  TPEHCORTHO  LOGUESMOUS  ECKCRMYLEV  SERQVLDAAD  FAFLEENSTS  1740
PYDYGENESD  FSDSPPCPDQ  FSLNFDRTFL  PALYSLLFL  LLLNGAVAA  VLLSQRTALS  1800
STDFTLLHLA  VADVLLVLT  PLWAVDAVQ  WVFGPGLCKV  AGALFNINFY  AGAFLLACIS  1860
FDRYLSIVHA  TQYRRDPRV  RVALTCIVVM  GLCLLPALPD  FIYLSANYDQ  RLNATHCQYN  1920
FPQVGRALR  LRAMRLVVVV  VVAFALCWTP  YHLVVLVDIL  MDLGALARNC  GRESRVDAVK  1980
CWTPVHLVVL  VDILMDVGV  ARNCGRESHV  DVAKSVTSGM  GYMHCCLNPL  LYAFVGVKFR  2040
EQMWMLFTRL  GRSDQRGPR  QPSSSRRESS  WSETTEASYL  GL
  
```

**A34 Protein sequence**

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Protein Accession #: P49682  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [70-318]  
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323  
 DRY box: 148-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MVLEVS DHQV LNDAEVAALL ENFSSSYDYG ENESDSCTTS PPCPDQFSLN FDRAFLPALY 60  
 SLLFLGLLG NGAVAVALLS RRTALSTDT FLLHLAVADT LLVLTPLWA VDAAVQWVFG 120  
 SGLCKVAGAL FNINFYAGAL LLACISFDXY LNIIVHATQLY RRGPPARVTL TCLAVWGLCL 180  
 LFLALPDFIFL SAHDERLINA THQYNFQPV GRTALRVLQL VAGFLPLLV MAYCYAHILA 240  
 VLLVSRGQRL LRAMRLVVVV VVAFALCWTP YHLVVLVDIL MDLGALARNC GRESRVDAVK 300  
 SVTSGLYGMY CCLNPLLYAF VGKFREREMW MLLRLGLCPN QRGLQRQPS SRRDSSWSET 360  
 SEASYSGL

**A35 DNA SEQUENCE**

Gene name: Differentially expressed CO16 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 Probeset Accession #: AA447522  
 Nucleic Acid Accession #: BC001291  
 Coding sequence: 44-541 (start and stop codons are underlined)

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1 11 21 31 41 51
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GGGGGCGCCG CGCGCTGACC CTCCTGGGGC ACCGCTGGGG ACGATGGCGC TGCTCGCCTT 60
GCTGCTGGTC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120
AGATCCAGAG GACTCCCAGC GAACGACGGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
TGAGAGAGAA AACACTTTTC AGTGCCAGAA CCAAGGAGG TGCAATAGGA CAGAGCCATA 240
CTGCGTTATA GCGGCCGTGA AAATATTTC ACCTTTTTTC ATGGTTGCGA AGCAGTGCTC 300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
GCCATGCCCT TCTTTTACC TCAAGTGTG TAAATTCGC TACTGCAATT TAGAGGGGCC 420
ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
GCTGTGGCTG GCCATCTCTC TGCTGCTGGC CTCATTGCA GCGGCGCTCA GCCTGTCTTG 540
AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTGCTCCA GACCGTTGTC 600
ACCTGTTGCA TTAACCTTGT TTTCTGTTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT 660
GGGATGGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
ACATTACAGG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTTC 780
AAATCAAACC TTGTAACCTA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCCCTCTG 840
CCTCTGAGGG TCTCAGTATT GATGGGGAGG GAGGCCTAAG TACCCTCAT GAGAGATATG 900
TGCTGAGATG CTTCGCACTT TTAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTC 960
GGGTGAAGAC ATCCCTGAGG TGAAGGACTC CTCAGCATGG GGGGCGATGG GCACACGTT 1020
AGGGCTGCCC CCATTCCAGT GGTGAGGCGC CTGTGGATGG CTGCTTTTCC TCAACCTTTC 1080
  
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5 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140  
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200  
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260  
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAACAAAT ACAAGGGGAC 1320  
 TTCAAAGTT CACGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

10 A36 Protein sequence:  
 Gene name: Differentially expressed CO16 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 Probeset Accession #: AA447522  
 Protein Accession #: AAH01291  
 Signal sequence: 1-17 (first underlined sequence)  
 Transmembrane domain: 146 - 162  
 Cellular localization: plasma membrane

20 1 11 21 31 41 51  
 MALLALLLVV ALPRVWTDAN LTARQRDPED SQRTDEGDNR VVCHVCEREN TFEQCNPRRC 60  
 KWTEPYCVIA AVKIFPPFFM VAKQCSAGCA AMERPKPEEK RFLLEPMPF FYLKCKCKIRY 120  
 CNLEGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSL

25 A37 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

30 1 11 21 31 41 51  
 35 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60  
 CCGTCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGGAACTTCA TCACCAATGA 120  
 GTGCAACATA CCAGCAACT TCATGTGCGC CAATGGACGG TGCAATCCCG GCGCCTGGCA 180  
 GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTCGAAATGT GGCCCAACT TCTTCCCTG TGCCAGCGCG ATCCATTGCA TCATTGGTCG 300  
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTCTG CTTTGTCTCA CGGCCGCTA CCACTGCAAG AACGGCTCT GTATTGACAA 420  
 GAGCTTCATC TCGATGGAGC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 AAGTTCTCAA GAACCGGCA GTGGGAGGT GTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 TTACCCAGC ATCACTATG CCACTATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 45 CCGTCTGGCA CTGGCTTTCG ACCACGAGG GAAGCGGAAC AACCTCATGA CGCTGCGCGT 660  
 GCACCGGCTG CAGCAGCGTG TGCTGTGTGC CCGCTGGTGG GTCTTGGACC ACCCCACCA 720  
 CTGCAACGTC ACCTACAAGC TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 GAATGCGCTG GAAGTAGGCT CCCCACCTC CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840  
 TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
 50 CGACCTGCCC CCCTACCGCT CCGGTCGCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960  
 CAGCAGCTCT CAGCAGGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020  
 GGGCAGCTCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACT GTTGCCATT TAACAATTTG 1140  
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 55 AACTATCTCT GCATTCCTCT CCTCCCCAG ACTTCAGAGA TGTTTTTCTG GCGTCTCAGT 1260  
 TGACATGATC TGTGTGCGGT CTTTCTGTGC AGGTCACTCT TCCCTTGGGA CCGAGATCA 1320  
 CACCTCATTT TTTCACTATA TTCTGTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380  
 AAATAGGCTG GAGAGAGACA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500  
 60 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAAT CCATTTGAGC 1560  
 ATCAAAACCT GCTTGCACA ATCCTATTG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620  
 AAGAAAACCT TGGACGTGAG TAACACCTTT CAGCAGTGGC AACGTTATTT TGGTTTGTG 1680  
 AAGGACTCTG AAACCATCTA CCGTGTATAA ATTCTGGCTT TAGAAATTTG CCCAAGAATG 1740  
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800  
 65 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920  
 ACCTGCCCCG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980  
 GTATGTCCTT GTGGCCACCA CCCAGCCTGT CTGTCTATT CATGCAGCCT CAACACTGGC 2040  
 CTCCAAAGTT CCCTTAACAC TTGCAAGTC CTTTTACCT GTGCATTGGG ACTTGAGGAC 2100  
 70 ACTGGTTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTGAGGGTC AGGCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 AGACAATTTC GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340  
 TGAAACAGTG TGTTTGTGTT TTCCCTTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400  
 75 AGCTGTCTCT TTTTGTGTT TTCTTTTAA AAGTCCAAA GAAAGATGCA AAAGGAGATC 2460  
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 AGAGGAGCTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640  
 TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCTGCA GGAATAAGGG GTAAAACTTT 2700  
 80 AGTGTGTTGT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGTAGAG 2760  
 CCACTCGGG CAGCTGTAC CCATTGAGAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820  
 AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAGG TGGCACTTCA 2880  
 TGATCCTGTT CTGTAGACTT TCTTTCTTT TTTTAAACAA ATCCAAAGGA TGTATACGAA 2940  
 AAGCTAGCCA CTGTATTTT GTTTTGTGTT AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000

AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTCATCT CTTGTGAGTC AGAAGGGCTT TATTCTCCC TTTGATGGG CCCCTTCTTC 3180  
 TTTCTGTGTC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATAGT 3300  
 AGATAAGGGA TGCCTACTAA TGCCTTTTAA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCAACACAG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTTACCTT GAAATTGACA 3660  
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 GAAAGGTTGT GTGTGCTTGC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780  
 TTATACTTTC TAATAAAATT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GNMCTAMARM 3840  
 AAMMAAAAC AMYWTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGCGCGG GGGCCCACTG AGGTACGGCG ACCACGCGGG CCCAACCGGG ACCCCAGAGG 3960  
 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAAGAAAAA ACCGCGCGGG 4020  
 GGAACCGCA GAGTGTGCG TAAACCAAC CCAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

### A38 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MWLLGFLCLL LSSAAESQLL PGNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECFKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSF ICDGQNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240  
 YVASQAQNA SEVGSPSPYS EALLDQRPAN YDLPPFPYSS DTESLNQADL PPRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV

### A39 DNA sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGCTGCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60  
 GGAAGAAAC TTCCTGGGGA GGCCTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCAGC 120  
 GACCGGGAGA GGGAGAGCGG GCGGAGGCT GCGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGAGGCGGG AGAAGGGGAA CCGGGCGGAG CGCCCGGCTT GATCCGCGC CCAGCAGCAG 240  
 CCGCGGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTC 300  
 CGCTCGCTC CTGGAACGTC CCGGGGAGG GTCCGCTTGC CAGTGAACCC TCCAGAGGCT 360  
 TCGGAGCAGC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGAAGGGGA TGGCTTAGGA 480  
 GCTCTGTGAC CTAGGGCCCG GGTGTGTGCT CTCTGGGCG TCGCGGCAGA GGGGAGTGCC 540  
 CCGCGCGGAA AGCGCGCGCG SACAGTCAGT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600  
 CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGGCCAG GGTGGTGCCA 660  
 TGTGGGGGCG TCGCGCTCG TCGCTCTCT CATCTTGAA CGCGGCTTCG CTCTGCGAGC 720  
 TGCTGCTGGC TCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780  
 TGGCTGGAGC CGCAGGGCGT CTGGGCGATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 GCGGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCGAG 900  
 GCGCGCTTGG ACCAGGGCGG CTGGGACAAT GACCGCGCAG AGGGCGCTGG CGAGCCTGGC 960  
 CCGGGGGAACA AAGACGGGCC CGGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGGG AGGGTGGCCC CCCACCGGTG AGGGCTTGGC AGCGGTGCTC CCCTGAAGGC 1080  
 TCCCGGAAAG GAAGGCAGCT CTTAGGGGCT TTCCCGGGGC TGTGCCCCG TGCCAGACGC 1140  
 CGCGGATTCC CATCTCTCC ACGGGGCGGC CCTCTTCCCC TGCAGCGGCC CGCCTTGCCT 1200  
 ATCTACGTGC CGTTCCTCAT TGTGGCTCC GTGTTGTGCG CTTTATCAT CTTGGGGTCC 1260  
 CTGTGGGAGC CCGTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320  
 GCGCCAGGGG GTAAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC 1380  
 CCGGGGTGCT CTTACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CCGCAACTCC 1440  
 GGGGCGCGGG CGCCCCAAC AAGGTCACAG ACCAAGTGT GCTTGCCGGA AGGGACCATG 1500  
 AACACGTGT ATGTCAACAT GCGCAGAAAT TTCTCTGTGC TGAAGTGTCA GCAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620  
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTTGCA GCCTGGCTAC 1680  
 AGGCAGATTG AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCGAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCAC TGTGTGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTGC GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860  
 GCTTACTTTG CCCCAGACT GTATGAAAC ATCTCGAAT TAGCATTCT GGATATGTTT 1920  
 CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGATTTTAA TAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100

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TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCCTGCTCTG TTGCCCAGGC TGGAGTGCAG 2220
TGGTGGGATC TGGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC 2280
AGCCTCCACG GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TGTATTTTTT 2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGTGCTCTC ACTCTCCTGA CCTCAAGCAA 2400
TCTGCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC 2460
TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAA TAACAGGACT 2520
ATTCTAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640
GGGCTATTTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCCTTC 2820
TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCCTTTT 2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
TGGTTATGGT TTGGCGTTTC CTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000
GAGTGCAAGT ACTTCTATTA CTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
AAAAATTTTC TGTCTTAGT TATAAAATTT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTTT 3180
GGAGATCATA AGCTCTTTTA TACTCTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
GATTGTTAAG AGAAAGCTT TTCAACGAAG GATGCTCTT CTCTCCCACT ACTGTTCTTG 3300
ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
CAAAATCAAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480
GTATGGTATG GTCTCTACCA CATTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540
TGTTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACCTA 3600
TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAAATA AAAAAAATA AAAAAAATA
  
```

**A40 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MLSGFLMSPS TOHRAQYTPG GKLPWEASI GAHRSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKNRGE PPWIRAOQQ PRPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPFPA 120  
 SGRQPRGPSD CIPRFPASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEBSGS 180  
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVV CGALAARPPS HPGTPLRSCS 240  
 CWNLCWRRG RGPSPGEYCHG WLDAQGVWRI GFQCPERFDG GDATICGSC ALRYCCSSAE 300  
 ARLDQGGCDN DRQQAGGEPG RADKDGPRRL GRASCLRGTG GDGBGAPFPV RAWQRCSPFG 360  
 SPKGRQLLRA PPGLLPRARR RGFPSPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS 420  
 LVAACCCRL RPKQDPQQR APGGNRLMET IPMIPASSTS RGSSSRQSSST AASSSSANS 480  
 GARAPPTRSQ TNCLPEGTM NNVTVMPTN FSVLNCQAT QIVPHQGYL HPFYVGYTVQ 540  
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQMYPV TV

**A41 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGTCACAG TTTCTTCCAA CCTTGCCATT 120  
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 ATGTTTATTG ATCACCTTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300  
 CAAATGAAG AAATACAAGA AATGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCTA 360  
 GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420  
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGCCTC GGGATTATAC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540  
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAAGT CAAATTTTAT 600  
 GAGAGAAACC TCTGGCATAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660  
 TTACTATTTA GTTTTAAATA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTAAATA 720  
 TCTGAAAAAA AAAAAAATA AAAAAAATA

**A42 Protein sequence:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

1 11 21 31 41 51  
 5 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60  
 PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDQYVPRIM 120  
 FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

#### 10 A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 20 ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCCT TATTATGCTG CTCTGGCCTT CTGCAGTCAT CAGTGTTTTA 240  
 25 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTGAAG AATTGAGTAA ACTTGTGCCA 360  
 CCAGAATGCC ATTGTGTGCG TGAAGGAAAA TTGAGCATA CACTTGCCCG AGACTTGGTT 420  
 CCAGGTGATA CAGTTTGCTT TCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTCT 480  
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTT 540  
 AAGGTGACAG TCCTTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
 30 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTGTGTCAT TGGACAGGA 660  
 GAAATCTCTG AATTGTGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGCAGA AGAGCATGGA CCTCTAGGA AAACAACCTT CTTTACTCT CTTTGTGATA 780  
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840  
 ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTTCACAGT 900  
 35 ACGCTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAGGG CCATTGTGAA AAAGCTGCCT 960  
 ATTGTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGG AACACTGAGC 1020  
 AAGAATGAAA TGACTGTATC TCACATATTT ACTTCAGATG GTCTGCTGTC TGAGGTACT 1080  
 GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTGTATG GTGATGTTGT TCATGGATT 1140  
 40 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAAAT 1200  
 AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCATGAAG 1260  
 ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTAGCTCT 1320  
 GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
 TGTTTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
 45 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500  
 ATGGGCTCAG CCGGACTCAG AGTTCTTGCT TTGGCTCTG GTCCCTGAAT GGGCAGAGCT 1560  
 ACATTCTTGT GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620  
 ACAACACTCA TTGCTCAGG AGTATCAATA AAAATGATTA CTGGAGATT CACAGAGACT 1680  
 GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCAAAAA CTCCCACTC AGTCTCAGGA 1740  
 50 GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTCTCACAAA TAGTACCAA GTGTGCAAT 1800  
 TTTTACAGAG CTAGCCCAAG GCACAGATG AAAATATTA AGTCGTACA GAAGAACGGT 1860  
 TCAGTTGTAG CCAATGACAG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920  
 ATGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980  
 CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040  
 55 AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100  
 ATCTCATGGG CTACATTAAT GAACCTTCTT AATCCTCTCA ATGCCATGA GATTTTGTGG 2160  
 ATCAATATTA TTATGATGG ACCCCAGCTC CAGAGCCTTG GAGTAGAAC AGTGATATAA 2220  
 GATGTCATTC GTAACCTCC TCGCAACTGG AAGACAGCA TTTTGACTAA AAATCTGATA 2280  
 CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTT CTCTGGCGT 2340  
 60 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACACAA TGACCTTCAC ATGCTTTGTG 2400  
 TTTTGTGACA TGTTCATGCG ACTAAGTCC AGATCCCGA CCAAGTCTGT GTTTGAGATT 2460  
 GGACTCTGCA GTAATAGAAAT GTTTGTCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520  
 CTAGTTATTT ACTTCTCTCC GCTTCAGAA GTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
 GATCTGTGTT TCTTTTGGG TCTCACCTCA TCACTGTGCA TAGTGGCAGA AATTATAAAG 2640  
 65 AAGGTTGAAA GGAGCAGGGA AAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTT 2700  
 CTGAGATAT GA

#### A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

1 11 21 31 41 51  
 80 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FRGWNEFDIS EDEPLWKYI 60  
 SQFNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQYRSEK SLEELSKLVP 120  
 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180  
 KVTAQPAAT NGDLASRNI AFMGTIVRCG KAKGVVIGTG ENSEPGVEPK MQQAEAPKT 240  
 PLQKSMOLLG KQLSPYSPGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPIVVTV 300



5 TLALGVMRMV KKRAIVKILP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360  
 GVGYNQFGEV IVDGDVVHGF YNPVSRIVE AGCVCDNAVI RNNTLMGKPT EGALIALAMK 420  
 MGLDGLQQDY IRKAEYFFSS EQKWMVAVKCV HRTQODRPEI CFMKGAYEQV IKYCTTYQSK 480  
 10 GQTLTLTQQQ RDVYQOEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV 540  
 TTLIASGVSI KMITGDSQET AVAIA SRLGL YKSTQSQSVSG BEIDAMDVQQ LSQIVPKVAV 600  
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADMI 660  
 LVDDDTFTTM SAIEBGGIY NNINFNVRFP LSTSLAALT ISLATLMNFP NPLNAMQILW 720  
 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780  
 ELRDNVITPR DTTMTFTCFV PFDMEALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840  
 15 LVYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVEREREKIQ KHVSTSSSF 900  
 LEV

**A45 DNA sequence**

15 Gene name: ESTs  
 Unigene number: Hs.157601  
 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

20  
 1 11 21 31 41 51  
 25 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60  
 TTTTATTTGC AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120  
 CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180  
 ACAAACAGGT GTCCACGCTG GCAGCCGCGC CCCGGGCGCC CTCTCTGTGA TCCCGTAGCG 240  
 CCCCTGGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGCGAC CGAGCGCTGG 300  
 30 TCGCCGCTCT CCTTCGCTTA TATCAACATG CCCCTTTTCC TGTGTCTGGA GGCCGTCTGT 360  
 GTTTTCTCTT TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA 420  
 GAAACCATCG GGAAGATTTT AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480  
 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAAG 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600  
 GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGGATTCAAT TTCAACCCAA 660  
 35 CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCRAAG GAGGGCGCAC GGAGACGGAA 720  
 CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCTGTGAG GCAGAAATGC TTCTGTGCCC 780  
 CAGATCCTCA TCATCGTCTC TGATGGGAAG TCCAGGGGGG ATGTGGCACT GCCATCCAAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGTGGGAG 900  
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGCAGCACG TGCTGTGGC TGAGCAGGTG 960  
 40 GAGGATGCCA CCAACGCCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020  
 ACGCCAGACT GCAGGGTCTG GGTCAACCCC TGTGAGCACA GGAAGCTGGA GATGGTCCGG 1080  
 GAGTTGCTCG GAAATGCCCC ATGCTGGAGA GATCGCGGCG GAGACCTTGG GGTGCTGGCT 1140  
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTCTCTAA CCCACCTTGC CACTGCTTAC 1200  
 45 AGGACCACTT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGAGG CACATGTGTT 1260  
 CCAGAGGAC TGAGCGGCTA CCAAGTGCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320  
 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCCAGCTCC TCTTCTGCTT GGACAGCTCT 1380  
 GCGGGCACCA CTCTGGACGG CTCTCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440  
 GCGTCTCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500  
 CTGGTGGCGG TGCTGTGGGG GGAGTACCAG GATGTGCTCG ACCTGGTCTG GAGGCTCGAT 1560  
 50 GGCATTCCCT TCGGTGTGCG CCCACCCCTG ACCGGGAGTG CCTTGGGCA GCGGCGAGAG 1620  
 CGTGGCTTGG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTGG 1680  
 CTCAGTGAAT CACACTCCGA GGAATGAGGT GCGGGCCCGC CGCGTCAACG AAGGGCGCGA 1740  
 GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800  
 GGCAAGCCAA AGCATGTGAT GGTCTACTCG GATCTCAGG ATCTGTTCAA CCAATCCCT 1860  
 55 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGGT GCGGACACA AGCCCTGGAC 1920  
 CTGCTCTTCA TGTTGAGCAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980  
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGG 2040  
 CTGTTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGACACCAA ACCCAACCGG 2100  
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTACGCCGGC 2160  
 60 ACCGCCCTGC TGACATCTTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220  
 GTCCCCAAG CTGTGGTGGT GCTCACAGGC GGGAGAGCGG CAGAGGATGC AGCCGTCTCT 2280  
 GCCCAAGAGC TGAGGAACAA TGGCATCTCT GTCTTGTGCG TGGGCGTGGG GCCTGTCTTA 2340  
 AGTGAGGGTC TGCGAGGGCT TGACAGTCCC CGGGATTCCC TGATCCAGCT GGCAGCTTAC 2400  
 GCGACCTGC GGTACCAACA GGACGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460  
 65 CAGTCAACC TCTGCAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520  
 GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCTACTGCGA GAACCGTGAG 2580  
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATTG TTGAGACGCC CCTGAGGCAC 2640  
 ATGGCTCCCG TGCGAGAGGG CAGCAGCCGT ACCCCTCCCA GCAACTACAG AGAAGGCCTG 2700  
 GGCACGTAAA TGGTGCCTAC CTCTGGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760  
 70 TTCCCGCGGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCAACA AACGATGTTG TTGAAAAGTT 2880  
 TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCT 2940  
 CTGCCACCTT TCCTTGTAGG ATAAACAAGG GGTCTCTGAG ACTTAAATTT AGCGGCTGTA 3000  
 CGTTCTCTTG CACACAATCA ATGCTGCCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060  
 75 AGGCTTTTAC TAGAGCATCC TTTGGAGGCG GAAGGCCACG GCCTTTCAAG ATGGAAGGCA 3120  
 GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG 3180  
 CTTGAGGAGC GTTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAGA GACTTGGAAA 3240  
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTGTG TGATGGGGGA GGGGCTGAGT 3300  
 80 TGTGCATGGG CCCAGGTCTG GAGGGCCAGC TAAATCGTGT CTGAGTCTGG ACAGATGTCC 3360  
 ACCTGAAGG TCCTC

**A46 Protein sequence**

Gene name: ESTs

Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

10 1 11 21 31 41 51  
 | | | | |  
 MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60  
 SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSPST QQEVKARIKR 120  
 15 MVFKGGRTRT ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180  
 FAVGVRFRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCM RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360  
 RAKVVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIFPRGGPT 420  
 20 LTGSALRQAA ERFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480  
 EAVRAELEEE TGSPKHMVMY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFMLD TSA 540  
 SVGPENFAQM QSFVRSCALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLGGVGA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRRNGI 660  
 SVLVVGVGV LSEGLRLRLAG PRDSLHVA YADLRVHQDV LIENLCGEAK QPVNLCKPSP 720  
 25 CMNEGSCVLQ NGSYRCRCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFW NVCAQGP

## COLON

30 A47 DNA SEQUENCE:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 35 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 | | | | |  
 CGGCACCAAG AGCACTGGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120  
 GCATAAAAA AGGAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 45 ATGTTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300  
 CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCTAGAAAT CATGTTTGT 420  
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGCTC GGGATTATACC CCTATTGATA GAAACATGA AGAAGCATT AAGACTTATT 540  
 50 CAGTCAGACC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAGAGAT CAAATTTTAT 600  
 GAAGAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660  
 TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720  
 TCTGAAAAA AAAAAAAAAA AAAAAAAAAA

55 A48 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 60 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

65 1 11 21 31 41 51  
 | | | | |  
 MMLHSALGLC LLLVTSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAQKSKK 60  
 PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETDKNLS PDGQVYPRIM 120  
 70 FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A49 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 56  
 Unigene number: Hs.6527  
 75 Probeset Accession #: AA478599  
 Nucleic Acid Accession #: NM\_005682  
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | |  
 CGGCAGCAGG GTCTCGCTCT GTACACAGG CTGGAGTGCA GTGGTGTGAT CTGGGCTCAT 60  
 CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120  
 ATTACAGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CAGTCGCTG 180

CTGCAGACGA CACTGTTCCT GCTGAGTCTG CTCTTCCTGG TCCAAGGTGC CCAACGGCAGG 240  
 GGCCACACAGG AAGACTTTGG CTCTGTCAGC CAGCGGAACC AGACACACAG GAGCAGCCTC 300  
 CACTACAAAC CCACACCAGA CCTGCGCATC TCCATCGAGA ACTCCGAAGA GGCCCTCACA 360  
 GTCCATGCCCC CTCTCCCTGC AGCCCAACCT GCTTCCCGAT CCTTCCCTGA CCCCAGGGGC 420  
 CTCTACCACT TCTGCCTCTA CTGGAACCGA CATGCTGGGA GATTACATCT TCTCTATGGC 480  
 AAGCGTGACT TCTTGCTGAG TGACAAAGCC TCTAGCCTCC TCTGCTTCCA GCACCAGGAG 540  
 GAGAGCCTGG CTCAGGGCCC CCCGCTGTTA GCCACTTCTG TCACCTCCTG GTGGAGCCCT 600  
 CAGAACATCA GCCTGCCAGC TGCCGCCAGC TTCACCTTCT CCTTCCACAG TCCTCCCCAC 660  
 ACGGCCGCTC ACAATGCCTC GGTGGACATG TGGAGCTCA AAAGGGACCT CCAGCTGTCTC 720  
 AGCCAGTTTC TGAAGCATCC CCAGAAGGCC TCAAGGAGGC CCTCGGCTGC CCCCAGGAGC 780  
 CAGCAGTTGC AGAGCCTGGA GTCGAAACTG ACCTCTGTGA GATTCAATGG GGACATGGTG 840  
 TCCTTTCGAG AGGACCCGAT CAACGCCACG GTATGGAAGC TCCAGCCAC AGCCGGCCTC 900  
 CAGGACCTGC ACATCCACTC CCGGCAGGAG GAGGAGCAGA GCGAGATCAT GGAGTACTCG 960  
 GTGCTGCTGC CTCGAACACT CTTCAGAGG ACGAAAGGCC GGAGCGGGA GGCTGAGAAG 1020  
 AGACTCTCTC TGGTGGACT CAGCAGCCAA GCCCTGTTC AGGACAAGAA TTCAGCCAA 1080  
 GTCTGTGGTG AGAAGTGTG GGGGATTGTG GTACAGAAAC CCAAGTAGC CAACCTACG 1140  
 GAGCCCGTGG TGCTCACTTT CCAGCACCAG CTACAGCCGA AGAATGTGAC TCTGCAATGT 1200  
 GTGTTCTGGG TTGAAGACCC CACATTGAGC AGCCCGGGGC ATTGGAGCAG TGCTGGGTGT 1260  
 GAGACCGTCA GAGAGAAAC CCAACATCC TGCTTCTGCA ACCACTTGAC CTACTTTGCA 1320  
 GTGCTGATGG TCTCTCGTGG GAGGTGGAC GCCGTGCACA AGCACTACCT GAGCCTCTCTC 1380  
 TCCTACGTGG GCTGTGTGTG CTCTGCCCTG GCCTGCCTTG TCACCATTCG CGCCTACCTC 1440  
 TGCTCCAGGG TGCCCTTGCC GTGCAGGAGG AAACCTCGGG ACTACACCAT CAAGGTGCAC 1500  
 ATGAACCTGC TGCTGGCCGT CTCTCTGCTG GACACGAGCT TCCTGCTCAG CGAGCCGGTG 1560  
 GCCCTGACAG GCTCTGAGGC TGGCTGCCGA GCCAGTGCCA TCTTCTGCA CTCTCCCTG 1620  
 CTCACCTGCC TTCTCTGGAT GGGCCTCGAG GGGTACAACC TCTACCGACT CGTGGTGGAG 1680  
 GTCTTTGGCA CCTATGTGCC TGGCTACCTA CTCAGCTGA GCGCCATGGG CTGGGGCTTC 1740  
 CCCATCTTTC TGGTGAAGCT GGTGGCCCTG GTGGATGTGG ACAACTATGG CCCATCATC 1800  
 TTGGCTGTGC ATAGGACTCC AGAGGGCGTC ATCTACCTT CCATGTGCTG GATCCGGGAG 1860  
 TCCTTGGTCA GCTCATACAC CAACCTGGGC CTCTTCAGCC TGCTGTCTT GTTCAACATG 1920  
 GCCATGTCTG CCACCATGGT GGTGCAGATC CTGCGGCTGC GCGCCACAC CCAAAAGTGG 1980  
 TCACATGTGC TGACACTGTC GGGCCTCAGC CTGGTCTTGG GCCTGCCCTG GGCCTTGATC 2040  
 TTCTTCTCTT TTGCTTCTGG CACCTTCCAG CTGTCTGCTC TCTACCTTTT CAGCATCATC 2100  
 ACCTCCTTCC AAGGCTTCTT CATCTTCATC TGGTACTGGT CCATGCGGCT GCAGGCCCGG 2160  
 GGTGGCCCTT CCCTCTGAA GAGCAACTCA GACTGGGCCA GGCTCCCAT CAGCTCGGGC 2220  
 AGCAGCTGTG CCAGCCGATC CTAGGCCCTC AGCCCACTGG CCATGTGAT GAAGCAGAGA 2280  
 TGGCGCTCG CTGAGGCTG CCTGTGGCCC CCGAGCCAGG CCGAGCCCA GGCAGTCTG 2340  
 CCGCAGACTT TGGAAAGCCC AAGSACCATG GAGAGATGGG CCGTTGCCAT GGTGAGCGGA 2400  
 CTCGCGGGGC TGGGGCTTTT GAATGGCCCT TGGGGACTAC TCGGCTCTCA CTCAGCTCCC 2460  
 ACGGAGCTCA GAAATGGGCC GCCATGCTGC CTAGGGTACT GTCCCCACAT CTGTCCCAAC 2520  
 CCAGCTGAGG GCCTGGTCTC TCCTTACAAC CCCTGGGCCC AGCCTCATTG CTGGGGGCCA 2580  
 GGCTTTGGAT CTGAGGGTGC TGGCACATCC TTAATCTGT GCGCTGCCT GGGACAGAAA 2640  
 TGTGGCTCCA GTTGTCTGT CTCTCGTGGT CACCTGAGG GCACTCTGCA TCCTCTGTCA 2700  
 TTTTAACCTC AGGTGGCACC CAGGGCGAAT GGGGCCAGG GCAGACCTTC AGGGCCAGAG 2760  
 CCTGGCCGA GGAGAGGCC TTTGCCAGGA GCACAGCAG AGCTCGCCTA CCTGTAGGCC 2820  
 G

**A50 Protein sequence**

Gene name: G protein-coupled receptor 56  
 Unigene number: Hs.6527  
 Protein Accession #: NM\_005682.1  
 Signal sequence: 1-26  
 GPS domain: 342-394  
 Pfam domain: 7tm\_2 [400-665]  
 Transmembrane domains: 410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MTQSQLQTT LFLLSLLFLV QGAHGRGHRE DFRPCSQRNQ THRSSLHYKP TPDLRISIEN 60  
 SEEALTVHAP PPAHPASRS PFDPRGLYHF CLYNNRHAGR LHLLYGKRDF LLSDKASSLL 120  
 CPQHQBESLA QGPPLLATSV TSWNSPQNIS LPSAASPTFS FHSPPHTAAH NASVDMCELK 180  
 RDLQLLSQFL KHPQKASRRP SAAPASQQLQ SLESKLTSVR PMGDMVSFEE DRINATVWKL 240  
 QPTAGQLDLH IHSRQEEQS EIMEYSVLLF RTLPQRTKGR SGEAEKRLLL VDFSSQALPQ 300  
 DKNSQVLGE KVLGIIVQNT KVANLTFVTV LTFQHLQPK NVTLCQVFWV EDPTLSSPGH 360  
 WSSAGCTVR RETQTSFCFN HLTTFVAVLMV SSVEDAVHK HYLSSLVYVG CVVSALACLV 420  
 TIAAYLCRSV PLPCRRKPRD YTIKVMNLL LAVFLLDTSF LLSEPVALTG SEAGCRASAI 480  
 FLHFSLLTCL SWMGLGYNL YRLVVEVFGT YVPGYLLKLS AMGWGFPFIFL VTLVALVDVD 540  
 NYGPILAVH RTEPGVIYPS MCWIRDSLVS YITNLGLPSL VFLFNMAMLA TMVQILRLR 600  
 PHTQKSHVL TLLGLSLVLG LPWALIFFSF ASGTFQLVVL YLFSIITSFQ GFLIFIWYWS 660  
 MRLQARGGPS PLKNSDCAR LPISSGSTSS SRI

**A51 DNA SEQUENCE**

Gene name: Hypothetical protein FLJ20063  
 Unigene number: Hs.5940  
 Probeset Accession #: AA053660  
 Nucleic Acid Accession #: AA053660  
 Coding sequence: 218-1360 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CCCCATGAC TTTGTACAGC TACTTCACTG CTTCCTCCCA ATTAGTACAC ATAGTTCCTC 60

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CACAATTCCT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCCTCCA CAATTCCTAT 120  
 ACCTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAT TCATTAGCTA CCTCTGACAT 180  
 AATCACCGCT TCATCTCCAA ATGATGGATT AATCACAATG GTTCCTCTG AAACACAAAG 240  
 TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGCCTC CCACTGGCAC 300  
 CGCTTTATTG GAGACCAAGC CCTTAAACAG CACAGGTCCC AGCAATCCTT GCCAAGATGA 360  
 TCCCTGTGCA GATAATTGCT TATGTGTTAA GCTGCATAAT ACAAGTTTTT GCCTGTGTTT 420  
 AGAAGGGTAT TACTACAAC CTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT 480  
 TTCAGTGACA GTATCAGAAA CATTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA 540  
 CTGTCATAGT GAAATTACTA GCTTGTTTAA AGATGTATTT GGCACATCTG TTTATGGACA 600  
 GACTGTAATT CTACTGTAA GCACATCTCT GTCACCAAGA TCTGAAATGC GTGCTGATGA 660  
 CAAGTTTGTG GATGTAACAA TAGTAACAA TTTGGCAGAA ACCACAAGTG ACAATGAGAA 720  
 GACTGTGACT GAGAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA 780  
 TGATTTGACC CTTCGGTGTG ATTATTATGG CTGTAACCAG ACTGCGGATG ACTGCCTCAA 840  
 TGGTTTAGCA TGGATTTGCA AATCTGACCT GCAAGGGCCT AACCACAGA GCCCTTTCTG 900  
 CGTTGCTTCC AGTCTCAAGT GTCTGATGC CTGCAACGCA CAGCACAGC AATGCTTAAT 960  
 AAAGAAGAGT GGTGGGGCCC CTGAGTGTGC CTGCGTGCCC GGCTACCAGG AAGATGCTAA 1020  
 TGGGAAGTGC CAAAAGGTGTG CATTGGGCTA CAGTGGACTC GACTGTAAAG ACAAAATTTCA 1080  
 GCTGATGCTC ACTATTGTGG GCACCATGCG TGGCATTGTC ATTCTCAGCA TGATAATTGC 1140  
 ATTGATTGTC ACAGCAAGAT CAAATAACAA AACGAAGCAT ATTGAAGAAG AGAACTTGAT 1200  
 TGACGAAGAC TTTCAAATC TAAAAGTGGG GTGACAGGC TTCAACAATC TTGGAGCAGA 1260  
 AGGGAGGCTC TTTCCTAAGG TCAGGATAAC GGCTCCAGA GACAGCCAGA TGCAAAATCC 1320  
 CTATTCAAGA CACAGCAGCA TGCCCGCCCC TGACTATTAG AATCATAAGA ATGTGGAACC 1380  
 CGCCATGGCC CCAATCCAAAT GTACAAGCTA TTATTTAGAG TGTTTAGAAA GACTGATGGA 1440  
 GAAGTGAGCA CCAATAAAGA TCTGGCCTCC GGGGTTTTTC TTCCATCTGA CATCTGCCAG 1500  
 CCTCTCTGAA TGGAAAGTGT GAATGTTTGC AAGCAATCCA GCTCACTTGC TAAATAAGAA 1560  
 TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGTG AGAGAGGTGG TTTTCTTCAA 1620  
 TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTCTTCT TAATCTTTT CCTGGTAGGG 1680  
 CAACAGAAC CCAATTTCAA CTAGAGGAAA GCTCCCCAGC ATTGCTTGCT CTTGGGCAAA 1740  
 CATTGCTCTT GAGTTAAGTG ACCTAATCC CCTGGGAGC ATACGCATCA ACTGTGGAGG 1800  
 TCCGAGGGGA TGAGAAGGGA TACCACCAT CTTCAGGGG TCACAAGCTC ACTCTCTGAC 1860  
 AAGTCAGAT AGGGACACTG CTCTATCCC TCCAATGGAG AGATTCTGCG AACCTTTGAA 1920  
 CAGCCAGAG CTGCAACCT AGCCTCACCC AAGAAGACTG GAAAGAGACA TATCTCTCAG 1980  
 CTTTTTCAGG AGGCGTGCCT GGAATCCAG GAACTTTTG ATGCTAATTA GAAGGCCTGG 2040  
 ACTAAAATG TCCACTATGG GGTGCACTCT ACAGTTTTTG AAATGCTAGG AGGCAGAGG 2100  
 GGCAGAGAGT AAAAACATG ACCTGGTAGA AGGAAGAGAG GCAAAGGAAA CTGGGTGGGG 2160  
 AGGATCAATT AGAGAGGAGG CACCTGGGAT CCACCTTCTT CCTTAGGTCC CCTCCTCAT 2220  
 CAGCAAGGGA GCACCTCTCT AATCATGCCC TCCGGAAGAC TGGCTGGGAG AAGGTTTAAA 2280  
 AACAAAAAT TCCAGGATTA GAGCCTTAGG TCAGTTTGAA ATTGGAGACA AACTGTCTGG 2340  
 CAAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCC GTCCAGCCTC GGGGTGTAGG 2400  
 TTCTGAGGT GTGCCATTGG GGCCTCAGCC TTCTCTGGTG ACAGAGGCTC AGCTGTGGCC 2460  
 ACCAACACAC ACCACACAC ACACACAAAT GGGGGCAACC ACATCCAGTA 2520  
 CAAGCTTTTA CAAATGTTAT TAGTGTCTT TTTTATTCT AATGCCCTGT CCTCTTAAA 2580  
 GTTATTATAT TTGTTATAT TATTGTCTT TGACTGTAA TTGTGAATGG TAATGCAATA 2640  
 AAGTGCCITT GTTAGATGTT GAAAAAATA AAAAAAATA AAAAAAATA A

**A52 Protein sequence:**

Gene name: Hypothetical protein FLJ20063  
 Unigene number: Hs.5940  
 Probeset Accession #: AA053660  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 289-311  
 EGF domain: 45-74  
 SEA domain: 80-196  
 Cellular Localization: plasma membrane

60  
65

1 11 21 31 41 51  
 MVPSETQSNN EMSPTTEDNQ SSGPPTGTAL LETSTLNSTG PSNPCQDDPC ADNSLCVKLH 60  
 NTSFCLCLEG YYNSSTCKK GKVPFGKISV TVSETFDPEE KHSMAVQDLH SEITSLFKDV 120  
 FGTSVYQTV ILTVSTSLSP RSEMRADDKF VDVITVILA ETTSNDEKTV TEKINKAIRS 180  
 SSSNPLNYDL TLRCDYYGDN QTADDCLNGL ACDCSKDLQR PNPQSPFCVA SSLKCPDACH 240  
 AQHKQCLIKK SSGAPEACV PGYQEDANGN CQKCAFYSG LDCDKKFLI LTIVGTIAGI 300  
 VILSMIILAI VTARSNNKTK HIEEENLIDE DFQNLKLRST GFTNLGAEBS VFPKVRITAS 360  
 RDSQMNPYS RHSSMPRPDY

**A53 DNA SEQUENCE**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80

1 11 21 31 41 51  
 ACCGGGCACC GGACGGCTCG GGTACTTTCTG TTCCTAATTA GGTCAATGCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCCTG AATAGTCTAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240

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TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTGTC ACCAGATGCA 300  
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360  
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
TCAGGGAGAT ACAGATGTGCT CATCATCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
GGAGTCTCGG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCATGTGCTC CGATGACTGG 600  
AAGGGTCACT ACSCAAATGT TGCCTGTGCC CAATGGGTT TCCCAAGCTA TGTGAGTTCA 660  
GATAACCTCA GAGTAGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
TGTGCTCTG GCCACGTGGT TACCTTGACG TGCACAGCCT GTGGTCTATG AAGGGGCTAC 840  
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
CTTCAGTTCC AGGGCTACCA CCGTGTGCGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960  
ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
CTAGTTTCCC TGTGTGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCCAC 1080  
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200  
GATGGAAGAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
TCCCCTGTC TGAACACAGC GGCCGTCCCT TTGATTTCCT ACAAGATCTG CAACCAAGG 1320  
GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
GTGGACAGCT GGCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
AAGTTAGTGG GAGCGACCCG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
TACACCCGTG TCACCTCCTT CTTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTTG AGGTGATGAA GACAGCCCGA 1620  
TCTTCCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
TTCCGGCACC AGTAGCAGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACTT 1740  
CAAGCTGCTT TTTGTTTTTT GTTTTTTGA GGTGAGTCT CGCTCTGTTG CCCAGGCTGG 1800  
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCTGTGTTCA AGCGATTCTC 1860  
TGCCTCTAGC TATCCAGTGA GCTGGGACCA CAGGTGCCCG CCACCAACAC CACTAATTT 1920  
TTGATTTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
CCTCAAAATGA TGTGCTCTGT TCAGCTCTCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040  
ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
AGGGGGCCTT TCCCACTGG TCCATCTGCT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160  
ACGAGATAAG CAGTATATG ACCTACGCTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
GCACAGCCCC AGAAGTGACG AACTGCAGTC ACTGCAGCTT TCTATCTCTA GGGACCAGAA 2280  
CCAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTTGTAGC ATTGTGTGCT TGACGTATTA 2400  
TTGCTCTTGG ATTCCAAATA ATATGTTTCC TTCCCTCATA AAAAAAAAAA AAAAAAAAAA 2460

## A54 Protein sequence:

Gene name: TMPRSS3a  
Unigene number: Hs.298241  
Probeset Accession #: AI538613  
Protein Accession #: BAB20077  
Signal sequence: none found  
Transmembrane domains: 43-65, 239-261  
Tryp\_SPC domain: 216-444  
Cellular Localization: plasma membrane

50  
55  
60

1 11 21 31 41 51  
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLPLKFFP IIVIGIIALI 60  
LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120  
TAASWKTMCs DDWKHYANV ACAQLGFPSY VSSDNLRVSS LGGQFREEFV SIDHLLPDDK 180  
VTALHHSVYV REBCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWVP QASLQFQGYH 240  
LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGVKVCW SGWGATEDGA GDASPVINHA 360  
AVPLISNLIK NHRDVYGGII SPSMLCAGYL TGGVDSQCGD SGGPLVCQER RLWLVLGATS 420  
FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

## A55 DNA SEQUENCE

Gene name: Putative G protein-coupled receptor GPCR150  
Unigene number: Hs.97101  
Probeset Accession #: AA215333  
Nucleic Acid Accession #: NM\_014373  
Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70  
75  
80

1 11 21 31 41 51  
GTGGCCTCGA GGTGGTGGCA GGGCCGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG 60  
GCCTCCGGAG GCAGGTTCCG CTGGAAGGAA CCGCTCTCGC TTGCTCTTAC ACTTGGCCAA 120  
ATGCTCTCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180  
AAATAACATA ATTGAAGGCA GTAAAGTGTA AATTAAATAG GAAGATCATC AGTCAAGGAA 240  
GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGTCT 300  
TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAACTGCTC TTTTCACTAC 360  
CAGTTACGTC AAACAAACCA GCGCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420  
GGGAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAAT 480  
TTTATGGAAT ATTTTGTGAT TTCACTAGCA TTGCTGTATC TTTTACTTTT GGTAAACATT 540  
TCCATTATAT TGTATTTCAG GGATTTTGTA CTTTAAAGCA TTAGGTTTAC TAAATACCAC 600  
ATCTGCCTAT TTTACTCAAT TATTTCTTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC 660  
CTGACAGCTT GTATAGATTA TTGCCTGAAT TTCTCTAAAA CAAACCAAGCT TTCAATTAAAG 720  
TGTCAAAAAT TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTTCAGT CCTTGCTTAT 780

5 GTTTTGGGAG ACCCAGCCAT CTACCAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840  
 TGTCTTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA 900  
 TTTGTAGCTT CATACACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960  
 ACTTCTTATA TGAATGAAAC TATCTTATAT TTTCTTTT CATCCCACTC CAGTTATACT 1020  
 GTGAGATCTA AAAAAATATT CTATCCAAAG CTCATTGTCT GTTTTCTCAG TACCTGGTTA 1080  
 CCATTGTGAC TACTTCAGGT AATCATIGTT TTACTTAAAG TTCAGATTCC AGCATATATT 1140  
 GAGATTGAAT TTCCCTGGTT ATACTTTGTC AATAGTTTTT TCATTGCTAC AGTGATTTGG 1200  
 TTTAATTGTC ACAAGCTTAA TTTAAAGAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260  
 10 TGAAGTGTCT GCTTCATTCC ACTTACAATT CCTAATCTTG AGCAAAATGA AAAGCCTATA 1320  
 TCAATAATGA TTGTGTAATA TTATTAATTA AAAGTTACAG CTGTCATAAG ATCATAATTT 1380  
 TATGACACGA AAGAACTCAG GACATATTAA AAAATAAACT GAACATAAAC AACTTTTGCC 1440  
 CCTGACTGTA TAGCATTTCA GAATGTGTCT TTTGAAGGGC TATACCAAGT ATTAATAGT 1500  
 GTTTTATTTT AAAACAAAA TAATTCCAAG AAGTTTTTAT AGTTATTTCAG GGACACTATA 1560  
 15 TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT 1620  
 GATGTTTGTG TTAATCAAAA AACTACTGG ATGCAAACTG TTATGTAAT CTGAGATTTC 1680  
 ACTGACAACT TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAT GTAAGCAAGA 1740  
 AAAAAAAA

20 A56 Protein sequence  
 Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Protein Accession #: NP\_055188  
 Signal sequence: none found  
 25 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297  
 Cellular Localization: plasma membrane

30 1 11 21 31 41 51  
 | | | | |  
 MTALSSENCs QYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRKNT CQNFMEYFCI 60  
 SLAFVLLLLL VNISIIILYFR DFVLLSIRFT KYHICLFTQI ISFTYGLHY PVFLTACIDY 120  
 CLNFSKTTKL SFKQCKLFYF FTVILINISV LAYVLGDPAI YQSLKAQNAV SRHCFYVSI 180  
 QSYWLSFFMV MILEVARIITC WEEVITLVQA IRTSYMMNET ILYPFSSHS SYTVRSKKIF 240  
 35 LSKLIVCFLS TWLPFVLLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300  
 LKDIGLPLDP FVNKKCCFIP LTIPNLEQIE KPISIMIC

40 A57 DNA SEQUENCE  
 Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 | | | | |  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 50 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCGAGA GCAGAGCCAG CGCGACTTT GGGGCTGAGG GGAGCCCCCG CCGACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCG GGGCCCTGCC CCGTCCCTCC TCCGGGCCCC CCGTCCCTGC CTGACGTGCC 360  
 55 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAGCG AGCTGGAGCA GGAGAAGTCG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCGCTGAGCC AGCAGGAGCG GGGACCTCTG 540  
 GATTCCACTG TCATCTAGTC CTGTGGGGCC GCGTGGGGCC CCAGGGCCAG CCTGGCACTC 600  
 AGCCCTTCGA GGGTGGGGCG CCGATCGCAC CCACCTCTC TGGCTGGAGA CCCCCGGCAG 660  
 60 GCCCAGGCAC AGTCCCGGAG TGGGGCGCTT CCTGCCGGCC TTGCCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTGTGTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTACTACTGG CCGCTGTGAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCCAGCGG TGCCGCGCTG 900  
 GGTCCCATCT TCAGGGAAAG GCATGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
 65 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTCGCC TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGCCAAAG CTGAGGGACC CTGGCTGAGC CGGATCGGCA GCGCGGGTGG GCGAGAGCTT 1200  
 GGCTGTCATG TGCTCTCCAC AGACCTGGG GTGATGGCCT TCCCGCTCTT GGCGGGGAGC 1260  
 70 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCAGCTCA TAGGCAAAAG CTGTTTCCCC CGACTCAGGA TTTCAGAGGC 1380  
 CTGGGGTCTT GCTCAACCCC CTTTGTCTCT ACGCCAGGCC TGCTCCCGAG TTTGAGCTGG 1440  
 GAGAGGGCAC CTCCCTCAGC CAAGGAAAAA GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAAGTCCC CTGTGGGTGT ACTCCCTCAG CCGCTGCCCA GGGCCACTCC CGCTGGTGTCT 1560  
 75 GGAGTACGCA CTGGTGGGGG GGGCTGTCTC AGCCCCAACC GGAGGGTCCC AGTGTACCCA 1620  
 GAACAGGGGG CAGCGCAACA GCATCGATGG GTTCTGCAGC CCGAGGGCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGGCGAG GGCTCCGAT GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1740  
 CCGATGCGGG GGTGAGTGGC TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCATTTGGT 1800  
 ACATGTCCTC ACAGGACAC TGTTCTCAGG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860  
 80 CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGCAGG GTGTGCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980  
 GCGCTCTTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCGCTG 2040  
 ACCTCTCGGG CAGGAAAGGG TGCAGTCTCT GAGGGCCTGT GCGCCACAGC CCCAGCACCC 2100  
 AGGTGGCATG CAGCGCAGTG GTGGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160  
 GGCTGGGGTC TGCCACCCAG GGCTCCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC 2220

5 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280  
 GGTGACTTCA TCAGGAGACC GCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340  
 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTCCG TGCAAGGTGA 2400  
 AAAGAAATAG GTCTCTCCAG TTACAGCTT GAAATCAGGC TAGTGAGTGG CCTTGAGAC 2460  
 CACGAGGGGA GAATTTAAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520  
 GCAGACCTTG CTTGGAGCCT GOCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580  
 GAGCAGCGTC CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAAGT ACATACACGT 2640  
 GCGTGACAC TGATGATACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700  
 10 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760  
 TTTTGTGTTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGGTTACGCG 2820  
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAAAAAA AAAAAGAAAG AAAAAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 15 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A58 DNA sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 20 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGGTAGAAG TGAAGTACTT 60  
 TTTTATTTCG AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120  
 CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCCGGTGTG GCGGCCCTCT CCCAGGAGAG 180  
 30 ACAAAACAGG GTCCACAGTG GCAGCCGCGC CCGGGCGGCC CCTCTGTGA TCCCGTAGCG 240  
 CCCCTGGGCC CGAGCCGCGC CCGGCTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300  
 TCGCCGCTCT CTTTCGGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GGCCGTCTGT 360  
 GTTTCTCTGT TTTCCAGAGT GCCCCATCTC CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420  
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480  
 35 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCCGGAAGG GGAGCTTTGA AAGGTCCAAG 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600  
 GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGGATTCTAT TTCAACCCAA 660  
 CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720  
 CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCTCTGGG GCAGAAATGC TTTCTGTCCC 780  
 40 GATATCTCTA TCATGTCAC TGATGGGAAG TCCAGGGGGG ATGTGSCACT GGCATCCAAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900  
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGG TGCTGTGGC TGAGCAGGTG 960  
 GAGGATGCCA CCAACGGCCT CTTACGACCC CTCAGCAGCT CGGCCATCTG CTCAGCGGCC 1020  
 ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080  
 45 GAGTTCTGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCTTTGC GGTGCTGGCT 1140  
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGTC CACTGTCTAC 1200  
 AGGACCACTC GCCCAGGCCCT CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260  
 CCAGAAGGAG TGGACGGCTA CCAATGCCCT TGCCCGCTGG CCTTGGAGGG GAGGGCTAAC 1320  
 TGTGCCCTGA ASCTGAGCCT GGAATGCAGG GTGACCTCC TCTTCTCTGT GGACAGCTCT 1380  
 50 GCGGGACCCA CTCTGGAGCG CTTCTGTGGG GCCAAGTCT TCGTGAAGCG GTTGTGCGG 1440  
 GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500  
 CTGGTGTGGG TGCCTGTGGG GGAATACCAAG GATGTGCTGT ACCTGGTCTG GAGCCTCGAT 1560  
 GGCATTCCCT TCCGTGTGGG CCCCACCTCG ACGGGCAGTG CCTTGGCGCA GCGCGCAGAG 1620  
 CGTGCTCTCG GAGCGCCAC CAGGACAGGC CAGGACCGGC CAGCTAGAGT GGTGGTTTTG 1680  
 55 CTCACCTGAGT CTCTGAGTCA GGATGAGGTT GCGGGCCACG CGGTGACAGT AAGGGGCGCA 1740  
 GAGCTGTCTC TGCTGGGTGT AGGCAGTGTG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800  
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1860  
 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGGT GCGGACACA AGCCCTGGAC 1920  
 CTGTCCTTCA TGTGGACAC CTCTGCCCTA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980  
 60 AGCTTTGTGA GAAGCTGTGC CTTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGG 2040  
 CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGG TGGACACCAA ACCCAACCGG 2100  
 GCTGCGATGG TCGCGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160  
 ACCGCCCTGC TGACATCTTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTCTGT 2220  
 GTCCCAAGAG CTGTGTTGGT GCTCAGAGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT 2280  
 65 GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGCGTGGG GCTGTCTTA 2340  
 AGTGAGGGTC TGCGGAGGCT TGCAAGTCCC CCGGATTCCC TGATCCACGT GGCAGCTTAC 2400  
 GCGGACCTGC GGTACCAACA GGAAGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460  
 CCAGTCAACC TCTGCAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCGTGCAGAT 2520  
 GGGAGCTACC GCTGCAAGTG TCGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580  
 70 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GATGGATTTC TTGAGACGCC CCGTAGGCGAC 2640  
 ATGGCTCCCG TGACAGAGGG CAGCAGCGGT ACCCTCCCA GCAACTACAG AGAAGGCGCTG 2700  
 GGCATCTGAA CTCTGCTTAC CTTCTGGAAT GTCTGTGCC CAGGTCTCTA GAATGTCTGC 2760  
 TTCCGCGCGT GCGCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 75 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCACA AACGATGTTG TTGAAAAGTT 2880  
 TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CTTTGTGAG GCTATGTCAT 2940  
 CTGCCACCTT TCCTTTGAGG ATAAACAAGG GGTCTGGAAG ACTTAAATTT AGCGGCTCTGA 3000  
 CGTTCCCTTG CACACAATCA ATGCTGCGCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060  
 AGGCTCTTAC TAGAGCATCC TTTGAGCGGC GAAGGCCACG GCCTTTCAAG ATGGAAGCA 3120  
 80 GCAGCTTTTC CACTTCCCCA GAGACATTCT GATGTCATTT GCATTGAGTC TGAAGGGGGG 3180  
 CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGGAAG GACTTGGAAA 3240  
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300  
 TGTGATGGG CCGAGGCTCG GAGGGCCACG TAAATCGTGT CTGAGTCGTG AGCAGTGTCC 3360  
 ACCTGGAAGG TCCTTC

A59 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
    SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QOEVKARIKR 120
    MVFKGGRTRT ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
    FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
20  SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEK RVDLLFLLDS SAGTTLDGFL 360
    RAKVFKRVFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIFFRGGPT 420
    LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
    EAVRAELEEI TGSFVKHVMVY SDPQDLFNQI PELQGLKCSR QRPGCRTQAL DLVFMLDTSA 540
    SVGPENFAQM QSPVRSALQ FEVMPDVTQV GLVVYGSQVQ TAPGLDTKPT RAAMLRAISQ 600
25  APYLGVGSGA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLNRNGI 660
    SVLVVGVGVFV LSEGLRRLAG PRDSLIVHAA YADLRVHQDV LIENLCGEAK QPVNLCKPSP 720
    CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
    RTPPSNYREG LGTEMVPTFW NVCAQGP
  
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 ProbeSet Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTACAGG ATCTGACAGG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
    AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGG CGAGATCAT CATTTGTGGT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGAOGGAGAG 240
    CTGGAAGTGC CCTTGGGGGA GGAAGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGGCT 300
45  GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACTGTG AGGTGCTGGA CTGCGCCACA 360
    GGAACCTGGT TCTCTGCTGT TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
    GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGGG GAACCTCAAGT 540
    GGGCCCTGTC CTTAGGGCTC CTGCTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
50  AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCCAGT AGCACAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CACTGGGTC 720
    CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
    GGCTCAGACA AACTGGGCAG CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
    TTCAACCCCA TCTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
55  ACTTCTCTCA GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
    GCCACCCAC TCTGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
    GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
    GGGTACGAGG GGGAGATCAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
    GACACTGCCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
60  GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCGAGG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTA
  
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 ProbeSet Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

```

1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLKIVILDKY 60
    YFLQGQPLHF IPRKQLCDGE LDCPLGEDEB HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120
    GWNFSACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELRMENSS 180
    GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHVV 240
    LTAAHCFRKH TDVFNWVRA GSKDLGSFPS LAVAKIIIE FNPMPKDNND IALAKLQFPL 300
    TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
    AYQGEVTEKM NCAIGPEGGV DTCQGDSSGP LMYQSDQWHV VGVISWGYGC GGPSTPGVYT 420
    KVSAYLNIWY NVWKAEL
  
```



**A62 DNA SEQUENCE**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
Unigene number: Hs.105484  
Probeset Accession #: AA314779  
Nucleic Acid Accession #: none found  
Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

```
10      1      11      21      31      41      51
      |      |      |      |      |      |
      CCAACAGAT TTGCAGATCA AGGAGAACC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
      CTGAGATCCT TGCCTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
15      CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
      AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
      AAGCTGAGGA ACTGCTCTGA TGCCGAGCTC GAGTGTCACT CTTACGGAAG CGGAGCCAC 300
      CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
      CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420
20      TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
      AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540
      AACAGCGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
      AACTCCTGCA CCAGCCCGCT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
      TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720
25      GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTCTAGCTC TAAATGTTTG 780
      CCOCGCCATC CCTTTCCACA GTATCCTTCT TCCTCCTCC CCTGCTCTG GCTGTCTCGA 840
      GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
      AAAGATTGTA AGACAGAAGG AAGAAACTCA GGAGTAAGCT TCTAGACCCC TTCAGTTCT 960
      ACACCTTCT GCCTCTCTC CATTCCTGAC ACCCCACCCC AGCCACTCAA CTCTGCTTG 1020
30      TTTTCTCTT GGCCTATAGA AGGTTTACCA GTAGAATCCT TGCTAGGTG ATGTGGGCCA 1080
      TACATTCCTT TAATAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
```

**A63 Protein sequence:**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
Unigene number: Hs.105484  
Probeset Accession #: AA314779  
Protein Accession #: none found  
Signal sequence: 1-22  
Transmembrane domains: none found  
C-type lectin domain: 47-156  
Cellular Localization: secreted

```
45      1      11      21      31      41      51
      |      |      |      |      |      |
      MASRMRLLLL LLCLAKTGV LGDIIMRPSC APGNFYHKSN CYGYFRKLNR WSDAELEQCS 60
      YNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG 120
      KSMGGNKHCA EMSSNNFNLT WSSNECNKRQ HFLCKYRP
```

**A64 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
Unigene number: Hs.2877  
Probeset Accession #: X63629  
Nucleic Acid Accession #: X63629  
Coding sequence: 54-2543 (start and stop codons are underlined)

```
60      1      11      21      31      41      51
      |      |      |      |      |      |
      GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
      TCCTCTGTGG ACCTCTGCGG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
      CCTCCGAGCC GTGCCGGCGG GTCTTCAGGG AGGCTGAAGT GACCTTGAGG GCGGAGGGCG 180
      CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
      CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
65      AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCATCCAAA CGTATCTTAC 360
      GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
      CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTCTCT 480
      ACAGCATCAC GCGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTGGCT GTAGAGAAGG 540
      AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
70      TCTTTGGCCA CGCTGTGTC GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
      TCATCGTGAC CGACAGCAAT GACCAACAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
      GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
      ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
      AGGACCCACA CGACTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
75      CCACTGGCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
      TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
      ACAATGCTCC CATGTTTGAC CCCAGAGAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080
      GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAGGC CCCCACTCA CCAGCGTGGC 1140
      GTGCCACCTA CTTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
80      CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGSGTTT GGATTTTGAG GCCAAAAACC 1260
      AGCACCCCTA GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
      CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACTGTG TTTGTCCAC 1380
      CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
      CTGCAGAAGA CCCTGACAAG GAGAATCAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500
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5  
10  
15  
20  
25  
30

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CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
ATGGAAGCCC TCCCACCCT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAAAG 1680
ACCATGGCCC AGTCCCTGAG CCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
ACCTGTCTGA CATCAAGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTTC CAGGCCCAGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAG CGAGGAAGGT GACACAGTGG 1860
TCTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTGGAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
TCAGGAGGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
AGGCCAGGGG GAGGTTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
TGTAACGTCC TAGGCCAGCG AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
AGGGCGCTAA CACAGACCCC ACAGCCCGCG CCTACGACAC CCTCTTGGTG TTCGACTATG 2400
AGGGCAGCGG CTCGAGCGG GCGTCCCTGA GCTCCCTCAC CTCCCTCCGC TCCGACCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAGAAGCTG GCAGACATGT 2520
ACGGTGGCGG GAGGAGCAGC TAGGGCGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580
CACAGAGCAT CTGCTCTTAC TCTCAGTTCC CCTCTCAGCT GAGGACTTGG GAGCTTGTCA 2640
GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCC AGSGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
TGCTCAACCC TGTGCTCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
CTGGAATGGA ACCTTCTTAT GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940
TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCACGA GCTGCTGGGC CCACTGGCCG 3000
TCCTGCATT CTGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCGTTTTT 3060
ATCTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CTGTGCGT TGCTATAGAT 3120
GAAGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAGAA A

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35  
40

A65 Protein sequence:  
Gene name: Cadherin 3, P-cadherin (placental)  
Unigene number: Hs.2877  
Probeset Accession #: X63629  
Protein Accession #: CAA45177  
Signal sequence: 1-24  
Transmembrane domain: 659-675 (second underlined sequence)  
Cellular localization: plasma membrane

45  
50  
55

```

1 11 21 31 41 51
MGLPRGPLAS LLLQLQCNLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDVW VAPISVPENG 120
KGPPFQRINQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGNLLLN KPLDREBIK 180
YELFGHAYNE NGASVEDPMN ISIIVTDQND HKPKFTQDTP RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TMDGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360
AWRATYLMG GDDGDHFTIT THPESNQGLL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480
DPAGNLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
VNDHGFVPEP RQITICNQSP VRHVLNITDK DLSFHTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKFEI KQTYDVHLIS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFIFLVL 660
GAVLALLFL LVLLLVRK RKIKEPLLLP EDDTRDNVFP YGEEGGGEED QDYDITQLHR 720
GLEAREPVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

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A66 DNA SEQUENCE  
Gene name: ATPase, Ca++ transporting, type 2C, member 1  
Unigene number: Hs.106778  
Probeset Accession #: N51919  
Nucleic Acid Accession #: AF189723  
Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

70  
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1 11 21 31 41 51
ATGATTCTCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTIGCAAGC 60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
TTTCATGTCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTCTCGGCTT CTGCAATCAT CAGTGTTTAA 240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTACAGTT 300
GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
CCAGAAATGCC ATTGTGTGGG TGAAGGAAAA TTGGAGCATA CACTTGCCTG AGACTTGGTT 420
CCAGGTGATA CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTCT 480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTT 540
AAGGTGACAG CTCTCAGCGC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTT TGAACACGGA 660
GAAATTTCTG AATTTGGGGA GGTTTTAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840

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ATTAGTGTA  GTTTGGCTGT  AGCAGCAATT  CCTGAAGGTC  TCCCCATTGT  GGTACAGTGT  900
ACGCTAGCTC  TTGGTGTAT  GAGAAATGGT  AAGAAAAGGG  CCATTGTGAA  AAAGCTGCCT  960
ATTGTTGAAA  CTCTGGGCTG  CTGTAATGTG  ATTTGTTTCA  ATAAACTGG  AACACTGACG  1020
AAGAAATGAAA  TGACTGTTAC  TCACATATTT  ACTTCAGATG  GTCTGCATGC  TGAGGTTACT  1080
GGAGTTGGCT  ATAATCAATT  TGGGGAAGTG  ATTGTTGATG  GTGATGTTGT  TCATGGATTG  1140
TATAACCCAG  CTGTTAGCAG  AATTGTTGAG  GCGGGCTGTG  TGTGCAATGA  TGCTGTAATT  1200
AGAAACAATA  CTCTAATGGG  GAAGCCAACA  GAAGGGGCT  TAATTGCTCT  TGCAATGAAG  1260
ATGGGCTTGT  ATGGACTTCA  ACAAGACTAC  ATCAGAAAAG  CTGAATACCC  TTTTAGCTCT  1320
GAGCAAAAGT  GAGTGGCTGT  TAAGTGTGTA  CACCGAACAC  AGCAGGACAG  ACCAGAGATT  1380
TGTTTTATGA  AAGGTGCTTA  CGAACAAAGT  ATTAAGTACT  GTACTACATA  CCAGAGCAAA  1440
GGGCAGACCT  TGACACTTAC  TCAGCAGCAG  AGAGATGTGT  ACCAACAAAG  GAAGGCAAGC  1500
ATGGGCTCAG  GGGGACTCAG  AGTTCCTGCT  TTGGCTTCTG  GTCCGTGAAT  GGGACAGCTG  1560
ACATTTCTTG  GCTTGGTGGG  AATCATTTAT  CCACCTAGAA  CTGGTGTGAA  AGAAGCTGTT  1620
ACAACACTCA  TTGCTCAGG  AGTATCAATA  AAAATGATTA  CTGGAGATTG  ACAGGAGACT  1680
GCAGTTGCAA  TCGCCAGTGT  TCTGGGATTG  TATTCACAAA  CTCCCACTG  AGTCTCAGGA  1740
GAAGAAATAG  ATGCAATGGA  TGTTCAGCAG  CTTTCACAAA  TAGTACCAAA  GGTTCAGTA  1800
TTTTACAGAG  CTAGCCCAAG  GCACAAGATG  AAAATTATTA  AGTCGTGACA  GAAGAAGCGT  1860
TCAGTTGTAG  CCATGACAGG  AGATGGAGTA  AATGATGCAG  TTGCTCTGAA  GGCTGCAGAC  1920
ATTGGAGTTG  CGATGGGCGA  GACTGGGTACA  GATGTTTGCA  AAGAGGCAGC  AGACATGATC  1980
CTAGTGGATG  ATGATTTTCA  AACCATAATG  TCTGCAATCG  AAGAGGGTAA  AGGGATTAT  2040
AATAACATTA  AAAATTTCTG  TAGATTCCAG  CTGAGCACGA  GTATAGCAGC  ATTAACITTA  2100
ATCTCATTTG  CTACATTAAT  GAACCTTCTC  AATCCTCTCA  ATGCCATGCA  GATTTTGTGG  2160
ATCAATATTA  TTATGGATGG  ACCCCAGCT  CAGAGCCTTG  GAGTAGAACC  AGTGGATAAA  2220
GATGTCATTG  GTAAACCTCC  TCGCAACTGG  AAAGACAGCA  TTTTGACTAA  AAACTTGATA  2280
CTTAAATATC  TTGTTTCATC  AATAATCATT  GTTTGTGGGA  CTTGTTTGT  CTCTGGCGT  2340
GAGCTACGAG  ACAATGTGAT  TACACCTCGA  GACACAACAA  TGACCTTCAC  ATGCTTTGTG  2400
TTTTTGACA  GTTTCATGTC  ACTAAGTTCC  AGATCCCAGA  CCAAGTCTGT  GTTTGAGATT  2460
GGACTCTGCA  GTAATAGAA  GTTTTGTAT  GCAGTTCTTG  GATCCATCAT  GGGACAATTA  2520
CTAGTTATTT  ACTTCTCTCC  GCTTCAGAAG  GTTTTTCAGA  CTGAGAGCCT  AAGCATACTG  2580
GATCTGTTGT  TTTCTTTGGG  TCTCACCTCA  TCAGTGTGCA  TAGTGGCAGA  AATTATAAAG  2640
AAGGTTGAAA  GGAGCAGGGA  AAAGATCCAG  AAGCATGTTA  GTTCGACATC  ATCATCTTTT  2700
CTGAAGTAT  GA
  
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**A67 Protein sequence:**  
 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

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1 11 21 31 41 51
| | | | |
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNFEFDS EDEPLMKKYI 60
SQFKNPLIML LLASAVISVL MHQFDVDAVS TVAILIVVTV APVQYRSEK SLEELSKLVP 120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSDIES SLTGTTTPCS 180
KVTAQPAAAT NGDLASRSNI AFMTGLVRGC KAGGVVIGTG ENSEFGEVFK MMQAEBAEPK 240
PLOKSMDLIG KQLSFYSFSGI IGIIMLVGNL LGRDILEMPT ISVSLAVAAI PEGLPPIVTV 300
TLALGVMRMV KKRAIVKGLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360
GVGVNQFGEV IVDGVDVHGF YNPAVSRIE AGVCNDVAI RNNTLMGKPT EGALIALAMK 420
MGLDGLQQDY IRKAEYFPSS BQKMAVKCV HRTQDRPEI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYVQEKAR MGSAGLEVLA LASGPGLQL TFLGLVGIID PPRTGVKEAV 540
TTLLASGVSI KMITGDSQET AVAIALSLGL YSKTSQSVSG EIDAMDVQQ LSQIVPKVAV 600
PYRASPRHKM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGTGT DVCKEADMI 660
LVDDDFQTIM SAIEEGKGIY NNIRKPFVRPQ LSTSIALLTL ISLATLMNFP NPLNAMQILW 720
INIMDGPPA QSLGVEFVVK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFPVFW 780
ELRENVITPR DTTMTFTCFV FFDMFNALSS RSQTSKVFEI GLCSNRMFCY AVLGSIMQQL 840
LVIFYPPLOK VFQTESLSIL DLLFLLGLTS SVCIVAEI IK KVERSREKI Q KVSSTSSSF 900
LEV
  
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**A68 DNA SEQUENCE**  
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CGGAGGCCCG GGTAGCGCGT AGAGCCGCG 120
CGATGCACGT GCGCTCACGT CGAGCTGCGG CGCGCACAG CTCTGTGGCG CTCTGGGCG 180
CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240
GCTTCATCCA CGGCGGCTCC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT CTGCGACCTG TACAACGCCA TGGCGGTGGA GAGGGCGGCG GGGCCCGGCG 420
GCCAGGGCTT CTTCTACCCC TACAAGGCGG TCTTCAGTAC CAGGGGCCCC CTTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
TGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCGCGGCA ATTCGGGATC TACAAGGACT 660
  
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ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCGG 780
AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT GGGCTTCGAG CTCTCGGTGG AGAOGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCGTATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
TCITCAAGGC CACGAGGTTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AACACAGCGCA 1020
GCCAGAACCG CTCGAAGAGC CCCAAGAACCC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTAGCGCGCC TACTACTGTG 1200
AGGGGGAGTG TGCTTCCCT CTGAATCTCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
AGACGCTGGT CCACGTATC AACCOCGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCAGAA TTCAGACCCT 1440
TTGGGGCCAA GTTTTCTCG ATCTCCATT GCTGCGCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCTTTTG TGAGACCTTC CCTTCCCTAT CCCCACCTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC ACATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCCTACAAGC TGTGACGGCA AAACCTAGCA GGAAAAAACA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTACTTGGCT GGGAACTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAGC AATGAATG
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A69 Protein sequence:  
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195  
Probeset Accession #: BE616633  
Protein Accession #: NP\_001710.1  
Signal sequence: 1-30  
Pfam domains: TGFb\_propeptide [37-281]  
Transmembrane domains: none found  
Cellular Localization: secreted

35  
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45

```
1 11 21 31 41 51
MHVRSIRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLSQSE RREMQRILS 60
ILGLPHRPRP HLQGHKNSAP MFMLDLINAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHRFRFDL SKIPGEAVT AAEFRYKDY 180
IRERFDNETF RISVYQVLQF HLGRESDLFL LDSRTLWASE EGWLVDITA TSNHVVNPR 240
HNLGLQLSVE TLDGGSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
QNRSTPKNQ EALRMANVAE NSSSDORQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
GECAPPLNSY MNATNHAIVQ TLVHFNPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
RNMVVRACGC H
```

#### Cervical

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A70 DNA sequence  
Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

55  
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1 11 21 31 41 51
CGCGGGGCGC GGAGTCGGCG GGGCTCGCG GGACGCGGGC AGTCCGGAGA CCGCGGCGCT 60
GAGGACGCGG GAGCCGGGAG CGCAOGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
CATAACCAAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
AATGTGGGCA CCAGAAAGA GGTGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360
TTGCGTGTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGAGCACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGGGG ACACCTCCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
CTGCCTCCAT TGAAAACAG AGATTTTGTG GATGGACCTA TACACCAAGG GGCTTTACTT 660
ATATCTGTGA CTGCTGTAG TTTGCTCTTG GTCTTATCA TATTATTTTG TTACTTCCGG 720
TATAAAGAGC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCCTCC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTAGAT GGTGAACAG 900
ATTGGAAGG TGCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT 960
GTGAAGGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGAGATAT CAAAGGGACA 1080
GGGTCTCGGA CCAAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
TATCTGAAGT CCAACACCTC AGAGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGCT 1200
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
CATCGAGATC TGAAAGTAA AAACATCTCG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
ACTCGAGTGT GCACCAACAG CTATATGCCCT CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTTGGGAG 1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TGTGTGTCAT CAAGAAGTTA 1620
```

CGCCCTCAT TCCAAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740  
 ACACCTGCCA AATGTCTAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800  
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920  
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTTGTG GCGGAGAAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

#### 10 A71 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51  
 | | | | | |  
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPPE DSVNNICSTD GYCFTMIEED 60  
 DSGLPVVTSQ CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120  
 25 GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYRS IGLEQDETYI PPGESLRDLI 180  
 EQSQSSSGSGS GLPLLVQRTI AKQIQMVKQI GKRGYGEVMM GKWRGEKVAV KVFFTTTEAS 240  
 WPRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KKNGTCCIAAD LGLAVKFISD 360  
 TNEVDIPNPT RVCTIKRYMPP EVLDESINRN HFQSYIMADM YSFGILILWEV ARRCVSGGIV 420  
 30 EEQQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS 480  
 RLTLARVKKT LAKMSESQDI KL

#### Bladder

##### A72 DNA SEQUENCE

35 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 | | | | | |  
 ATGTTACAGG ATCTTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60  
 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120  
 45 CTGAGCTCGG CGAGTATCAT CATTTGTGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180  
 TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240  
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300  
 CGAGTGGCAG TCCGCTCTTC CAAGGACCGA TCCCACTGTC AGGTGCTGGA CTCGGCCACA 360  
 50 GGGAACTGGT TCTCTGCTTG TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420  
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480  
 GATCTGGATG TTGTTGAART CACAGAAAC AGCCAGGAGC TTCGATGCG GAACCTCAAGT 540  
 GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTC 600  
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660  
 55 AGCATCCAGT ACAGACAAAC GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACCTGGTC 720  
 CTCACGGCAG CCCACTGCTT CAGGAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780  
 GGCTCAGACA AACTGGGCGC CTTCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840  
 TTCACCCCA TGTACCCCAA AGACAATGAC ATGCCCTTCA TGAAGCTGCA GTTCCCACTC 900  
 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960  
 60 GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020  
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGCTGCAA TGCAGACGAT 1080  
 GCGTACCAGG GGAAGTCAC CGAGAAGATG ATGTGTGAGC GCATCCCGGA AGGGGGTGTG 1140  
 GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200  
 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260  
 65 AAGGTCTCAG CTTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

#### A73 Protein sequence:

70 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 75 LDLa domain: 54-94  
 Tryp\_SpC domain: 204-429  
 Cellular Localization: plasma membrane/ER

80 1 11 21 31 41 51  
 | | | | | |  
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIVV VLKIVLDKY 60  
 YFLOGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPPEGP AVAVRLSKDR STLQVLDSAT 120

GNWFSACFDN FTEALAEAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180  
 GPCLSGSLVS LHCLACGKSL KTPRVVGEE ASVDSWPQV SIQYDKQHC GGSILDPHV 240  
 LTAHCFRKH TDVFNWVRA GSKLGSFSP LAVAKIIIE FNPMPKND IALMKLQFPL 300  
 TFSGTVRPIK LPFDEELTP ATPLIWIGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360  
 AYQGEVTEKM MCAGIPEGGV DTCQGSDDG LMYQSDQHWV VGIVSWGYGC GGPSTPGVYT 420  
 KVSAYLNWII NVWKAEI

**A74 DNA SEQUENCE**

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]

Unigene number: Hs.19322

Probeset Accession #: AA088458

Nucleic Acid Accession #: AA088458

Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | | |  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACAGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCGGGGCCCC CTTGCCCTGC CTTGACGTCC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCGCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTTGTGGGCC CGGTGGGCCC CCAGGGCCAG CCTGGCACTC 600  
 AGCCCTTCGA GGGTGGGCGC CCCATGCGAC CCACCTCTCT TGGCTGGAGA CCCCAGGCG 660  
 AGCCAGGCAC GGTCTCGGAG TGGGCGCCTT CTTGCCGCCC TTGCCAGATG GGCTCCCGAG 720  
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**A75 DNA SEQUENCE**

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor

Unigene number: Hs.227948

Probeset Accession #: AB035089

Nucleic Acid Accession #: AB035089

Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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 GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60  
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	TTTTTCTCTG	GTTCCGTGGG	CTAGCACGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
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	ATCTAAAGCT	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAG	TGGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTTG	10140
	TAAATCCCTT	TTCTTATTCT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCCATAGA	TGCAATTAGT	CTGTCACTCC	ATTTAGAAAA	TGTTCACTTA	10260
	GAGGTGTTCT	GGTAAACTGA	TTGCTGGCAA	CAACAGATTG	TCTTGGCTCA	TATTTCTTTT	10320



5 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTGA ATGATTAAAA TAGCATGCCT 10380  
 TTCTCTCTTT CTCTTAATAA GCCACATAT AAATGTACTT TCCTTCCAG AAAAATTTC 10440  
 CTTGAGGAAA AATGTCCAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTGAA 10500  
 ATATAATTCT GTTCTTGACC TGTTTAAAT GAACCAACC AAATCATACT TTCTCTTCA 10560  
 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620  
 GTTTCTAAT TTTGTGATTC TATAAACAC ATCATCAATA AAATAATGAC ATAAATCAT 10680  
 TTTTGCTTTA CCGTGTCTCT CTCTGGAAAG GGCAAGTGTC CAGTTACACA TAGGAAAGAT 10740  
 AATTAGAGA TATATTAATC ATATATAAAG GAAATTAATA AACAGACTAG TTCATGATGA 10800  
 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACACA TAGGAACTTC 10860  
 10 CTATTTTATG CTAAAGGAT AAGAACTCA TTACAGGCTT TGATGGTGTG TTGTCAAAGA 10920  
 GGGGCATAAA ATTATCATAT CCACATCTAG AAAATACATC TCTGGCTACG CTGATATCAA 10980  
 TGGATCGAG GAAAGAACAG TGTGGTTACC ATATATAAAT TAGGAAATCA TTAGAGTATT 11040  
 GGGAGTGGAA ATGGAGAGAA AGAAGAGGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100  
 AGAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAGAATA TCTTGTCTT 11160  
 15 GAGAGAAAAA AAGACTTTGG GTTTAAATTT GTACTTGATG AATTAAGGTA CTTTATATAT 11220  
 TCAAATGGAT TTGCTGGCA GGCACCTGAA GATATTAGTC TAAATCTCAG AAACAGAATA 11280  
 TGATCTGAAG CTCTAAATTT GTGATATTCA ATATAAATAC TTTAGAGTCA TTGGGATAAA 11340  
 TATGGTAGTT GTAGCTAAAA GCAAAAATAA GATACTAGGG AGAAGGATA AAGTTAGAAG 11400  
 20 AAGAAGAAAT CTAGAATTGA CCTTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460  
 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTACTCC CATAGATTCT 11520  
 TCCC

25 A76 Protein sequence:  
 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 Unigene number: Hs.227948  
 Probeset Accession #: AB035089  
 Protein Accession #: BAB21525  
 30 Signal sequence: none found  
 Transmembrane domains: none found  
 Serine Proteinase Inhibitor domain: 13-390  
 Cellular Localization: secreted

35 1 11 21 31 41 51  
 MNSLSEANTK FMFDLFQOFR KSKENNIFYS PISITSALGM VLLGAKDNTA QQISKVLHFD 60  
 QVTENTTEKA ATYHVDRSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFGK KTYQLQEYL 120  
 40 DAIKKFYQTS VESTDFANAP EESRKKINSW VESQINEKIK NLFPDGTIGN DTLVLVNAI 180  
 YFKQGWENKF KENNTKEEFK WPNKNTYKSV QMMRQYNSFN FALLEDVQAK VLEIPYKGRD 240  
 LSMIVLLPNE IDGLQKLEEK LTAELMEWT SLQNMRETCV DLHLPRPKME ESYDLKDTLR 300  
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAATATAVV VVELSSPSTN 360  
 EEFCCNHFFL FFIRQNKNTS ILFYGRFPSSP

45 A77 DNA SEQUENCE  
 Gene name: hypothetical protein FLJ13459  
 Unigene number: none found  
 Probeset Accession #: XM\_047266  
 50 Nucleic Acid Accession #: XM\_047266  
 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 60  
 CACCATGCCA GGCCTCTCTA ACCTCTTCAA GTCTGTITTC TCATCTGCAA AACAGAGGTA 120  
 ATAAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTTCAT TCATTGTTAT 180  
 CATAAATGAG GACTAACCTG TCTCCCGTTG GGAGTTTGA ACCTAGACCT CATGTCTTCA 240  
 TGACGTATC ACTGCCCGAG GCCACGCTGT GTCCTACAC CAGCCCCAGC TGAAGCATCT 300  
 60 TCTTTTCTG CCGTAGAGA TGGTTACAT GCCTGGCGTG ATGCATTCTG GCCTTCGAG 360  
 ATCCTGGCGG GCGTGTGCCA ACGCTGTGGC CTCCTGCCCC CTGAATACCG AGCGGTGCT 420  
 TCAAGGTGG GCAGCAAGT CTTCTGACA CCAACGAGA CCCTGCCCCC AGGGATCTCT 480  
 TCACATGTGG ATTGACATCT TTCTCAAGA TGTGCTGCT CCACCCCCAG TTGACATCAA 540  
 GCCTCGCGAG CCAATCAGCT ATGAGCTCAG AGTTGTATC TGGAAACAGG AGGATGTGGT 600  
 65 TCTGGATGAC GAGAATCCAC TCACCGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660  
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGAGCTT CACTTCAACT CCCTGACTGG 720  
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTTGAC TACCTGCCCA CGGAGCGGGA 780  
 GGTGAGCGTC TGGCGCAGGT CTGGACCTTT TGCCCTGGAG GAGGCGGAGT TCCGCGAGCC 840  
 TGCAGTCTG GTCTCGCAGG TCTGGGACTA TGACCGCATC TCTGCCAATG ACTTCTCTTG 900  
 70 ATCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCCGG AGCTCTGCTC 960  
 TGTGCAGCTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTGCTT GCCGCGCCT 1020  
 GAGGGGCTAG TGGCCGCTAG TGAAGCTGAA GGAGGCAGAG GACGTGGAGC GGGAGGCGCA 1080  
 GGAGGCTCAG GCTGGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCCAGAAGA 1140  
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCTC ACGGGCAAGG TGGAGGCAGA 1200  
 75 GTTTGAGCTG CTGACTGTGG AGGAGGCGGA GAAACCGCCA GTGGGAAGG GCGGAGGCA 1260  
 GCCAGAGCCT CTGAGAAAC CCAGCCGCCC CAAAACCTTC TTCACTGGT TTGTGAACCC 1320  
 GCTGAAGACT TTTGTCTCT TCACTGGCG CCGGTACTGG CGCACCTCTG TGCTGCTGCT 1380  
 ACTGGTCTG CTACCGTCT TCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG 1440  
 CCAGGTCTC TCGCTGCCC TCCACAAGT ACTCTGCTG ACCTTGACA CTCACCCAGG 1500  
 80 GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTTCTTA CCCATGTGAG CTACCCAGG 1560  
 GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG

A78 Protein sequence:  
 Gene name: hypothetical protein FLJ13459

Unigene number: none found  
 Probeset Accession #: XM\_047266  
 Protein Accession #: XP\_047266  
 Signal sequence: none found  
 Transmembrane domains: 291-313  
 C2 domain: 27-86  
 Cellular Localization: plasma membrane / ER

10 1 11 21 31 41 51  
 | | | | | |  
 MWIDIFPDQV PAPPFVDIKP RQPISEYELRV VINWTEDEVVL DDENPLTGEM SSDIYVKSUV 60  
 KGLEHDKQBT DVHFNSTLGE GNFNWRPFVR FDYLPTEREV SVWRRSGPFA LEEAEFRQPA 120  
 VLVLQWWDYD RISANFLGS LELQLPDMVR GARGPELCSV QLARNAGAPR CNLPRCRLR 180  
 15 GNVFVVKLKE AEDVEREAOE AQAGKKGRKQ RRRKGRPEDL EFTDMGQNVY ILTGKVEAEF 240  
 ELLTVEEAEK RVPVGKGRKQP EPLEKPSRPK TSFNWFWNPL KTFVFFIWRN YWRTLVLVLLL 300  
 VLLTVFLLLV FYTIPGQISQ VIFRPLHK

20 A79 DNA SEQUENCE  
 Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Nucleic Acid Accession #: AL137708  
 25 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51  
 | | | | | |  
 GGCAITGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60  
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGCT CCCTTCTGT CTGTCTCCCT GCTCTGCCCC 120  
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180  
 ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCGAG 240  
 CTCTTGTGGG CAAGCAGGGG GAGGCCGCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300  
 35 CTGCTCTCTG GAGCGGTGGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCA CCGTGGGCTG 360  
 GGGTCACCGT AGGCCCATG TAGCACCTCG GTTCCCTGCG CTGTAGGTGA CAGGAGCCAG 420  
 CCCAGCCAGG TGTGTCTCCT CCCAGGCCCG TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480  
 CGCCCGCCCC ACCTTCTCTT CCACCCACAT GCCAAGGGT GGGCAGGCAG GCAGGTGGAC 540  
 GAGTCCAGCT AGCGGCTGAG TCAGTGTGTG TGGAAATGTC TGGCCGCTCC CAGCTGCACC 600  
 40 CTGCCCTTAC CTGCCACCAT CTACACTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCTGCG 660  
 CAGGAATGCA CCTTTAGCCC AGGCCGTGCT AGTGAGCTCC GCGCAGACCC AGCCCTGCTC 720  
 CTCCCGCCAT GACCTTGCAG ACCCTCTCTG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC 780  
 ATGCTCCACC TGATGGCTG GCAAAACCAT GTGGGCCCCA GCTGTGTGTC GTGCTGGGGT 840  
 45 AGAGGCAAGG AAGTGTAGGG ACCGACAGAG TGAGACCCCC AGGGATGAGA TGGGACCCCC 900  
 AGGCAAGGCC CAGGGTCCAG GGGCCAGGAG AGAGAAGCAG GAGGAGGAGG AGCTTCTCTG 960  
 TGGAGGACGC ATCTACAGT GGGGCGAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020  
 AGGCTGCCCA GGGCTTGCCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080  
 GCTGGGCGTG GGCAGCTAAG CTGGAGCTTT GGGCAGGGTC CAGAGCTTCC CTCCCTTCAG 1140  
 50 CTCTCTGCTG CACAGAACCC TGGCCCTGCG CCAACCCGTC CTGCTCTCTT GCGCTGGCAG 1200  
 ACCCAGCACT GGCTGTGCTT AGTCAGATGG GGTAGCGGGC AGGGGCCCGA GGGGCCACCC 1260  
 TCCAGCTGA CCGAGTCCC TGGGCCGCTT CTCCAAACC AGCAGGGTAG AAAGATGGGG 1320  
 CACCCACAGG TCTCTCCAG TGGCCCGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380  
 ATTCCAGACC TTGTGCGCGG GACCCCTGTG GAGTTGTGGG ATTCCAGAAG GGGGTGTGGG 1440  
 55 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500  
 CCAGGCGCCC GCTGGGCTCT CATTGCCGCG GCCCTTGGCG GGGGCGTCTT CTCTGCTTCC 1560  
 TGCCCTCTCT GTGCTGCTCT CTGCTGCTGC CGCCGCCACA GGAAGAAGCG CAGGGACAAG 1620  
 GAGTCTGTGG GTCTGGGCGG TGGCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680  
 TCCTTGCTCA CTAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740  
 60 GGCAGATCA GCGCCAGGGA TGGTTTAAAC CCCACAGAGG CAGGGCGTTG AGGACCTTCC 1800  
 TGGCAGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT 1860  
 GGGCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920  
 TTTGGGTGGG TTTGGCGGT CTACAGAGC GAAGCCGACG ATTTGTGCTT GTTGGGTGGC 1980  
 CTGGCTTGA GGCGGGGGGT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCAGGG 2040  
 65 CTCTGATGAG GCATGATGTC AGCACCACTT GCCCTTGTTC CCAACTCACT CCAGGTGCAA 2100  
 CCTGATGAG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCCCTGAG 2160  
 CTCTCCCTGG AGTTGCACTT TGGAAAGCCAG GAGGTGAAGG GCCCGCTGCG GCAGGACCA 2220  
 CGGTCTGCGC AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280  
 TGGGGAGCTG ACAGGGCAGG GGCCTTGGC TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340  
 70 GTGGGCGTGA GGCAGGCAGC CGAAGTGAAG CCTGGGGGCA CCGTGGACCC CTATGCCCGG 2400  
 GTACAGCTCT CCAACAGGCG CGGACACAGA CATGAGACAA AAGTGACACG AGGCAAGCTC 2460  
 TGCCCGCTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGCTGGGTGG 2520  
 GCCTGGAAGG CTGGATGGGC CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580  
 GCTGGGTGGG CTTGAGCTAG GGCAGCAGG CCTGGCTCAC GCGCTGGCTC CAGATCCCGC 2640  
 75 AGGCGGAGCT GCGAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700  
 GGCATGAGCC CTTGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGATCTG CAGCATGTTT 2760  
 TGGAGCTGT GTACCTGCTG GGCAGCGCGG CTGCCACTCA GGTGAGGTGC TGGTCAACAG 2820  
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CTTGCCCTAT GGGCCATCGG AAAGACAGGC 2880  
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAGATCAC CTTCCCGGGC 2940  
 80 TGAAGCCCTT CTTGCTGCCC ACAGCCCGAG CAGGTGGGGG AGCTGTGCTT CTCTCTCCGG 3000  
 TACGTGCCCA GCTCAGGCGG GCTGACCGTG GTGGTGTGAG AGGCTCGAGG CTTGGTCCA 3060  
 GGCCTTGACG GACCTACGTG GAAGGTCCAG CTATGCTGA ACCAGAGGAA GTGGAAGAAG 3120  
 AGAAGACAG CCAACCAAAA GGGCAGCGCG GCCCCTACT TCAATGAGGC CTTCACTTCC 3180  
 CTGGTGCCTT TCAGCCAGGT CCAGAAATGTG GACCTGGTGC TGGCTGTCTG GAGCCGAGC 3240  
 CTGCCGCTCC GAACAGGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGCG CTCGGGGCAG 3300

CCCTGCGCAGC ACTGGGCGAGA CATGCTGGCC CACGCCCGGC GGCCCATTCG CCAGCGGCAC 3360  
CCCTGCGGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCCG CCTTCGCTG 3420  
CGCGTCCCTT TCGCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCG CTGAGCCACG 3480  
GCATTGCCC AGGCCGCCCT GCAGGCCAC TGCAATAAAC GCCTTCTCCT GCC

**A80 Protein sequence:**

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)  
Unigene number: Hs.161031  
Probeset Accession #: AL137708  
Protein Accession #: CAB70885  
Signal sequence: none found  
Transmembrane domains: 69-85  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
MGHPVPSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60  
STFGPRWALI AGALAAAGVLL VSCLLCAACC CRRHRKPKR DKESVGLGSA RGTTHLVR 120  
SGSLLTQSRE GLKSRLLQSPG QRGEFSRDRG LTPTEAGR

**A81 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
Unigene number: Hs.2877  
Probeset Accession #: X63629  
Nucleic Acid Accession #: X63629  
Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51  
GCGGAACACC GCGCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGCG 60  
TCCCTCGTGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCAGCG 120  
CCTCCGAGCC GTCCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG CGCGGAGGCG 180  
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240  
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300  
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCGATCCAAA CGTATCTTAC 360  
GAAGACACAA GAGAGATTGG TGGSTTGCTC CAATATCTGT CCGTGAATAAT GGCAAGGGTC 420  
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGCTTGTGCT GTAGAGAAGG 540  
AGACAGGCTG GTTGTGTGTT AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600  
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660  
TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGA 720  
GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
ATGATGCGAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840  
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900  
CCAGTGGGCT CCGCGGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020  
ACAATGCTCC CATGTTTGAC CCCGAGAAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080  
GCCATGAGT GCAGAGGCTG ACGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140  
GTGCCACCTA CCTTATCATG GCGCGTGAAG ACGGGGACCA TTTTACCATC ACCACCCACC 1200  
CTGAGGCGCA CGCTGTGATC CTGACCAACA GGAAGGGTTT GGATTTTGGG GCCAAAAACC 1260  
AGCACACCCCT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACT 1320  
CCACAGCCAC CATAGTGGTC CAGCTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380  
CTTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GGAGCCTGTG TGTGTCTACA 1440  
CTGCAGAAAG CCCTGACAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500  
CAGGTTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTTCAG AGCTGTGGGC ACCCTCGACC 1560  
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
ATGGAAGCCC TCCCAACCAT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
ACCATGGCCC AGTCCCTGAG CCCGTCAGA TCACCATCTG CAACCAAGC CCTGTGGGCC 1740  
ACGTGCTGAA CATCAAGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTC CAGGCCACG 1800  
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
TCTTGTCCCT GAAGAAGTTC CTGAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920  
ACCATGGCAA CAAAGAGCAG CTGACGTTGA TCAGGSCCAG TGTGTGGGAC TGCCATGGCC 1980  
ATGTGGAAG CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
TCAGGAGCC CTCTTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
AAGAGGGGGG TGGCGAAGAG GACCAAGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACCTGGCACC AACCATCATC CCGACACCCA 2280  
TGTAACCTCC TAGGCCAGCC AACCCAGATG AATCGGCAA CTTTATAATT GAGAACCCTGA 2340  
AGGCGGCTAA CACAGACCCC ACAGCCCGCG CCTACGACAC CCTCTTGTGT TTGACTATG 2400  
AGGGCAGCGG CTCGAGAGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCCC TCGACCAAG 2460  
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520  
ACGTTGGCGG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580  
CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640  
GGAAGTGGCC GTAGCAACTT GCGCGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
TCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
CACCTGGGCC AGGTTGGCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820  
TGCTCAACCC TGTGTCCTGG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880  
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT CCAACTTAAT TTTTTTTTTT AATGCTATCT 2940  
TCAAAAAGTT AGAGAAAGTT CTTCAAAGT GCAGCCACGA GCTGCTGGGC CCACTGGCCG 3000  
TCTGTATTT CTGTTTCCA GACCCCAATG CCTCCCATC GGAATGATCT CAGGTTTCT 3060  
ATACTGAGTG TGCTAGGTT GCGCTTATT TTTTATTTTC CCGTGTGCT TGCTATAGAT 3120  
GAAGGGTGAG GACAACTGCT TATATGTACT AGAATTTTT TATTAAGAA A

**A82 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)  
 Cellular localization: plasma membrane

10

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1      11      21      31      41      51
|      |      |      |      |      |
15  MGLPRGPLAS LLLLVQCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGOA LGKVFMGCPG 60
    QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
    KGPFQRLNQ LKSNKDRDRTK IPYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREBIK 180
    YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
    DEDDAIYTYN GVVAYSISHS EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
    TDMGGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVQRLT VTDLDAPNSP 360
    AWRATYILMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
    PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRIIR 480
    DPAGHLAMDV DSGQVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLTLLTID 540
    VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
    TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFIPVL 660
    GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGGEED QDYDITQLHR 720
    GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
    DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEDED
  
```

**A83 DNA SEQUENCE**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Probeset Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

35

```

1      11      21      31      41      51
|      |      |      |      |      |
40  AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCACGCGTG CTGTGGCCTC 60
    GGGGAGTGGG AAGTGGAGGC AGGAGCCITC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
    CTCAGCATC ATGATTAACCT CCCAAATACT ATTTTGTGGA TTTGGGTGGC TTTTCTTCAT 180
    GCGCCAAATG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCCTCTCCGT 240
    GAGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
    GAATAGCAGC TCCCGTTATT TTCACTGGAA AATGAACCTG TGCGTAATTC TGCTGATCCT 360
    GGTTTTCATG GTGCCCTTTT ACATTGGCTA TTTTATGTG AGCAATATCC GACTACTGCA 420
    TAAACAACGA CTGCTTTTTT CCGTCTCTTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
    ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
    CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTTCTTTCG GATTTGSTGC 600
    TGTCACCTGC CCATACACTT ACATGTCTTA CTTCTCAGG AATGTGACTG ACACAGATAT 660
    TCTAGCCCTG GACGCGGAC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
    GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
    TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
    TATTCAACAG GAGATGGATG CTTTGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
    TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTT 960
    TAATTTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
    CAATATGTTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
    TGTGAATTAT CTGGAATCC AATTGTATGT GAAGTTTGG TCCCAACACA TTCTCTTCAT 1140
    TCTGTGTGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT 1200
    CTTTATGCC ATCTCTAGCA GTAAGTCCTC CAATGTCTAT GTCTGCTAT TAGCAGAT 1260
    AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320
    CCGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTGTGTT 1380
    TGATGTGATC TTCCTGTGCA GCGCTCTCTC TAGCATATCT TTCCTCTATT TGGCTCACAA 1440
    ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
    CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAATG GAACCCAGGC CTGACATTTT 1560
    ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCTCTC 1620
    AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTAAG 1680
    ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CCGAGAGGAG 1740
    CCAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
    TGAGCCAAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAGGTTA TAGCTTTGCC 1860
    TTGAGATGTA CTCATTAAAA TCAGAGACTG T
  
```

**A84 Protein sequence**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Protein Accession #: NP\_057418.1  
 Signal sequence: none found  
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402,  
 424-446  
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
  
```

	MSFLIDSSIM	ITSQILFFGF	GWLFMRQLF	KDYEIRQYVV	QVIPSVTFAF	SCTMFELIIF	60
	EILGVNLSSS	RYFHWKMLNC	VILLILVFMV	PFIYGYFIVS	NIRLLHKQRL	LPSCILLWTF	120
	MYFFWKLQDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
5	VTDTLILALE	RRLLQTMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGFVGM	IKSVTTSASG	240
	SENLTILQOE	VDALIELSRQ	LFLETADLYA	TKERIEYSKT	FKGKYFNFLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDPVF	RGIEITVNYL	GIQEDVKFWS	QHSIFILVGI	IIVTSIRGLL	360
	ITLTKFFYAI	SSSKSSNVIV	LLLAQIMQMY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSALSSILF	LYLAHKQAPE	KQMAP			

## A85 DNA SEQUENCE:

Gene name:	TTK protein kinase
Unigene number:	Hs.169840
Probeset Accession #:	M86699
Nucleic Acid Accession #:	NM_003318
Coding sequence:	1026-3551 (underlined sequences correspond to start and stop codons)

20	1	11	21	31	41	51	
	GGAAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCTCCCG	GGTTCAGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACTAATTT	180
	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCGT	240
25	ACCTCAGGTG	ATCCACITTC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAACCTG	300
	TGCTGGCTCG	ATCTTTTTTT	TGTTGTTGGA	TTTTTGAAC	AGGGTCTCCC	TTGGTCGCCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATAACCC	TCCACCTCCT	GGTTTCAAGT	420
	GATCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	GCGTGCACCA	CCACACCCGG	480
	CTAATTTTTG	TATTTTATT	AGAGACAGGG	TTTCAACATG	TTGGCCAGCG	TGTTTCTCAA	540
30	CTCCTGGACT	CAAGGGATCC	GCCTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACACTG	CCTGACCTTA	TAATCTTAA	GTCAATTTTT	CTGGTCCATT	TCTTCTTAG	660
	GGTCTCTACA	ACAAATCTGC	ATTAGCCGGT	ACAATAATCC	TTAATCTCAT	GATTCACAAA	720
	AGGAAGATGA	AGTGATTCAT	GATTTAGAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
	GGATGATGAT	CTTAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
35	TTTGGTTTAA	ATTAATATAT	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
	ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCGCCAG	960
	TGCAGTTTTC	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAATGAA	CAAGATGAGA	GACATTAATA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
	AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAACT	GTTAACCATA	1140
40	TTATGATGAT	GGCAACAAC	CCAGAGGACT	GGTTGAGTTT	GTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTGGTTAC	AGTCAAGCAA	1260
	TTGAAGCGCT	TCCCCAGAT	AAATATGSCC	AAAATGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
	GATTTGCTGA	ATTAAAGACT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAATATG	1380
	CCAGAGCAAA	CTGGAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
45	CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
	TACCAGACTG	AATGCTGGAA	ATTGCCCTGC	GGAAATTTAA	CCTCAAAAAA	AAGCAGCTGC	1560
	TTTCAGAGGA	GGAAAAGAAG	AATTTATCAG	CATCTACSGT	ATTAACCTGCC	CAAGAATCAT	1620
	TTTCCGGTTC	ACTTGGGCAT	TTACAGAATA	GGAAACACAG	TTGTGATTCC	AGAGGACAGA	1680
	CTACTAAGCC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAATATAGTT	1740
50	ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCATTT	GGAAAGATCC	1800
	CAGTTATCC	GCTAAGTAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
	GTTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
	AACCAAGTGG	AAATGATCCC	TGTGAATTAA	GAAATTTAAA	GTCGTGTTCA	AATAGTCATT	1980
	TCAGGAAGCC	CTGGGTGTCA	GATGAAAAGA	GTTCTGAACT	TATTATTACT	GATTCAATAA	2040
55	CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAACAAGA	GGTTCAGAG	AGTAAACAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAACCA	GAATCCTGCT	GCATCTTCAA	ATCACTGGCA	GATTCGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTTTTCTA	GTTTCAAAAC	2280
	AGTCACCACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
60	CGAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AAGATGACT	2400
	TTCCACCTGC	TTGTCAAGTT	TCAACACCTT	ATGGCCAAAC	TGCTGTGTTT	CAGCAGCAAC	2460
	AGCATCAAT	ACTTGGCACT	CCACTTCAAA	ATTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGTTTAAA	GGAAGAAATT	ATTCCATATT	AAAGCAGATA	GGAAAGTGGAG	2580
	GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAATATG	2640
65	TGAATTAAGT	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATAAAGT	ACAACACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCAAGG	2760
	ACCAGTACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCAG	2880
	TTACACAAAT	CCATCAACAT	GGCATTGTTT	ACAGTGATCT	TAAACAGACT	AACTTTCTGA	2940
70	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAATG	CAACCAAGTA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAGCAAA	3060
	TCAAGATAT	GTCTTCTCTC	AGAGAGAAATG	GGAAATCTAA	GTCAAGATA	AGCCCCAAAA	3120
	GTGATGTTG	GTCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTT	3180
	AGCAGATAAT	TAATCAGATT	TCTAAATTAC	ATGCCATAAT	TGATCTTAAT	CATGAAATTG	3240
75	AATTTCCCGA	TATTCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
	ACCAAAACA	GAGGATCTCC	ATTCTGAGC	TCCTGGCTCA	TCCATATGTT	CAAAATCAAA	3360
	CTCATCCAGT	TAAACCAATG	GCCAAAGGAA	CCACTGAAGA	AATGAAATAT	GTTCTGGGCC	3420
	AACTTGTGTT	TCTGAATTCT	CCTAACTCCA	TTTTGAAAGC	TGCTAAACT	TTATATGAAC	3480
	ACTATAGTGG	TGGTGAAGT	CATAATTCTT	CATCCTCCAA	GACTTTTGAA	AAAAAAGGG	3540
80	GAAAAAATAT	ATTGCAAGTT	ATTCGTAATG	TCAGATAGGA	GGTATAAATAT	ATATTGGACT	3600
	GTATATCTCT	TGAATCCCTG	TGGAATCTCA	CATTGGAAGA	CAACATCACT	CTGAAGTGTG	3660
	ATCAGCAAAA	AAAAATTCAGT	GAGATTATCT	TTAAAGAAAA	ACTGTAAAAA	TAGCAACCAAC	3720
	TTATGGCACT	GTATATATGT	TAGACTTGTG	TTCTCTGTTT	TATGCTCTTG	TGTAATCTAC	3780
	TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GTATATTCTA	AAAAACTTTG	3840

TAAATAAAGT TTTGTGGCTA AAATGA

**A86 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51  
 15 MNKVRDIKNN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLKLEKNS 60  
 VPLSDALINK LIGRYSQAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120  
 ANCKKPAFVH ISFAQFELSQ GNVKKSQKLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180  
 EEEKQNLAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR 240  
 20 NSLRQTNKTK QSCPFGRVFV NLLNSPDCDV KTDSDVVPFC MKRQTSRSEC RDLVVPKSKP 300  
 SGNDSCELRN LKSVQNSHFV EPLVSDEKSS ELIITDSITL KNKTESLLA KLEETKEYQE 360  
 PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTPE QPVFVSQKQS 420  
 PPISTSKWFD PKSICKTPSS NTLDDVMSCF RTPVVKMDFP PACQLSTPYG QPACFQQQKH 480  
 QILATPLQNL QVLASSSANE CISVKGRIYS ILKQIGSGGS SKVFQVLNEK KQIYAIKYVN 540  
 25 LEADNQTLTD SYRNEIAYLN KLQQHSKII RLYDYEITDQ YIYMVMCEGN IDLNSWLKKK 600  
 KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPFANFLIV DMLKGLIDFG IANQMPPDQT 660  
 SVVKDSQVGT VNYMPPPEAIK DMSSSRENGK SKSKISPKSD VMSLGCILYY MTYQKTPFPQ 720  
 IINQISKLIA IIDPNEHIEF PDIPKDLQD VLKCKLKRDP KQRISIPELL AHPYVQIQTH 780  
 PVNQMAKGTI EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK 840  
 K

**A87 DNA SEQUENCE**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 40 GGGGCGACGG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCGCCCCCT 60  
 CTGCCACCTG GGGCGGTGCG GGGCCGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120  
 CGATGCAGCT GCGCTCACTG CGAGCTGCGG CGCCGACACG CTTCGTGGCG CTCTGGGCAC 180  
 45 CCTGTTCCT GCTGGCTCTC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240  
 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGGCGGA GATGCAGCGC GAGATCCTCT 300  
 CCAITTTGGG CTGTGCCACG CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360  
 CCAITTCAT GCTGGAACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGCG GGGCCGCGCG 420  
 GCCAGGGCTT CTCTACCCG TACAAGGCCG TCCTCAGTAC CCAGGGCCCG CCTCTGGCCA 480  
 50 GCCTGCAAGA TAGCCATTTC CTCACCGAGC CGCAGTGGT CATGAGCTTC GTCAACCTCG 540  
 TGAACATGA CAAGGAATTC TTCCACCCAC GCTACCAACA TCGAGAGTTC CGGTTTGATC 600  
 TTTCAGAT CCAGAAAGGG GAAGCTGTCA CGGCAGCGGA ATTCCGGATC TACAAGGACT 660  
 ACATCCGGGA ACCTCTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720  
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCCT TGGGCTCGG 780  
 55 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACACGCAA CCACTGGGTG GTCAATCCGC 840  
 GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900  
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGTGGCTT 960  
 TCTTCAAGGC CAGGAGGTTC CACTTCGCA GCATCCGCTC CAGGGGAGC AAACAGCGCA 1020  
 GCCAGAACCG CTCGAAGAGC CCCAAGAACC AGGAAGCCCT GCGATGGCC AACGTGGCAG 1080  
 60 AGAACAGCAG CAGCAGCCAG AGGCAGGCCG GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140  
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200  
 AGGGGGAGTG TGCCCTTCCCT CTGAACCTCT ACATGAACGC CACCAACACC GCCATCGTGC 1260  
 AGAGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320  
 AGCTCAATGC CATCTCCGTC CTCTACTTCC ATGACAGCTC CAAGCTCATC CTGAAGAAAT 1380  
 65 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GGCCTAGCT CCTCCGAGAA TTCAGACCCT 1440  
 TTGGGGCCAA GTTTTCTCGG ATCTCTCCAT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500  
 CTGCTTTTGG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560  
 AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAGA 1620  
 TCCTACAGC TGTGCAGGCA AAACCTAGCA GGAAAAAACA ACAAGCATA AAGAAAAATG 1680  
 70 GCGGGGCCAG GTCATTGGCT GGGAAAGTCT AGCCATGCAC GGAAGCTTTT CCAGAGGTAA 1740  
 TTATGAGCGC CTACACGCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800  
 GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCTCTGA ATAAATGTCA 1860  
 CAATAAACG AATGAATG

**A88 Protein sequence:**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 Signal sequence: 1-30  
 Pfam domains: TGFb\_propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIIHRLRSQE RREMQREILS 60
   ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
   LQDSHFLTDA DMVMSFNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
   IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVDITA TSNHWVUNPR 240
   HNLGLQLSVE TLDGQSINPK LAGLGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
   QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
10  GECAFPPLNSY MNATNHAIVQ TLVHFIPNET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
   RNMVVRACGC H

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**A89 DNA SEQUENCE:**

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15  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Nucleic Acid Accession #: AC012478
   Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

```

```

20  1      11      21      31      41      51
   |      |      |      |      |      |
   ATGCGCGCCG TGCCGCTGCC CGCCCGGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC 60
   GCTCCGCGCG CCGCGCCGAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
25  CGCGAGTCCG GCGCACCGCC CGGCCCGGGG CCGCGGAACA CCACCGGTTT TGGGTCTGGG 180
   CGCGCGGGCG GCAGCGGCAG CTCAGCTCC AACAGCAGTG GCGACGCTT GTGACCCGCG 240
   ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CGGTGATCGT GCGTTCGCC 300
   TTTACACCCC TCCTCATCGC CTGCTGCTGC CTGCGGCTCT TCAGGTCGGG AAAGAGGTTA 360
   AAGAAGACAC GCAAGATAGA TATCATCACC ACTCCAGCAG AGCGAGTGA AATGGCGCCA 420
30  CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
   TCCTTCCCGG CTGCTCATGA AGCTCAGCTG CCAGGGTGCC AGAGCTACT GACAGTTCTT 540
   GTGCCCCAC CCITCATCCT CGACATTGAC CTTCCAGCAA GATCAGTGG AAGGCCTGAT 600
   GGTGGAATCA GACCTGGTAA AACCTGTTT CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660
   TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720
35  GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTG AGGCATCTGC 780
   TCAGACTGTG ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840
   TTTGGGCATC CTTTAAAGT GCCCCTACT TCTACTCCC ATGGTTTTCG ACAACTGCAG 900
   CTGAATCTCA TGGAAAGGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT 960
   GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CTTTCCAAAT 1020
40  CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAACCATG 1080
   AGTACTTGGG GCTTGATGAT TTTCTGGT GCGGCCAGC GGGGCACCTT TTGTGAAGAC 1140
   AGAGCAGTGA CTAAGTTCTT CCAGGAGTGC TCTTCTCCA AACAGCTGGG CTGGAAGCCA 1200
   GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTC TCCGCTGAGC 1260
   ACCCATCTCG TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCTT GACCGGGAGG 1320
45  AGGGTGTTCG GGCCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
   TGCCCTTTTG TTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
   ATCTGTCTCC CCTGCTGTGC CGTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCCTTGCGT CATTTGAGCA GAGCCACAA AAGGCAGCTG CTGCCACCGG GGAGCCTGTC 1560
   AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
50  GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCACGCTGA GGATGTCACT 1680
   CACCTCTGGG GAGACTTGGG TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GCCAGAAGAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860
   TCCCCCGCAG AGCCCTGTT TCTGTCCAGG CCTTGA

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**A90 Protein sequence:**

```

60  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Protein Accession #: FGENESH predicted
   Signal sequence: 1-27
   Transmembrane domains: 94-115, 448-469
   Cellular Localization: not determined

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```

65  1      11      21      31      41      51
   |      |      |      |      |      |
   MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
   AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAIVIVAF FTTLLIACIL LRVFRSGKRL 120
70  KKTRKYDIIT TPAERVEMAP LNEEDEDDED STVPDIKYRV SLPAALRRQL PGQTLTLTVP 180
   VPPPFILID LPARCSGRPD GGIRPGKTCF PANWHFVESW SAATWGVKDW TWKPSCVGGV 240
   ETKTNVMYKT PAPSCVSGIC SDCHQWQRFH VTMELLPLP FGHFPKVPPT STPHGFRQLQ 300
   LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLPN PWHFVSATGS PIKTLTYQTM 360
75  STLGLDVFCG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPPLS 420
   THPVRLARSD ARGQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEPV KRGPSSQLTR HTCPGWGITH 540
   ANLQTIPTDQ QQEGPREDVT HPGGDLQDVA NFYLEEBEPQ DGRQCKNVLN SEEGPPSLTG 600
   CERLTGSHHF SSHSKWSWPL SPRQPLFLSR P

```

**EWING****A91 DNA SEQUENCE**

```

Gene name:      G protein-coupled receptor 64
Unigene number: Hs.184942

```

Probeset Accession #: AA435577  
Nucleic Acid Accession #: NM\_005756  
Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60  
CTGCGGTCAG GGATGGTTTT CTCTGTGAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120  
GTTTACTCGA CGTTCAAGAT ATTCTGTGTC ATCATTGTGC TTCAATGTCG TCTGGTAACA 180  
TCCCTGGAAG AAGTACTGTA TAATCCAGT TTGTCAACCAC CACCTGCTAA ATTATCTGTT 240  
GTCAGTTTTG CCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300  
AGCTTACTCC CTTCAAACGA AACAGAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360  
GCTTCAGGCG TCAAAACCCA GAGAAATATC TGCAATTTGT CATCTATTG CAATGACTCA 420  
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT 480  
CAACATATAA CGAATGGCAC CTAACTGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA 540  
GAGCTCAACA AAACCTGACA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600  
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660  
TGTGCTGCAA TAGCGCTTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720  
TCTGTGAGGA TACCTGCCCC TTCTTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780  
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840  
TCCATCCGAG TGGTGCCTCG GGCCACTGTG CTTTCCCAGG TCCCAAAAGC TACCTCTTTT 900  
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTC CCTCTCCAAT AGGGGAGATT 960  
CAACCCCTTT CACCCAGGCC TTCAAGTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020  
CCACAGTCTG AAACGATCTC TTCCCTATG CCCCACAAACC ATGTCTCCGG CACCCACGCT 1080  
CCTGTGAAAG CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140  
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200  
CAAGTGTGCG AGATGAGAGG GGCTGTGCTC TTGGGCGAGC TGGAGCCTAA CCTCGCAGGA 1260  
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCGCCCG CTGACATGCT GGCCCTCTG 1320  
GCTCAAGAT TGCTGAAGT AGTGGATGAC ATTGGCCTAC AGCTGAAGTT TTCAACACAG 1380  
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440  
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAATC TTCAGTTTC TCTGGAAACC 1500  
CAAGCTCCTG AGAATGAGAT TGGCACAATT ACTCTTCTT CATCGCTGAT GAATAATTTA 1560  
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTITGA AACACCTGCT 1620  
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680  
GTTGCAACC TGACCGGTACG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740  
AACCCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800  
GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860  
ATCTGTACCT GTAGCCATCT AACAGCTTC GGCGTCTGCG TGGACCTATC TAGGACATCT 1920  
GTGCTCCTCG CTCAATGAT GGCTCTGAGG TTCAATACAT ATATTGGTTG TGGGCTTTCA 1980  
TCAATTTTTT TGTCAGTAGC TCTGTGAACC TACATAGCTT TTGAAAGAT CCGGAGGAT 2040  
TACCTTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CTTGGTCTTC 2100  
CTCTGGAGCT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160  
TTTCTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCCTAGAAGC ATTCCATATG 2220  
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTGTC 2280  
ATTGTGCGTT GGGGGGTACG AGCTGTGGTT GTGACCATCA TCTGACTAT ATCCCCAGAT 2340  
AACTATGGGC TTGGATCCTA TGGGAAATTC CCAATGGTT CACCGGATGA CTTCTGCTGG 2400  
ATCAACACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTG 2460  
CTGAACGTC AATATTCTGA CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT 2520  
CAACTGGGAG CCGAGCGAAA AACCAATATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580  
TTTTTACTGG GAATAACTTG GGGCTTGGCC TTCTTTGCC TGGGACCAAT TAACGTGACC 2640  
TTCAATGATC TGTTTGCCAT CTTTAAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700  
TTGTGGCCCA AAGAAATGTT CAGGAAGCAA TGGAGGCGGT ATCTTTCTTG TGGAAAGTTA 2760  
CGGCTGGCTG AAAATTCTGA CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT 2820  
GTAAACCAAG GAGTGTCCAG CTCTTCAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC 2880  
TCCACCACAC TGCTAGTGAA TAATGATTGC TCAGTACAGC CAAGCGGGA TGGAAATGCT 2940  
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAAATG GAGATGTGTG CCTTACGAT 3000  
TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCGGT 3060  
ATGGCTCTCA AAGGAGCTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTTC 3120  
CTTCTCTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180  
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240  
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300  
TTTAGACATT TCTGATTTGG TTCTTATCT TTCAATTTAT AAGAAGTTG GTTTTAAACA 3360  
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420  
TTTAAGAGG CTAAAGTTATC TTGTATAACA TCATATAAAG CAACTGTTGA CTTGAGCCTG 3480  
TTGGTGAGTT TAGTTGTGCA TGCTTTGTT GTATATAAGC TAAATCTTAG TGACCATATG 3540  
GTCAAAAATC TTACTTCTAC ATTTTTTGT ATTTATTTTC TACTGTGTAA ATGTATTCTT 3600  
TTGTAGAATC ATGGTTGTTT TGCTCACGTT GATAATTCAG AAAATCCTTG CTGTTCCGC 3660  
AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAA 3720  
TCAGAAATA ATGATCCGAG CCAGACTGAG AAAATGTAG CAGACAGTGC CACAGTTAGC 3780  
TCATACAGT CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840  
TGGGTGATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900  
GTGACAGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCGCAT 3960  
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020  
AGAGGGATGA ACTGTATCCT AGACCATGTG TCAGGAAAT TGTGAACGTA GATGAGGTAC 4080  
ATACACTGCC CATTCTCAAA TCCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140  
CTTCTCTTAA AAGGTACAT ATATATGGAA AAAATCATA TTGCGTTCT TTAAGAGGCA 4200  
ACTGCAATGT ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260  
TTGTTTTTAA AATGTGTCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320  
GGGAACCTGC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380  
TATACAGGGT CTATCTTCTT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440  
TTATTAGGAA CATTTCAAAC CCCTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGATCAT 4500  
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560  
CTGACTAGT TTTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTGTA TTTATATGTT 4620



AAAAACAAAA ATGTTAAAAAT CAATGAAATA AATTGTCAGT TAAGA

# A92 Protein sequence

Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSPP	PAKLSVVSFA	60
PSSNEVETTS	LNDVTLSELL	SNETEKTKIT	IVKTFNAGSV	KPQRNICNLS	SICNDSAFFR	120
GEIMFYDKE	STVPONQHIT	NGTLTGVLSL	SELKRSELNK	TLQTLSETYF	IMCATAEAQS	180
TLNCTFTIKL	NNTMNAACAI	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
VCLADHPRGP	PFSSSQSIPV	VPRATVLSQV	PKATSFAPPP	DYSPVTHNVP	SPIGELIPLS	300
PQPSAPIASS	PAIDMPPQSE	TISSPMPQTH	VSGTPPPVKA	SFSSPTVSAP	ANVNTTSAPP	360
VQTDIVNTSS	ISDLENQVLQ	MEKALSLSGL	EPNLAGEMIN	QVSRLLHSPP	DMLAPLAQRL	420
LKVVDIDIGK	YLKFCIVG	TSPSLALAVI	RVNASSFNIT	TFVAQDPANL	QVSLETQAPE	480
NSIGTITLPS	SLMNNLPAHD	MELASRVQFN	FFETPALFQD	PSENLISLIS	YVISSSVANL	540
TVRNLTNRVT	VILKHINPSQ	DELTVRVCFW	DLGRNGGRGG	WSDNGCSVKD	RRINETICTC	600
SHLTSPGVLL	DLRSVSLPA	QMMALTFITY	IGCGLSSIFL	SVTLVTYIAF	EKIRRDYPSK	660
ILIQLCALAL	LLNLVFLDLS	WIALYKMQGL	CISVAVFLHY	FLLVSTFMWG	LEAFHMYLAL	720
VKVFNTYIRK	YLKFCIVG	GVPVAVVTII	LTISPNDNYL	GSYGKFPNGS	PDDFCWINNN	780
AVFYITVVGY	FCVIFLLNVS	MFIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFLLG	840
ITWGFAPFAW	GFVNVTIFMYL	FAIFNTLQGF	FIFIFYCVAK	ENVRKQWRRY	LCCGKLRLAE	900
NSDMSKTATN	GLKKQTVNQG	VSSSSNSLQS	SSNSTNSTTL	LVMNDCSVEA	SGNGNASTER	960
NGVFSFVQNG	DVCLHDFGTG	QHMFKNEKEDS	CNGKGRMALR	RTSKRGSLSHF	IEQM	

## Fibrosis

### A93 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CCGCAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCCCCA	GCCCTCCCCC	AGGCCGCGAG	60
CGCCCCCTGCC	CGCGTGCCCTG	GCCTCCCTTC	CCAGACTGCA	GGGACAGCAC	CCGCTAACTG	120
CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
ATGCCTCTGC	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
GGGAACGCGG	CCAGTGCAAG	GCATCAQGGG	TTGTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
TGTCACTATG	GAATCAAACT	GGCTGTCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
TGTGAAGCTA	CATGCGAACC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
AGATGCTTTC	CAGGATACAC	CGGGAAAACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACAAG	GAAGCTACAA	GTGCTTTTGC	600
CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
TCAGGACTCC	GCCTGGGCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCTCTT	780
GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGTGAAG	CTACTACTGC	840
AAATGTGCTA	TGGTTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
GGGTCTCTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
ATCCCTGAAA	ATTCTGTGAA	GGAAGTCCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
AAGAAGTTGC	TTGCTCAACA	AAACAGCATG	AAAAAGAAGG	CAAAAATTAA	AAATGTTACC	1140
CCAGAAGCCA	CCAGGACTCC	TACCCCTAAG	GTGAACTTGC	AGCCCTTCAA	CTATGAAGAG	1200
ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAATGAAA	1260
GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
AGCCTGGGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCTGATT	1380
CTGTGTCAAA	GGAAGCGCTG	AACTTCCAAA	CTGGAACATA	AAGATTTAAA	TATCTCGGTT	1440
GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
GGTCACAAGA	AAGACATGG	CCGATTGAAA	CTTCTCTTAC	CTGACCTGCA	ACCCCAAAGC	1620
AACTTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCGGAGACAA	AAGTCGGGAA	ACTTCGAGTG	1680
TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
TGGAAGACAG	CGAAAATTCA	GTTGTATCAA	GGAACCTGATG	CTACCAAAAG	CATCATTITT	1800
GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
TCAGGCTTAT	GTCCAGATAG	CCTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
TTGACTTTGT	ATGTGAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCAIT	1980
TAGAAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040
TCCTGTATAA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCAGTGTATC	TTCTCAGTCA	2100
TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAAT	GTCAGTTTAT	CTCCCTCTCT	2160
CAGTATATCT	ATTGTTGATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
TAGAAAAAAA	AGCACAGAGA	AATGTTTAA	TGTTTGACTC	TTATGATACT	CTTGGGAAAC	2280
TATGACATCA	AGATAGACT	TTTGCTTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340
TGTATATTCA	TAATCTTTGT	AATAATAATA	TCCAAATCAT	CAAAAAAAA	AAAAAAA	

A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

1 11 21 31 41 51  
 15 MPLPWSLALP LLLSWVAGGP GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60  
 CEATCEPGCK FGECVGPWNC RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKCF 120  
 LSGHMLMPDA TCVNSRSCAM INCQYSCEDT EEPQCLCPSS SGLRLAPNGR DCLDIDECAS 180  
 GKVICPNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240  
 20 GSPKCKCKQG YKNGRLRCSA IPENSVKEVL RAPGTIKDRI KLLAHKNSM KKKAKIKNVT 300  
 PEPTRTPTPK VNLQPFNYEE IVSRGONSHG GKKNEEKMK EGLEDEKREE KALKNDIEER 360  
 SLRGDVFFPK VNEAGEGLI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WKQDREDDFD 420  
 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFYRL AGDKVGLRV 480  
 FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGGKGTG EIAVDGVLLV 540  
 25 SGLCPDSLLS VDD

GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51  
 35 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GCGCGCTGTG 60  
 CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGGAAACAAT TCACCAATGA 120  
 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCAATCCGG GCGCCTGGCA 180  
 40 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTCGAAATGT GGCACAACCT TCCTCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG 300  
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCTCTGC CTTTGCTCCA CGGCCGCTA CCATGCAAG AACGGCTCT GTATTGACAA 420  
 GAGCTTCATC TGGATGGAG AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 45 AAGTTCTCAA GAACCCGCGA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 TTACCCGAGC ATCACTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCTGCTGGCA CTGGCTTGGC ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660  
 GCACCGGCTG CAGCAGCTGT TGCTGCTGTC CGCCTGGGTG GTCTCTGGAC ACCCCACCA 720  
 CTGCAACGTC ACCTACAAGC TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 50 GAATGCGTCG GAAGTAGGCT CCCCACCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840  
 TGGCTGGTAT GACCTTCCTC CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGCCC CCTACCGCT CCGGTCGCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960  
 CAGCAGCTCT CAGCAGCTGG AAGACACGAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020  
 GGGCAGCTGT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 55 AGTTATTCCA AAGCTCATAT GGGTTAATCT GCTCTGACT GTTGCCATTG TAACAATTG 1140  
 TGCTCATGGG AAGCTCTTGA AGCACTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GCATTCCCCT CCTCCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260  
 TGACATGATC TGTGTGCGT CTTTCTGTC AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320  
 CACCCCTATT TTTCACATTA TTCTGTTCT GTTGAGAGGA CAGCATATAA AACAGTATTG 1380  
 60 AATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATCTCTCT GCTGGGTAGT TACCTTAGAG CATTTGGGGA TTGGGTTAG 1500  
 ATGATCTAAC CAGGAGGCCA TCACCTGGATG GTCACCCCCC CAATAAATTT CCATTTGAGC 1560  
 ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCCG TTCAGCAGAG TCAGTGGCCA 1620  
 AAGAAACTT TGAGCGTGAG TAACACCTT CAGCAGTCGC AACGTTATT TTGGTTTGTG 1680  
 65 AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTG CCCAAGAATG 1740  
 CTCATTCTAG GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCTAA AATAGGCAGG 1800  
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920  
 AACTGCCCTG AGCCAGGAA TGAGGACCTA ACTTGAGTGT GCCCAAGTGC TGACCTGGCT 1980  
 70 GTATGTCCCT GTGGCCACA CCCAGCCTGT CTTGCTCAIT CATGCAGCCT CAACACTGGC 2040  
 CTCGAAAGTT CCCTTAACAC TTGCAAGATC CTTTTTACCT GTGCATTGG ACTTGAGGAC 2100  
 ACTGGTTTCT ATCAGAGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CAGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTGAGGCTG AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 75 AGACAATTG GAGTCAAGAT TTCCATTG GATCTATTTT AAATCTTTTA GAAATGCAIT 2340  
 TGAAGCAGTG TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400  
 AGCTGTCTCT TTTTGTGTT TTCCTTTAA AAGGTCCAAA GAAAGATGCA AAGGAGATC 2460  
 ACACCTTGC CCCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGOCAG 2520  
 ACATTGTGC ATTTGTGCAC TTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580  
 80 AGAGGAGTCT CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTT 2640  
 TTCTCTGTGT CCAGTCAGCG ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAAAGTT 2700  
 AGGTGTGTTG TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760  
 CCACTCCGGG CAGCTGTAC CCATTGAGAA CTTCTTCCG CAGCTGAAGA AATGTTCACT 2820  
 AACCTGTTTG ACGCTAATTA AAACAGAGCC TGACGGAAGT GGGGCTAAG TGGCATTCAG 2880

5 TGATCTCTGT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA 2940  
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAGAA CTTTGATGA CAGCCAGAAT GTGTAGAAC TCTGGCTGAA 3120  
 CATTTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180  
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCACTTTAG GAAAAACAAA TGGTTTTAGT 3300  
 AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 10 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTGT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC TAATCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600  
 AGTTACACTG TGATCACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 15 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTTGT GTGTCGTTGC TTTTGTGTT TTGGTTAGGC TTGGTTTTGT TTTTAAATT 3780  
 TTATACCTC TAATAAATT GCAGTTTCAT TCTTCTGTT TTGTGCAANG GWMCTAMARM 3840  
 AAMMAAAAC AWYTTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCATCTCGGG 3900  
 TGGGGCGGG GGGCCACGT AGGTACGGG ACCACGGGG CCCAAACGG ACCCCAGAAG 3960  
 20 GAAACCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGGCGCGGG 4020  
 GGAACCGCA GAGTGTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

25 A96 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 30 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 | | | | |  
 MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGANQCD GLPDCFDKSD 60  
 EKCEPKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENCTANP LCSTARYHC 120  
 40 KNLGLCIDKSF ICDQNNQCD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHQQRK NNLMTLHVHR LQHPVLLSRL VVLDHPHHCN VTYNVNGIQ 240  
 YVASQAEQNA SEVGSPSPYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PFYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEV

#### 45 LUNG

A97 DNA SEQUENCE  
 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 50 Unigene number: Hs.256897  
 Probeset Accession #: BE001836  
 Nucleic Acid Accession #: BE001836  
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 | | | | |  
 ATGGCCGTCA AATCTTTTTC CTTCAACACT GGGATGATG GGCTAGACCC AGACCCAATC 60  
 ATGTTAAGTA TGATAGGGAT CAGTGGCCCA GCTGGTGTGG AAGACAAGTG GGTCACTACTG 120  
 GGTTTAGGCC CACATAGCAC TAAAGGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC 180  
 60 GGGAAATATG TCACTCTAA AAAAGATGTT TCTATTAGAA TTACTTACT CTTTCATGAA 240  
 AACATAGATG CTTCTCTTTT CTTGATTAGT GATGCCATC AGTTAACCCA AGTGCACTCA 300  
 GAGAAGTCAA ATTCTGACAC AATCCAGCAA GTAACATATA AACTGATGG CCCAGTCGAA 360  
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAG AGATTGAGA 420  
 AATTTTCTGA AGCTCTTGAA GCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480  
 65 AGAGCAAAGG CTACCAAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540  
 GACAGCTACA CCTGTTTTC TCCCTCATG CTTGATCCCC AGAAGTCTA CTTTCACAGC 600  
 GCTGGAGCAC TCCCAAGCTG TGAATGTCAT CTCACCAACC TCAGCCAGAG TGTCAATTC 660  
 TGTGAGAGAA CAAAGATTG GGGCACTTTC AAAATTAATG AAAGGTTTAC AAATGACCTT 720  
 TTGAATTCAT CTTCTGCTAT ATACTCCAAA TATGCAATG GAATTGAAAT TCAACTTAAA 780  
 70 AAAGCATATG AAAGAATTCA AGGTTTTGAG TGGTTTCAAG TCAACCAATT TCGAAATGGA 840  
 AGCATGTTG CTGGGTATGA AGTTGTGGC TCCAGCAGTG CATCTGAAGT GCTGTGAGCC 900  
 ATTGAACATG TTGCGAGAA GGCTAAGACA GCCCTTCACA AGCTGTTTCC ATTAGAAGAC 960  
 GGCTCTTTCA GAGTGTTCGG AAAAGCCAG TGTAAATGACA TTGTCTTTGG ATTTGGGTCC 1020  
 AAGGATGATG AATATACCTT GCCCTGCAGC AGTGGCTACA GGGGAAACAT CACAGCCAG 1080  
 75 TGTGATCCT CTGGGTGGCA GGTCACTAGG GAGACTGTGT TGCTCTCTCT GCTTGAAGAA 1140  
 CTGAACAGA ATTTCAATG GATTGTAGGC AATGCCACTG AGGCAGCTGT GTCATCCTTC 1200  
 GTGCAAAATC TTCTGTGCTAT CATTOGGCAA AACCATCAA CCACAGTGGG GAATCTGGCT 1260  
 TGGTGTGTTG CGATTCTGAG CAATATTTC TCTCTGTGAC TGGCCAGCCA TTTCAGGGTG 1320  
 TCCAATTCAT CAATGGAGGA TGTCACTAGT ATAGCTGACA ATATCCTTAA TTCAGCTCAA 1380  
 80 GTAACCAACT GGACAGTCTT ACTGOGGGA GAAAGATATG CCAGCTCAGC GTTACTAGAG 1440  
 ACATTAGAAA ACATCAGCAC TCTGGTGCTT CCGACAGCTC TTCCTCTGAA TTTTCTCGG 1500  
 AAATTCATTG ACTGGAAGG GATTCCAGTG AACAAAAGCC AACTCAAAAG GGGTTACAGC 1560  
 TATCAGATTA AAATGTGTCC CCAAAATACA TCTATTCCCA TCAGAGGCCG TGTGTTAATT 1620  
 GGGTCAGACC AATTCAGAG ATCCCTTCCA GAAACTATTA TCAGCATGGC CTCGTTGACT 1680  
 CTGGGGAACA TTCTACCGGT TTCCAAAAAT GGAATGTCTC AGGTCAATGG ACCTGTGATA 1740

5 TCCACGGTTA TTCAAACTA TTCCATAAAT GAAGTTTTC TATTTTTTC CAAGATAGAG 1800  
 TCAAACTGA GCCAGCTCA TTGTGTGTT TGGGATTICA GTCAATTGCA GTGGAACGAT 1860  
 GCAGGCTGCC ACCTAGTGAA TGAAACTCAA GACATCGTGA CGTGCCAATG TACTCACTTG 1920  
 ACCTCCTTCT CCATATTGAT GTCACTTTT GTCCCTCTA CAATCTTCCC CGTTGTAAAA 1980  
 TGGATCACCT ATGTGGGACT GGTATCTCC ATTGGAAGTC TCATTTTATG CCTGATCATC 2040  
 GAGGCTTTGT TTTGGAAGCA GATTAAAAA AGCCAAACCT CTCACACACG TCGTATTGTC 2100  
 ATGGTGAACA TAGCCCTGTC CCTCTTGATT GCTGATGTCT GGTATTATTG TGGTGCCACA 2160  
 GTGGACACCA CGGTGAACCC TTCTGGAGTC TGCACAGYTG CTGTGTTCTT TACACACTTC 2220  
 10 TTCTACCTCT CTTTGTTCTT CTGGATGCTC ATGCTTGCCA TCCTGCTGGC TTACCGGATC 2280  
 ATCCTCGTGT TCCATACAT GCCCAGCAT TTGATGATGG CTGTGGATT TTGCCTGGGT 2340  
 TATGGGTGCC CTCTCATTAT ATCTGTCAIT ACCATTGCTG TCACGCAACC TAGCAATACC 2400  
 TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCCTGGCT 2460  
 TTTGTTGTC CTGCACTGGC TATTGTGGCT GTGAACCTCG TTGTGGTGTCT GCTAGTTCTC 2520  
 15 ACAAAGCTCT GGAGCGCGAC TGTGGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC 2580  
 ATCCGCTGG GGAAGAGCCT CCTCATTCTG ACCCTCTGCT TAGGGCTCAC CTGGGGCTTT 2640  
 GGAATAGGAA CAATAGTGA CAGCCAGAAT CTGGCTTGGC ATGTTATTTT TGCTTTACTC 2700  
 AATGCATTCC AGGATTTTTT TATCTTATGC TTGGAATAC TCTTGGACAG TAAGCTGCGA 2760  
 CAACTTCTGT TCAACAAGT GTCTGCCTTA AGTTCTTGA AGCAAAACAGA AAAGCAAAAC 2820  
 20 TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAAGCCTT TCAACCCACT GCAAAACAAA 2880  
 GGCCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940  
 GTCTCAAATG AATAA

## A98 PROTEIN SEQUENCE

25 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 Unigene number: Hs.256897  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Pfam domain: 7tm\_2 [561-820]  
 30 Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 MHALLLCFSV LNGASGLSL QSPVEEYQL LQVYRDSKE KRDLRNFKL LKPPLLWSHG 60  
 LIRIIRAKAT TDCNSLNGVL QCTCEDSYTW FPPSCLDPOQ CYLHTAGALP SCECHLNLS 120  
 QSVNFCERTK IWTFFKINER PTNDLLNSSS AIYSKYANGI EIQLKKAYER IQGFESVQVT 180  
 QFRNGSIVAG YEVVSSSSAS ELLSAIEHVA EKAKTALHKL FPLEDGSFRV FGKACNDIV 240  
 40 PGFSGKDEY TLPSCSSYRG NITAKCESSG WQVIRETCVL SLLEELNKNF SMIVGNATEA 300  
 AVSSFVQNL S V I I R N P S T T V G N L A S V S I L E N I S S L S L A S H F R V S N S T M E D V I S I A D N I 360  
 LNSASVINWT VLLREEKYAS SRLLETLENI STLVPPTALP LNFSPKFDW KGIPVNKSQL 420  
 KRGYSQIKM CPQNTSIPR GRVLIGSDQF QRSLEPTIIS MASLTGLNLI PVSKNGNAQV 480  
 NGPVISTVIQ NYSINEVFLP PSKIESNLSQ PHCVFWDPSH LQWMDAGCHL VNETQDIVTC 540  
 45 QCTHLTSFSI LMSFPVPSTI FVVKWITYV GLGISIGSLI LCLIIELFW KQIKKSQTS 600  
 TRICMVNIA LSLIADVWF IVGATVDTTV NPSGVCTAAV FPTHFFYLSL FFWMLMLGIL 660  
 LAYRIILVPH HMAQHLMMAV GFCLGYGCPL IISVITIAVT QPSNTYKRKD VCWLNWSNGS 720  
 KPLLAFFVPA LAIVAVNFV VLLVLTKLWR PTVGERLSRD DKATIIIRVGK SLLILTPLLG 780  
 LTWGPFGITI VDSQNLAWHV IFALLNAFQV RTVTITYCIV K

## A99 DNA SEQUENCE

55 Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 ProbeSet Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51  
 AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCCAGCGTG CTGTGGCCTC 60  
 GGGAGTGGG AAGTGGAGGC AGGAGCCTTC CITACACTTC GCCATGAGTT TCCTGATCGA 120  
 CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTGTGGA TTTGGGTGGC TTTTCTTCAT 180  
 65 GCGCAATTG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240  
 GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300  
 GAATAGCAGC TCCGTTATT TTTACTGGAA AATGAACCTG TGCSTAATTC TGCTGATCCT 360  
 GGTTTTCATG GTGCCCTTTT ACATTGGCTA TTTTATTGTT AGCAATATCC GACTACTGCA 420  
 TAAACAACGA CTGCTTTTCT CCGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480  
 70 ACTAGGAGAT CCCTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGTC 540  
 CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTTCTCG GATTGGTGC 600  
 TGTCACTGTC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660  
 TCTAGCCCTG GAACGGCGAC TGCTGCAAC CATGGATATG ATCATAGCA AAAAGAAAAG 720  
 GATGCAATG GCAAGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780  
 75 TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAAGCATCA GGAAGTGAAT ATCTTACTCT 840  
 TATTCAACAG GAAGTGGATG CTTTGAAGA ATTAAGCAGG CAGCTTTTCT TGGAAACAGC 900  
 TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTT 960  
 TAAATTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020  
 CAATATTGTT TTTGATCGAG TTGGGAAAC GATCCTGTG ACAAGAGGCA TTGAGATCAC 1080  
 80 TGTGAATTAT CTGGGAATCC AATTGTATGT GAAGTTTGG TCCCAACACA TTTCTTCTAT 1140  
 TCTGTGTGA ATGATCATCG TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200  
 CTTTATGCC ATCTCTAGCA GTAAGTCTC CAATGTCAIT GTCTGCTAT TAGCACAGAT 1260  
 AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320  
 CGCACCATA ATCACTGAAG TCCTTGAGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT 1380  
 TGATGTGATC TTCTGTGCA GCGCTCTCTC TAGCATACTC TTCTCTATT TGGCTCACAA 1440

	ACAGSCACCA	GAGAAGCAA	TGGCACCTTG	AACTTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAAATTTAGA	TATAAGAGGG	GGGAAAAATG	GAACCAAGGC	CTGACATTTT	1560
	ATAAACAAAC	AAATGCTAT	GGTAGCATTT	TTCACTTCA	TAGCATACTC	CTTCCCCCTC	1620
5	AGGTGATACT	ATGACCATGA	GTAGCATCAG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGGAGAGGAG	1740
	CCAAGAAACT	AAAGGTGAAA	AATACACTGG	AACTCTGGGG	CAAGACATGT	CTATGGTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTAA	GGTTCACATG	GAAGAGGTTA	TAGCTTTGCC	1860
	TTGAGATTGA	CTCATTAATA	TCAGAGACTG	T			
10	<u>A100 Protein sequence</u>						
	Gene name: putative G-protein coupled receptor						
	Unigene number: Hs.16085						
	Protein Accession #: NP_057418.1						
	Signal sequence: none found						
15	Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446						
	Cellular Localization: plasma membrane						
	1	11	21	31	41	51	
20	MSFLIDSSIM	ITSQILPFGF	GWLFMRQLF	KDYEIRQYVV	QVIFSUTFAP	SCTMFELIIF	60
	EILGLVNSSS	RYFHWKMNLC	VILLILVFMV	PFYIGYFIVS	NIRLLHKQRL	LPSCLLWLTF	120
	MYFFWKLSDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTMSYFLRN	180
	VTDDILALE	RRLQTMDMI	ISKKRMAMA	RRTMPQKGEV	HNKPSGFWGM	IKSVTTSAGS	240
25	SENLTLIQOE	VDALBELSRQ	LPLETADLYA	TKERIEYSKT	PKGKYFNPLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDPTV	RGIEITVNYL	GIQFDVKFWS	QHSFILVGI	IIVTSIRGLL	360
	ITLTKPPYAI	SSSKSSNVIV	LLLAQIMGY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRNFDVIF	LVSALSSILF	LYLAHQAPE	QKMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]						
	Unigene number: Hs.19322						
	Probeset Accession #: AA088458						
	Nucleic Acid Accession #: AA088458						
35	Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)						
	1	11	21	31	41	51	
40	GCCCTTGGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAGG	GAGGTGCTGC	TGCAGGGTTT	GGAGATGATG	120
	CGCGGGGGCC	CGGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCGCG	180
	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAAGGTACA	AGAGGTGGCC	CGGTGCCTGG	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCCCTGCC	CCGTCCTCC	TCCGGGGCCC	CCTGCCCTGC	CCTGAAGTCC	360
45	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
	CTCACCCAGT	AGGTGACCCA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAAGTCG	480
	CGCGCTCATT	GCAGAGCTGT	TGAGGCCCGC	GCCCTGAGCC	AGCAGGACGG	GGGACCTCTG	540
	GATTCCACCT	TCATCTAGTC	CTTGTGGGCC	GGGTGGGGCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTCCA	GGGTGGGGCC	CCCATCGCAC	CCACCTCTCT	TGGCTGGAGA	CCCCCGGCAG	660
50	GCCACAGCAC	AGTCCCGGAG	TGGGGCGCTT	CCTGCCGGCC	TTGCCAGATG	GGCTCCCCAG	720
	GCCTGCCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTTTKGGCTC	CTGGTTGYTG	780
	ACATGGGCTG	GGGGCTCTCT	TGAGTCCGCA	TAGTCCGCGC	CTACTACTGG	CCGCTGTGAG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCCCGG	TTTCCAGCGG	TGCCGCCCTG	900
	GGTCCCATTA	TCAGGGAAGG	GCCTGCCCCA	CGCCAGGCTG	CACCTTCAAC	AACGGGCAGC	960
55	AGAGGGCGCG	GGGCGGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGTCCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TCCGACGAGC	GGAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAAGCGGG	GGGGCTCTGG	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTGCG	ACTTCAGGTT	1140
	CTGGCCACAG	CTGAGGGAAC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GGAGAGAGCT	1200
	GGCTGTGATG	TGCTCCCAAC	AGACCTGGGG	GTGATGGCCT	TCCCTCTCTT	GGCGGGGAAG	1260
60	TTGCCCCAGC	TTGAGTCCCA	CAACAATCC	TGTGAGCCTG	GCTCCCCAGG	AGSGCCCCCA	1320
	GACAGCTCCC	AGGCACGTCA	TAGGCAAAAG	CTGTTTCCCC	CGACTCAGGA	TTTCAAGGCG	1380
	CTGGGCTCTT	GCTCACCCCC	CTTTGCTCTC	ACGCCAGGCC	TGTCCCCAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAGC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCTTGCCCC	GGCCCACTCC	CGCTGTGTCT	1560
65	GGAGTAGCCA	CTGGTGGGGG	GGCCCTGCTC	AGCCCAACCT	GGAGGGTCCC	AGTGTACCCA	1620
	GAACCAAGGG	CACGGCAACA	GCATCGATGG	GTTCTGCAGC	CCAGGGCCCC	CGATGCGGGG	1680
	TCAGTGTGTG	TGGGGGCGAG	GGCCTCCGAT	GCGGGGTGAG	TGCGTGGGGG	GCGCAGGGCC	1740
	CCCGATGCCG	GGTCAGTGCG	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCATTTGGTT	1800
	ACACTGTCCG	ACAAGGCACC	TGTCTCAGAG	GAGGGGCCCT	GGCAGGCAGC	GTGGCAACTC	1860
70	CCTTCGCGAG	CCAGCTCCA	TGCTAACCTG	CCACAGCAA	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCAG	GACAGGCCCA	AGTCAGCCCA	GCATGCAGCT	1980
	GCCCTCTTAC	CTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCTTGG	2040
	ACCTCTCTGG	CAGGAAAGGG	TGCAGGTCTT	GAGGGCCCTG	GCCCCACAGC	CCAGCACACC	2100
	AGGTGGACATG	CAGCGCAGTG	GCTGGGGCCG	TGGCAGCCAG	GGAGAAAGCC	CCCGTCAGCA	2160
75	GGCTGGGGTC	TGCCCAACAG	GGCCTCCCCA	CGTCTGCCTT	TGAGGGTGCC	TGCCATGCCC	2220
	TGGGGGATCC	TGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGAGTTCA	TCAGGAGACC	GCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCTCCG	GAAAAATGCG	CTTTCAGCCT	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATGC	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAGTGG	CCCTGGAGAG	2460
80	CACGAGGGGA	GAAATTAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCTCG	CCTGGAGCCT	GCCCTAGGAC	GCTGGGGCGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGGCTC	ATCCGCGCTC	TGCCAGTAGC	GTGTGCAGGT	ACATACAGTG		2640
	CGGTGCACAT	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
	CAGAAGTGTG	CCAGTGTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTGTGTGTT	ATCAAGTTCC	AAGGAAAGG	AACATCTCAG	CGGGCGCTGG	TGGTTCAGCG	2820

CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

**A102 DNA SEQUENCE**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ACCGGGCACC GGACGGCTCG GGTACTTTTC TTTCTAATTA GGTTCATGCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120  
 CCACTCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCTCG AATAGTACAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGGG CCTTGATGAT TTGAAAATAA GTCTGTGTGC ACCAGATGCA 300  
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTGACTGTC 420  
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGAA CGGGGAGGAC GAGTACCGCT GTGTCGGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAAG CCACTGTGTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGTG TGCCCTGTGC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAAACCTCA GAGTGAGCTG GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT TCCATTCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTCG CCACGCTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCAGCCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTGTGAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGACAA TCACGCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCAGGTTCA ATGAAATGAT CCAGCCTGTG TGCTTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGGAAAGG TGTGCTGGAC GTCCAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTGCC TGAACACGCG GGCCGTCCCT TTGATTTCCT ACAAGATCTG CAACCCACAG 1320  
 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT AGTACGAGCG CAGCGGGGGG CCGCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCCAGCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTCG GACTCCCTGT TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGCG CCGAAAGAGG CACCCCTTCA TCTGATTCCA GCACAACCTT 1740  
 CAAGTGTGCT TTGTGTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGTTTCA AGCGATTCTC 1860  
 TTGCTTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACCTAATT 1920  
 TTGTATTTTT AGTAGAGACA GGGTTTCACT ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCTGCTC TCAGCCTCCC ACAGTGTGCG GATTACAGGC ATGGGCCACC 2040  
 ACGCTAGGCC TCACGCTCCT TTCTGATCTT CACTAAGAAG AAAAAGAGCA GCAACTTGCA 2100  
 AGGGCGGCGT TTCCCATCGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160  
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCTCTCTA GGGACCAGAA 2280  
 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCTTAT TTTCTGATTT TCTTTGTAGC ATTTGGTGTCT TGACGTATTA 2400  
 TTGTCTCTTG ATTCCAATA ATATGTTTCC TTCCCTCAAA AAAAAAATA AAAAAAATA 2460  
 AAAAAA

**A103 Protein sequence:**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGENDPFAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLEPLKFFP IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLPV 120  
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEQGFREFFV SIDHLLPDDK 180  
 VTALHHSVTV REGCASHVTV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240  
 LCGSVITPL WIIIAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VVHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGKVCWT SGWGATEDGA GDASPLVNLHA 360  
 AVPLISNKIC NHRDVGII SPSMLCAGYL TGGVDSQGGD SGGPLVCQER RLWLKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51  
 | | | | | |  
 ATGCACACCG TGGCTACGTC CGGACCCAAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC 60  
 GGCTGCCCGG GCTGTGGCGC CAACGCCTCG GACGGCCCGC TCCCTTGGCC GCGGGCCGTG 120  
 GACGCCTGGC TCGTGCCGCT CTCTCTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180  
 TCGCTGGTCA TCTACGTCAT CTGCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240  
 ATGCCAACCC TGGGGGCCAC GGAAGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300  
 15 CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360  
 ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CGCCATGAG TGTGGACGCG 420  
 TGGTACGTGA CGGTGTTCCC GTTGGCGGCC CTGCACCGCC GCACGCCCGC CTGGCGCTG 480  
 GCTGTGAGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTGCGCCTG 540  
 CACGCGCTGT CACCGCGGCC GCGGCGCTAC TGCACTGAGG CCTTCCCGAG CCGCGCCCTG 600  
 20 GAGCGGCGCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCGCT CTCTGCCACC 660  
 TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGGTGCG CCGCGCGCCC 720  
 GCCGATAGCG CCCTGCAAGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAA 780  
 GTCTGCGCGC TGCTGCGCGC CTGTGCTCTG CTCTTCCGCC CTGCTGGGG CCGCATCCAG 840  
 CTGTCTCTGG TGCTGCAAGC GCTGGGCCCC GCGGCTCTCT GGCACCCACG CAGCTACGCC 900  
 25 GCCTAGCGCG TTAAGACTG GGTCACTGCG ATGTCTTACA GCAACTCCGC GCTGAACCCG 960  
 CTGCTCTACG CCTTCTCTGG CTGCACTTTC CGACAGGCGT TCCGCGCGGT CTGCCCTGCG 1020  
 GCGCGCGCGC GCGCGCGCGC CCGCGCGCGC CCGGAGCCCT CGGACCCCGC AGCCCCACAC 1080  
 GCGGAGCTGC ACCGCTCTGG GTCCCAACCG GCGCGCAGAA GCGAGGGAGC 1140  
 30 AGTGGGCTCG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm\_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

45 1 11 21 31 41 51  
 | | | | | |  
 MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFPA ALMLLGLVGN 60  
 SLVIYVICRH KPMRTVTNFI IANLAATDVT PLLCCVPFTA LLYPLPGWVL GDFMCKFVNY 120  
 IQQVSVQATC ATLTAMSVDR WYVTVPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180  
 HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240  
 ADSALQQLV AERAGAVRAK VSRVAAVVL LFAACWGIQ LFLVLQALGP AGSWHPRSYA 300  
 50 AYALKTNAHC MSYNSALNP LLYAFILGSHF RQAFERVCPC APRPRRRPRR PGSPDPAAPH 360  
 AELHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

A106 DNA SEQUENCE

Gene name:

integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM\_002214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51  
 | | | | | |  
 CCCAGAGCGG CCTCCCCCTG TGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGAGC 60  
 CTGCGGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAGCTGCG AACTAATGGT 120  
 GTTGGCCCTC CTGCCCCACT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180  
 65 TCCCTCTGAC CTGCGCGCGG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240  
 TAGGGTGGTT TCCCCCCCAG CTGCGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTGG 300  
 CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360  
 TGTCCCGGAG CAGGCTCGCG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCGGGGCCCT 420  
 TGGCGGTGGA AGGAGGTGCT TCTGCGGAG ACCGCGGGAC CCGCGTGCC GAGCGGGGAG 480  
 GGCGGTAGGG GCCCTGAGAT GCCGAGCGGT GCGCGGGGCC GCTTACCTGC ACCGCTTGCT 540  
 70 CCGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAAAGCT CCTAGCGACA CTCGCCGCGG 600  
 GGCCCGGAGG TCGCCCGGGA GGCGAGCCCC GCGTCCGAAA GGCAGCCAGG CCGCGGGCGC 660  
 GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITTAAC GCTGCATTGG 720  
 TCTGCCGTGA AAAGACCGCG CGAGGTCCCG CCTCGTTCCT CTGGGCGAGC TGGGTGTTTT 780  
 75 CACTTGTGCT TGGAAGTGGC CAAGGTGAAG ACAATAGATG TGCACTTTCA AATGCAGCAT 840  
 CCTGTGCGAG GTGCTTGGCG CTGGGTCCAG AATGTGATG GTGTGTTCAG GAGGATTTC 900  
 TTTCAAGTGG ATCAAGAAAT GAAGTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT 960  
 GCTCAGTTGA TTCAATAGAA TACCACCTG TGCAATGTTT AATACCCACT GAAATAGAAA 1020  
 TTAATACCCA GTGACACCAA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCGGAAGCTA 1080  
 80 ATTTTATGCT GAAAGTTTCT CCTCTGAAGA AATATCTCTG GGATCTTTAT TATCTTGTG 1140  
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCGTTGGA AACGATTAT 1200  
 CTAGAAAAAT GGCATTTTTC TCCGTGACT TTCGTCTTGG ATTGGCTCA TACGTTGATA 1260  
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAAGTACT 1320  
 ACAATTTAGA CTGCATGCTT CCGCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA 1380  
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440

5 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620  
 ACGTCAAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AATTTAATAG 1680  
 ACAACAACAT TAATGTCATC TTTGCAGTTC AAGGAAACA ATTTTCATGG TATAAGGATC 1740  
 TTCTACCCCT CTGGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800  
 ATAATTTGGT AGTGAAGCC TATCAGAAGC TCATTTTACA AGTGAAGTT CAGGTGGAAA 1860  
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920  
 CAGGCATGGA AGGATGACGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980  
 10 TTACAAATGAA AAAATGTGAT GTCAAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040  
 GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTGAG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAG TGTTCCTCAGT 2160  
 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTT TCTGAGAGT TGCAAGTCAC 2220  
 15 ACAAGATCA GCCTGTTTGC AGTGGTCTGAG GAGTTTGTGT TTGTTGGGAA TGTTCATGTC 2280  
 ACAAAATTA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340  
 CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520  
 20 CACCGATGCC AGGAGCATC GGCCTTTCT GTGAACACTG CCCACCTGT TATACAGCCT 2580  
 CGAAGAAAA CTGGAATGTT ATGCAATGCC TTCAACCTCA CAATTTGTCT CAGGCTATAC 2640  
 TTGATCAGTG CAAACCTCA TGTGCTCTCA TGGAAACAAC CATTATGTC GACCAAACTT 2700  
 CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTT ATAGTTACAT 2760  
 TCTTGATTGG GTTGCTTAAA GTCTGTGATC TTAGACAGGT GATACTACAA TGGAAATAGTA 2820  
 25 ATAAATTAAG GCCTCATCAT GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATTC 2880  
 TGCAAAATGT TTGCAACAGA GCACTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CACTTCTAA AAAAAAGATT 3000  
 TTAACACTTT AATGGGAAAC TGGAAATGTT AATAATTTCT CCTAAAGATT ATAATTTTAA 3060  
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACCTCGAAC 3120  
 30 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTAATCTGTT TTGAGACTAG TGTGTTGTTA GCATTTTACT GTAATATATA 3240  
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360  
 CACTACAGG GTACAGTAAT CCTGCACGTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 35 TATATTCTAA GGTGTCACAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTAAATCTTA 3540  
 AAGATTATTT GCTTTTAAAT GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT 3600  
 TTTGCAAGAT GGATACTAAT TCCAGATTG TCTCTCTTT GCCTTTATGT TTTGTTTTCT 3660  
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 40 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780  
 GAATGTAA

**A107 Protein sequence:**

45 Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 50 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane

55 1 11 21 31 41 51  
 60 MCGSALAFFT AAFVCLQND RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60  
 LGPECGWCVQ EDFISGGSRS ERCDIVENLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120  
 GEVSIQLRPG AEANFMLKVH PLKYPVDVLY YLVDVSASMH NNIEKINSVG NDLSRKMAFF 180  
 SRDFRLGFGS YVDKTVSPYI SIHPERIHNO CSDYNLDCMP PHGYIHVLSL TENITEPEKA 240  
 VHRQKISGNI DTPEGGPDAM LQAAVCESHI GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV 300  
 VPNDGNCHLK NNIVYKSTTM EHPSLGLQSE KLIDNNINVI FAVQKGQFHW YKDLLPLLP 360  
 65 TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420  
 NVTNDEVLFP NVTVMKKCD VTGGKQYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480  
 CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKQDPVC SGRGVCVCGK CSCHKIKLKG 540  
 VYGYKCEKDD FSCPVYHGNL CAGHGECEAG RCQCPGSGWEG DRQCPSAAA QHCVNSKGV 600  
 CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660  
 70 CALMEQHYV DQTECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNLIKSSS 720  
 DYRVASAKKO KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETPRCNF

**A108 DNA sequence**

75 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 ATGCTGTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60  
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GTGCGGCACA CCTCCCGAGG GCGAGGCAGC 120  
 GACCGGGAGA GGGAGAGCCG GCGGAGGCT CCGGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCGCGCT GGATCCGCGC CCAGCAGCAG 240



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CCGCGGCCGC GCAGGCTGCC GGGACTGCGG CTGGGGGCGC GCAGGACCCT 300  
 CGCCTGCGTC CTGGACGTTT CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360  
 TCCGAGCAGC AGCCCCGGGG GCCTTCTGAC TGACATCCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCCTGGAC CTAGGGCCCG GCGTGTGCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540  
 CCGCGCGGAA AGCGCGCGG GACAGTCAGT GACGAGGCC GGGGGTCGCC GGGGCCAOGA 600  
 CTCTCTGGAG ACCGTCTCTG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
 TGTGGGGCGC TCGCGCTCTG TCCGTCTCTT CATCTGGAA CCGCGCTTCG CTCCTGCAGC 720  
 TGCTGTGGC TGCGCTGCTG GCGGCGGGGG CGAGGGGCCA GCGGCGAGTA CTGCCACGGC 780  
 TGGCTGGAGC CGCAGGCGGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 GGGGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGGCGGAG 900  
 GCGCGCTGG ACCAGGGCGG CTGGGACAA GACCGCCAGC AGGCGCTGG CGAGCCTGGC 960  
 CGGCGGGA CAAGACGGGC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGG AGGTGCGGCC CCCACCGTG AGGGCTGGC AGCGGTGCTC CCTGGAAGGC 1080  
 TCCCCGAAAG GAAGCGAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140  
 CGCGATTCC CATCTCTCC ACGCGCGGCG CCTCTCCCC TGCAGCGGCG CGCTTGGCCC 1200  
 ATCTAGTGC GTTCTCTCAT TGTGGGCTCC GTGTTTGTG CCTTTATCAT CTTGGGGTCC 1260  
 CTGTGGCAG CCTGTGCTG CAGATGTCTC CGGCTTAAGC AGGATCCCCA GCAGAGCCGA 1320  
 GCGCCAGGGG GTAAACCGCT GATGGAGACC ATCCCATGA TCCCGAGTGC CAGCACCTCC 1380  
 CGGGGTGCT CCTCAGGCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCAACTCC 1440  
 GGGCGCGGCG GCGCCCAAC AAGGTCACAG ACCAACTGTT GCTTGGCGGA AGGACCATG 1500  
 AACACGTGT ATGTCAACAT GCCCAGCAAT TTCTCTGTGC TGAAGTGTCA GCAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT AGTGGGGTA CAGCGTGCAG 1620  
 CAGACTCTGC TGGCCATGAG AGCTGTGCCA CCTTTATGG AGCGCTGCA GCCTGGCTAC 1680  
 AGGCAGATT AGTCCCGCTT CCTCACACC AACAGTGAAC AGAAGATGA CCCAGCGGTG 1740  
 ACTGTATAC CGAGATCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTGC GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860  
 GCTTCATTGG CCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920  
 CATCCAGGGT ATCATGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAAATTA TAACTGATA AATTAAGGAT TTTTATTATG TTGTATTAT TATTCTTTT 2100  
 TTGTTGTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160  
 TTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTGTCTG TGCCCAAGC TGGAGTGCAG 2220  
 TGGTGCATG TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCCTGCCCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCAT GGCTAATTTT TTGTATTTT 2340  
 TGTAGAGAT TGGGTTTACC ATGTTGGCTG GGTGCTCTC ACTCTCTGA CCTCAAGCAA 2400  
 TCTGCTGTC TCAGCCTCCC AAAGTGTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460  
 TGAGCCTTT TTTTTTTCTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT 2520  
 ATTCATAAAG GAAACCTGTT TGAACCTGT GAGATCAGT ATCAGTCTCA GTATTCCACA 2580  
 GGCACACCTT AATTTCTATG TAAAGGATA TATATATTT GTCTATTTT GTGCTTTTGG 2640  
 GGGCTATTG TTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTACA 2700  
 TTAAGAGAG ACTGAATAA ATTGTATAGT TACTTAAGTA ATGAAGCAT TTCAGAACTC 2760  
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 TTGATTGTAT CTAAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880  
 TATATTGAAA TCATAAACTA TCACCGCTG CTCTCTGAG TTAATTTTAA TTTTGGCTTG 2940  
 TGGTATGTT TGGGCTTTTC CTCTGTTTG GTTTTCAGAG CCCAAGTCT ATATAGTCTC 3000  
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCTTA GATCTGATAA 3060  
 AAAAAATTT CTGTCTTAGT TATAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACGAGATAC GATTACTTT 3180  
 GCAGATCAT AGGCTTTTTA TACTCTGTT ATCAAATGG CTTATTTTC AGGCACTAAG 3240  
 GATTGTAAAG AGAAAGCTT TCAACGAAG GATTGCTTT CTCTCCAC ACTGTTCTG 3300  
 ATTTCTCTC TCTTTCAGG CTCAACAGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360  
 CAAATTCAG TGAATTTATT TGTGTGTTCT TACTTTATAT AAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACAGTATT TTGTAATTAA ACAAATGCT 3480  
 GTATGGTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540  
 TGTTTCAATG CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660  
 TGAATAAATA AAAAAAATA AAAAAAATA

**A109 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

70  
 75  
 80

1 11 21 31 41 51  
 MLSGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKGNRGE PPANIRAQQQ PRPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPEA 120  
 SGRQPRGSD CIPRFPSSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEGSG 180  
 PRKRRGTYS DEARGSPGPR LLGDRPALSG DALSAPEVVP CGALAARPSF HPFTPLRSCS 240  
 CCLRCWRRG RPSGGEYCHG WLDAQGVWRI GFQCFERFDG GDATICGSC ALRYCCSSAE 300  
 ARLDQGCCDN DRQQAGGEPG RADKDGPRRL GRASCLRGTO GDGBGAPFPV RAWQRCSPG 360  
 SPKGRQLLRA FPGLLPRARR RGFPSPPRG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420  
 LVAAACCCRL RPKQDPQQR APGGRNLMET IPMIPASSTS RGSSSRQSST AASSSSSANS 480  
 GARAPPTRSQ TNCCLPEGTM NNVYVNMFTN FSVLNCQOAT QIVPHQGYL HPPVVGTVQ 540  
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQMYPAV TV

**A110 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCAGAG TTCTCTCCAA CCTTGCCATT 120
   GCAATAAAGA AGGAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCCTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGACC 300
   CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTATGCGAT 360
15 GAACCACTG ATAAGAATT ATCACCCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTG 420
   GACCCCTTCT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTACCC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCCTTCACT TCAAAGAAGT CAAATTTCAT 600
   GAAGAAAAAC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
20 TTAATTATTA GTTTTITTA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTITAAA 720
   TCTGAAAAAA AAAAAAATA AAAAAAATA

```

25 A11 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

30

```

1      11      21      31      41      51
|      |      |      |      |      |
35 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQSKSK 60
   PLMVIHLED CQYSQALKKV FAQNEBIQEM AQNKPIMLNL MHETTDKNLS PDGQYVPRIM 120
   FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

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A112 DNA SEQUENCE  
 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

```

1      11      21      31      41      51
|      |      |      |      |      |
50 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
   AATACCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCCTATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCG CGAAGGGCCT 300
   GCAGTGGCAG TCGGCTCTC CAAGGACCGA TCCACTGTC AGGTGCTGGA CTGGGCCAGA 360
55 GGAACCTGGT TCTCTGCTCG TTTGACACAC TTCAAGAGAG CTCTGCTGGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAAT CACAGAAAAA AGCCAGGAGC TTGSCATGCG GAACCTAAGT 540
   GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
   AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
60 AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCTTGGACCC CCACTGGGTC 720
   CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCGAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
   TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
65 ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCAACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTCAA TGCAGACGAT 1080
   GCGTACCAGG GGAAGATCAG CGAGAAGATG ATGTGTGCGA GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCGAGG AGTATACACC 1260
   AAGGCTCAGC CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

```

75 A113 Protein sequence:  
 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

80

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1      11      21      31      41      51
|      |      |      |      |      |
5  MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPFDEGP AVAVRLSKDR STLQVILDSAT 120
GNWPSACFDN FTEALAEAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GPCLSGSLVS LHCLACGKSL KIPRVVGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHV 240
LTAACHCFRKH TDVFNWKVRA GSKLGSFSPS LAVAKIIIE FNMYPKQND IALMKLQPL 300
TFSGTVRPIK LPFFDEELTP ATPLNIIIGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAGIPEGVG DTCQGDSSGP LMYQSDQWHV VGVSWGYGC GGPSTPGVYT 420
KVSAYLNIWY NWNKAEI

```

A114 DNA SEQUENCE:

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15  Gene name:          TTK protein kinase
Unigene number:       Hs.169840
Probeset Accession #: M86699
Nucleic Acid Accession #: NM_003318
Coding sequence:      1026-3551 (underlined sequences correspond to start and stop codons)

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```

20      1      11      21      31      41      51
|      |      |      |      |      |
25  GGAATTCCTT TTTTITTTT TTTGAGATGG AGTTTCACCT TTGTTGGCCA GGCTGGAGTG 60
CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCTCCCG GGTTCAGCG ATTCTCCTGC 120
CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180
CTTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
ACCTCAGGTG ATCCACTTGC CTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300
TGCTGGCTG ATTCTTTT TGTGTTGGA TTTTGAAC AGGCTCTCCC TTGTCGCC 360
AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTCAGT 420
GATCCTCCCA CTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGCACCA CCACACCGG 480
CTAATTTTGT TATTTTATT AGAGACAGGG TTTCACCATG TTGGCCAGCG TGTCTCAAA 540
CTCCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAA GTCCCGAGAT TACAGGTGTG 600
AGTCACCATG CTTGACCTTA TAATCTTAA GTCATTTT CTGCTCCATT TCTTCTTAG 660
GGTCCTCACA ACAATCTGCT ATTAGCGGT ACAATAATCC TTAACCTCAT GATTCACAAA 720
AGGAAGATGA AGTGATTCAT GATTTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT 780
GGATGATGAT CCTAATCCA GATACAGTAA AATGGGGTA TGGGAAGSTA GAATACAAAA 840
TTTGTTTAA ATTAATTATC TAAATATCTA AAACATTTT TGGATACATT GTTGATGTGA 900
ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTGGGTT CCATCTTTT TCTTCCCG 960
TGCAATTTTC GTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAAATG ACAATTGATT 1020
CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080
AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAAC GTTAAACCAA 1140
TTATGATGAT GGCAACAAC CCAGAGGACT GGTGTAGTTT GTTGCTCAA CTAGAGAAAA 1200
ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTGTGTTA AGTCAAGCAA 1260
TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTGCTAGA ATTCAAGTGA 1320
GATTTGCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAATGG 1380
CCAGAGCAAA CTGCAAGAAA TTTGCTTTT TCTATATATC TTTTGACAA TTTGAACCTG 1440
CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG 1500
TACCAGTACT AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560
TTTCAGAGGA GGAAGAAAG AATTATCAG CATCTACGCT ATTAAGTACC CAAGAATCAT 1620
TTTCCGGTTC ACTTGGGCTT TTACAGAATA GGAACAACAG TTGTGATTCC AGAGGACAGA 1680
CTACTAAGCC CAGGTTTITA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740
ACCGGAATTC ATTGAGACAA ACTAACAACA CTAAACAGTC ATGCCCATTT GGAAGAGTCC 1800
CAGTTAACTT CTAAATAGAT CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGTACCTT 1860
GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGTTGTG CCTGGATCTA 1920
AACCAGTGG AAATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980
TCAAGGAACC TCTGGGTGCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATAA 2040
CCCTGAAGAA TAAACGGGAA TCAAGTCTTC TAGCTAAATT AGAAGAACT AAAGAGTATC 2100
AAGAACCAGA GGTTCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160
GTATTAACCA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCGGAG TTAGCCCGAA 2220
AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC 2280
AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGTG AAGACACCAA 2340
GCAGCAATAC CTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGATGACT 2400
TTCCACCTGC TTGTCAAGTG TCAACACCTT ATGGCCAAAC TGCCGTGTTT CAGCAGCAAC 2460
AGCATCAAT ACTTGCCACT CCACTTCAA ATTACAGGT TTAGCATCT TCTTCAGCAA 2520
ATGAATGCAT TTGGTTTAAA GGAAGAATTT ATTCATATT AAAGCAGATA GGAAGTGGAG 2580
GTTCAAGCAA GGTATTTTCT GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
TGAATTTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA COGGAACGAA ATAGCTTATT 2700
TGAATAAATC ACAACACAC AGTGATAAGA TCAATCCGACT TTATGATTAT GAAATCAGG 2760
ACCAATGATC CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2820
AGAAAAATC CATGATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG 2880
TTCAACAAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCAAGT AACTTTCTGA 2940
TAGTTGATGG AATGCTTAAAG CTAATTGATT TTGGGATTGC AAACCAAATG CAACAGATA 3000
CAACAAGTGT TGTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060
TCAAGATAT GTCTTCTCCT AGAGAGAAATG GGAATCTAA GTCAAGATA AGCCCAAAA 3120
GTGATGTTG GTCTTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180
AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG 3240
AATTTCCCGA TATTCCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTGTT TAAAAAGGG 3300
ACCCAAAAA CAGGATATCC ATTCCTGAGC TCCTGGCTCA TCCATATGTT CAAATCTCAA 3360
CTCATCCAGT TAACCAATG GCCAAGGGA CCACTGAAGA AATGAATAT GTTCTGGGCC 3420
AATTTGTTG TCTGAATCT CCTAACTCCA TTTTGAAGC TGCTAAAACT TTATATGAAC 3480
ACTATAGTGG TGTGAAAGT CATAACTCT CATCTCCAA GACTTTGAA AAAAAAGGG 3540
GAAAAAATG ATTTGCAAGT ATTCGTAATG TCAGATAGGA GGTATAAAAT ATATTGGACT 3600
GTTATCTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660
ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3720

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TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780  
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAAGCTTG 3840  
TAAATAAAGT TTTGTGGCTA AATGCA

**A115 Protein sequence:**

Gene name: TTK protein kinase  
Unigene number: Hs.169840  
Probeset Accession #: M86699  
Protein Accession #: NP\_003309  
Signal sequence: none found  
Transmembrane domains: none found  
Protein Kinase Domain: 510-775  
Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51  
MNKVRDIKKN FKNEEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLLKLEKNS 60  
VPLSDALLNK LIGRYSQAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120  
ANCKKFAFVH ISFAQFELSQ GNVKKSQQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180  
BEEKKNLSAS TVLTQAQESFS GSLGHLQNRN NSCDNRGQTT KARFLYGENM PPQDAEIGYR 240  
NSLRQTNTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPQSKP 300  
SGNDSCELRN LKSVQNSHF EPLVSDEKSS ELIITDSITL KNKTESLLA KLEETKEYQE 360  
PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHITFE QPVFSVSKQS 420  
PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVQNDFF PACQLSTPYG QPACFQQQQH 480  
QILATPLQNL QVLASSANE CISVKGRIS ILKQIGSGGS SKVFQVLNEK KQIYAIFYVN 540  
LEEADNQTLN SYRNEIAYLN KLQHSKDKII RLYDYEITDQ YIYMVMCEGN IDLNSWLKKK 600  
KSIDPWERKS YWKNMLEAVH TIHQHGVHS DLKPNANFLIV DGMLKLIDFG IANQMOPDTT 660  
SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYV MTYGTTPFPQ 720  
IINQISKLHA IIDPNHEIEF EDIPEKDLQD VLKCCCLKRDP KQRISIPELL AHPYVQIQTH 780  
PVNQMAKGT EEMKYVLQGL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK 840  
K

**OVARIAN****A116 DNA SEQUENCE**

Gene name: G protein-coupled receptor 39  
Unigene number: Hs.85339  
Probeset Accession #: AA349893  
Nucleic Acid Accession #: NM\_001508  
Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60  
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCCTA TTCTGGTGTG CTTGATCATC 120  
TTCTGATGAG GCCTCTCTGG GAACAGCGCC ACCATTCGGG TCACCCAGGT GCTGCAGAG 180  
AAAGGATACT TGCAGAGGA GGTGACAGAC CACATGGTGA GTTGGCTTG CTGGGATC 240  
TTGGTGTTC TCATCGGCAT GGCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300  
AOGTCCAGCT ACACCTGTG CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGTAC 360  
GCTACGCTGC TGCAGTGTG GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTACCCC 420  
TTCAAGTACA AGCTGTGTG GGGACCTTGC CAGGTGAAGC TGCTGATGG CTTGCTCTG 480  
GTCACTCCG CCTGTGTGG ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540  
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGC CCACCCAGAG 600  
CAGCCCGAGA CCTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660  
CAGTCCAGCA TCTTGGGCGC CTTCTGTGTC TACCTGTGG TCCTGCTCTC CGTAGCCTTC 720  
ATGTCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCTGGGGC 780  
ACGCGGCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGCCAG 840  
ACCATCATCT TCTGAGGCT GATTGTGTG ACATTGGCGG TATGCTGGAT GCCCAACCCAG 900  
ATTTCGAGGA TCATGGCTGC GSCCAAAACC AAGCAGGACT GGACGAGTCT CTACTTCCGG 960  
GGGTACATGA TCTCTCTCCC CTCTCTGGAG ACGTTTCTT ACCTCAGCTC GGTCTATCAC 1020  
CGCTCTCTGT ACACGCTGTC CTCGAGCAG TTTGGGCGGG TGTTCTGTGA GGTGCTGTGC 1080  
TGCGGCTCTG CGCTGCAGCA CGCCAACCC GAGAAGCGCC TGCGGTGACA TGCGCACTCC 1140  
ACCACCGACA GCGCCGCTT TGTGAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200  
TCTGCAAGGA GAAGTGAAGA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260  
TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCCAGC 1320  
AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

**A117 Protein sequence:**

Gene name: G protein-coupled receptor 39  
Unigene number: Hs.85339  
Probeset Accession #: AA349893  
Protein Accession #: NM\_001508, NP\_001409  
Signal sequence: none found  
Pfam domains: 7tm\_1 [72-172, 224-344]  
Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
NASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK 60

KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120  
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFMAMTEYPL 180  
 VNVPSHRLGT CNRSSTRHHE QPETSNSIC TNLSSRWTVF QSSIFGAFVW YLVVLLSVAF 240  
 MCWNMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIPLRLIVV TLAVCWMPNQ 300  
 IRRIMAAKP KHDWTRSYFR AYMLLPFSE TFFYLSVSVN PLLYTVSSQQ FRRVFVQVLC 360  
 CRLSLQHANH EKRLRVHAHS TDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPO 420  
 SKSQSLSLES LEPNSGAKPA NSAAENGQFE HEV

**A118 DNA sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.87223  
 Probeset Accession #: AA250737  
 Nucleic Acid Accession #: NM\_001203  
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGCGGGGCGG GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGCAGAGA CCGCGGCGCT 60  
 GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGTGGGAGTT CAGCCTACTC TTTCTTAGAT 120  
 GTGAAAGGAA AGGAAGATCA TTTTCATGCT TGTGATATAA GGTTCAGACT TCTGCTGATT 180  
 CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGGGAAGTGC AGGAAAATTA 300  
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360  
 TTGGCTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480  
 GGTTCCTTAG GACATAAGG CTCAGATTTC CAGTGTGGGG ACACCTCCAT TCCTCATCAA 540  
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600  
 CTGCCTCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCCTTACTT 660  
 ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCCTTATCA TATTATTTTG TTACTTCCGG 720  
 TATAAAGAC AAGAAACAGG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780  
 ATTCTCTCTG GACATACCTT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
 TCAGGCTTCC CTCTGCTGGT CCAAGGAGCT ATAGCTAAGC AGATTGAGT GGTGAAACAG 900  
 ATTGAAAAAG GTCCGATATG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT 960  
 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020  
 ACAGTGTGTA TGAGGACATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080  
 GGTCTCTGTA GCTAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCTTA CTCTTCTGTC 1200  
 AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260  
 CATCGAGATC TGAAGAGTAA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320  
 GACCTGGGCC TGGCTGTAA ATTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
 ACTCGAGTTG GCACCAAGCG CTATATGCGT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440  
 AATCACTTCC AGTCTTACAT CATGCGTGAC ATGTATAGTT TTGGCTTCAT CCTTTGGGAG 1500  
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560  
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620  
 CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGGC GGTTAAGAAA 1740  
 ACCTTGCCCA AATGTGAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAGTAAG 1800  
 CATCTCTGCA GAAAGCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920  
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTTGTG GCGGAGAGAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

**A119 Protein sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCPTMIEED 60  
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNDLHPTL PPLKNRDFVD 120  
 GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
 EQSQSSSGSGS GLPLLVRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVPFTTEAS 240  
 WFRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNILV KNGTCCCIAD LGLAVKPFISD 360  
 TNEVDIPPNT RVGTRKYMPP EVLDESLENN HFQSYIMADM YSFLGLINEV ARRCVSGGIV 420  
 EYQLPYHDL VPSDPSYEDM REIVCIKLR PSPPNRWSSD ECLRQMKLM TECWANNPAS 480  
 RLTLRVKKT LAKMSQSQDI KL

**A120 DNA SEQUENCE**

Gene name: LTV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Probeset Accession #: U41060  
 Nucleic Acid Accession #: NM\_012319.2  
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	CTCGTGCCGA	ATTCGGCAGC	AGACCGCGTG	TTCGCGCCTG	GTAGAGATTT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAC	CAAACTCTGC	CGCGTGGCCG	GGCGGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCTG	ACCTTTGCCC	180
5	TCTCTGTAC	AAATCCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTGTAAGGGT	360
	TCAGAAAAAT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
10	ACCACGACCA	TCACCTCAGC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
	AGCATCACTC	AGACCAGCAG	CATCACTCTG	ACCATGATCA	TCACCTCTAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAAG	CGAAAAGCTC	TTTGCCCGAG	CCATGACTCA	GATAGTTTCAG	600
	GTAAAGATCC	TAGAAACAGC	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAAGGACAGT	GTAGTGCTA	GTGAAGTGAC	CTCACTGTG	TACAACTCTG	720
	TCTCTGAAGG	AACCTCACTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
15	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTCAATC	AAAGAGCCGG	GTGAGCCGGC	840
	TGGCTGGTAG	GAATCTGTGA	GTGAGCCCG	AAAAGGCTTT	ATGTATTCCA		900
	GAAACACAAA	TGAAAATCCT	CAGGAGTGT	TCAATGCATC	AAAGTACTG	ACATCTCATG	960
	GCATGGGCAT	CCAGTTCCTG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
20	TCACCAAAAT	TGATGCTAGA	TCTTGTCTGA	TTTATACAA	TGAAAAGAA	GCTGAAATCC	1080
	CTCCAAAGAC	CTATTCTATTA	CAATAGCCT	GGGTGGTGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCTT	GTCTCTGCTG	GGGTTATCT	TAGTGCTCT	CATGAATCGG	GTGTTTTTCA	1200
	AATTTCTCCT	GAGTTTCTCT	GTGGCACTGG	CCGTGGGAC	TTTGAGTGGT	GATGCTTTTT	1260
	TACACCTTCT	TCCCATTTCT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
	CAATGAAAT	GAAAGAGGGA	CCACTTTTCA	GTCACTCTGC	TTCTCAAAAC	ATAGAAGAAA	1380
25	GTGCTATTTT	TGATTCACAG	TGGAAGGGTC	TACAGCTCT	AGGAGGCCGT	TATTTTCATG	1440
	TTCTTGTGTA	ACATGCTCTC	ACATTGATCA	AACAATTAA	AGATAAGAAG	AAAAGAATC	1500
	AGAAGAAACC	TGAAAATGAT	GATGATGTGG	AGATTAAGAA	GCAGTTGTCC	AAGTATGAAT	1560
	CTCAACTTTC	AACAAATAG	GAGAAAGTAG	ATACAGATGA	TGAACTGAA	GGCTATTTAC	1620
	GAGCAGACTC	ACAGAGAGCC	TCCCACTTTG	ATTCTCAGCA	GCGCTGAGTC	TGGAAGAAG	1680
30	AAGAGGTCT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
	CTCAGCTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTGCCCACTT	1920
	TGGCTGAGAT	GGTGATTAATG	GGTGATGGCC	TGCACAAATT	CAGCGATGGC	CTAGCAATTG	1980
35	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTGTCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GSTGACTTTG	CTGTTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CCTTTATAAT	GCATTGTCAG	CCATGCTGGC	GTATCTTGGA	ATGCAACAG	2160
	GAATTTTCAT	TGCTCAATTAT	GCTGAAAATG	TTTCTATGTG	GATATTTGCA	CTTACTGCTG	2220
40	GCTTTATCAT	GTATGTGCTC	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
	GTGACCATGG	ATGATGCGCG	TGGGGGTATT	TCITTTTACA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTTGGAAT	TATGTTACTT	ATTTCCATAT	TGAAACATA	AATGCTGTTT	CGTATAAATT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
45	TTGTATTGAA	TATGTCTGTC	TGTTACAAAG	TCAGTTAAAG	GTACGTTTAA	ATATTAAAGT	2580
	TATTCTATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAGAG	ATTTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAATGT	CTTTAATGCT	2700
	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAAGTCTGCG	2760
	TGTTTAGGAA	TAAAGATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAAATTTA	2820
50	AGCAAAGAAA	TAAAGAGAGAA	AAGAGAAAGAA	TCTGAGAAAT	GGGGAGGCAT	AGATTCTTAT	2880
	AAAAATCACA	AAATTTGTGT	TAAATTAGAG	GGGAGAAATT	TAGAATTAA	TATAAAAAGG	2940
	CAGAATTAGT	ATAGAGTACA	TTCATTAAAC	ATTTTGTCTA	GGATTATTTC	CGTAAAAAAC	3000
	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAC	TTTGATAAT	ACAGAAATCT	3060
	AAATATATTT	AATGAATTCA	AGCAATATAC	ACTTGACCAA	GAAATTGGAA	TTTCAAAATG	3120
55	TTGCTGCGGG	TTATATATCA	CAAAAGCTG	TATGAGTACA	GTGAGTAGTT	TATGTATCAC	3180
	TATTGCCAAG	TTATATATCA	CAAAAGCTG	TATGAGTACA	TGTTCTCGTT	ACCTGGTTTA	3240
	CAAAATTATC	AGAGTAGTAA	AACITTTGATA	TATATGAGGA	TATTAATACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTGAGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTTG	3360
	GAGCAATTGT	CTTTATATAC	GATACTGTAG	CCATACCTAG	CCTGCTCTGT	GCATTCTCTA	3420
60	GATGTTTCTT	TTTTACACAA	TAAATTCCTT	ATATCAGCTT	G		

**A121 PROTEIN SEQUENCE**

Gene name: LIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Protein Accession #: NP\_036451  
 Signal sequence: 1-21  
 Pfam domain: Zip[591-743]  
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
	MARKLSVILI	LTFALSVTNP	LHELKAAAFP	QTTEKISPNW	ESGINVDLAI	STRQYHLQQL	60
	FYRYGENNSL	SVEGRFKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDHEHSDH	120
75	EHSDHDS	HNNHAAAGKN	KRKALCPDHD	SDSSGKDPFN	SQKGHAHRE	HASGRNRVND	180
	SVSASEVST	VYNTVSEGT	FLETIETPRP	GKLPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
	NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMGIQV	PLNATEFNVL	CPALINQIDA	300
	RSLIHTSEK	KAEIPPKTYS	LQIAWVGFI	AISIISFLSL	LGVLVPLMN	RVFFKFLLSF	360
80	LVALAVGTLS	GDAPLHLLFH	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIESAYFDS	420
	TKWGLTALGG	LYFMYLVEHV	LTLIKQFKDK	KKNQKQKPN	DDVVEIKKQL	SKYESQLSTN	480
	EEKVDTDDRT	EGVLRADSQE	PSHFDSSQPA	VLEEEVEMIA	HAHPQEVYNE	YVPRGCKNKC	540
	HSHFMDTLGQ	SDDLHSHHHD	YHHILHSHH	QNHHPHSHSQ	RYSREELKDA	GVATLAWMVI	600
	MGDGLHNFSD	GLAIGAAFT	GLSSGLSTSV	AVFCHELPH	LGDFAVLLKA	GMTVKQAVLY	660
	NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720

RWGYFFLQNA GMLLGFGLM LISIFEHKIV PRINF

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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10      1      11      21      31      41      51
      |      |      |      |      |      |
COGCAGAGGA GCGTGGGCCA GGCTAGCCAG GCGGCCCCCA GCCCTGCCCC AGGCCGCGAG 60
CGCCCTGGCC GCGGTGCGCTG GCGTCCCTTC CCAGACTGCA GGGACAGCAC CCGGTAACGT 120
15      CGAGTGGAGC GGAGGAGCCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGCGCC GCGGCCCTCC CGAGGGGGGG TCAGGAGGAG GAAGGAGGAC CCGTGGCAGA 240
ATGCCTCTGC CCGGAGCCTT TCGCTCCCG CTGCTGCTCT CCGGGTGGC AGGTGGTTTC 300
GGGAACGCGG ACATGGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
20      TGTGAAGTCA CATGCGAACC TGGATGTAAG TTTGGTGAAT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
25      TCAGGACTCC GCGTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTTCT 780
GGTAAAGTCA TCTGTCCCTA CAATGGAAGA TGTGTGAACA CATTGGGAAG CTACTACTGC 840
AAATGTGACA TTGTTTTCGA ACTGCAATAT ATCAGTGGAG GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCTACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGTCCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
30      ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC 1080
AAGAAGTTTC TTGCTCAACA AAACAGCATG AAAAAGAAGG CAAAATTAA AAATGTTACC 1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGGA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
35      GAGGSGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTGGGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
CTGGTCCAAA TGGTCAACA AACCTCCAAA CTGGAACATA AAGATTAAA TATCTCGGTT 1440
GACTGCGACT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTGAC 1500
TGGAACTCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA 1560
40      GGTCAACAAG AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
TTTGTGAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGGAAAGCAG GGAATAATCA GTTGTATCAA GGAACGTATG CTACCAAAAG CATCATTTT 1800
GAAGCAGAGA GTGGCAAGGG CAAAACCGGC GAAATGCGAG TGGATGCGCT CTTCCTTGTT 1860
45      TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTGTG ATGTGAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGATTAA TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCCT 2040
TCTGTATAA GATATGCCAA TATTGTCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAAT TTTCCACATT ATATTATAAA ATATGGAAT GTCACTTTAT CTCCCTTCCT 2160
50      CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
TAGAAAAAAA AGCAGAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
TATGACATCA AAGATAGACT TTTGCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
TGTATATTTA AATTCTTGTG AATAATAATA TCCAAATCAT CAAAAAATA AAAAAAAT

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55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

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65      1      11      21      31      41      51
      |      |      |      |      |      |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60
CEATCEPGCK FEGCVGNPKC RCPFGYTGKT CSQDVNECGM KPRPCQHRVC NTHGSYKFC 120
70      LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EGGPQCLCPS SGLRLAPNGR DCLDIDECAS 180
GKVICPYNRR CVNTFGSYIC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTQ 240
GSFKCKKQGG YKGNGLRCSA IPENSVEKVL RAPGTIKDRI KKLALHNSM KKKAKIKNTV 300
PEPTRTPFPK VNLQPFNYEE IVSRGNSHG GKKGNBEKMK BGLEDEKREE KALKNDIEER 360
75      SLRGDVFPFK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNEGICD WKQDREDDFD 420
WNPADRNDNI GFYMAVPALA GHKKDIGRLK LLLPDLPQPS NFCLLPDYRL AGDKVGKLRV 480
FVKNSNNALA WEKTTSEDEK WTKTKIQLYQ GTDATKSIIF EAERGKGTG EIAVDGVLLV 540
SGLCPDLSLLS VDD

```

80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

```

5      1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG GGGCCGCTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGGCCGAGAG CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACTG GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240
GCTTCATCCA CCGCGCGCTC CGCAGCCAGG AGCGCGGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCGG 420
GCCAGGGCTT CTCTACCCG TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACGAAG CCGACATGGT CATGAGCTTC GTCAACTTCG 540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGCAGCCGGA ATCCCGGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAG AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCCTC TGGGCTCCGG 780
AGGAGGGCTG GCTGCTGTTT GACATCACAG CCACAGCAAA CCACTGGGTG GTCAATCCCG 840
GGCACAACCT GGGCGCTGCG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCGTATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACCGAGGTC CACTTCCGCA GCATCCGCTC CACGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCTC GCGGATGGCC AACGTGGCAG 1080
AGAAACAGCA CAGCCACGAG AGGCAGGCCT GTAGAGAACG CGAGCTGTAT GTCAAGCTTC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGGAGTG TGCCTTCCTT CTGAATCCTT ACATGAACGC CACCAACCAA GCCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCAAGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAACGTCACT CTGAAGAAAT 1380
ACAGAAACAT GTGTGTCGGG GCCTGTGGCT GCACTAGCTC CTTCCGAGAA TTCAAGCCCT 1440
TTGGGGCCAA GTTTTCTGG ATCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCTCCCTAT CCCCACCTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCTTACAAGC TGTGAGGACA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
GCGGGGCGAG GTCAATGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGCTGTGTC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAGC AATGAATG

```

#### A125 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 Signal sequence: 1-30  
 Pfam domains: TGFb\_propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

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50      1      11      21      31      41      51
|      |      |      |      |      |
MHVRSRAAA PHSFVALWAP LFLRSALAD FSLDNEVHSS FIIHRLRSQE RREMQRILS 60
ILGLPHRPPR HLQVKHNSAP MFMLDLNLYM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFFRFDL SKIPEGAVT AAEFRIYKDY 180
IRERFDNETF RISVYQLQBE HLGRESDLFL LDSRTLWASE EGWLVEFDITA TSNHWVNVPR 240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMWAF FKATEVHFERS IRSTGSKQRS 300
QNRSKTPKQK EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PBGYAAYICE 360
GECAPPLNSY MNATNHAIVQ TLVHFIPNET VPKPCCAPTQ LNAISVLIFD DSSNVILKKY 420
RNMVVRACGC H

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#### A126 DNA SEQUENCE

Gene name: integrin, beta 8

Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Nucleic Acid Accession #: NM\_002214

Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

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70      1      11      21      31      41      51
|      |      |      |      |      |
CCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCGAGCTTC CTCCCTGCC AGCCAGGACG 60
CTGCGCACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
GTTGGCCTCC CTGCCACCTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
TCCCTCGACG CTGCGCGGCG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
TAGGGTGTTT TCCGCCCCAG CTTGCGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTGG 300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT 360
TGTCCCGAGC CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCGGGGCCCT 420
TGGCGTGAAG AGGAGGTGCT TCTCGCGGAG ACCGCGGAGC CGCGCGTGCC GAGCGGGAG 480
GGCCGTAGGG GCGCTGAGAT GCGGAGCGGT GCGCGGGGCC GCTTACCTGC ACCGCTTGCT 540
CCGAGCTAGG GGTCTCGCCT GCTAGGCGCT CGGAAAAGCT CTTAGCGACA CTGCGCCGCG 600
GGCCCGGAGG TGCGCCGGGA GGCAGAGCCC GCGTCCGGAA GGCAGCCAGG CGCGGGCGCG 660
GGGGCGGGCT GTTTTGCAIT ATGTGCGGCT CGGCCCTGGC TTTTITTACC GCTGCAITTG 720
TCTGCTGCA AAACGACCGG CGAGGTCCCG CCTGTTCTCT CTGGGAGACC TGGGTGTTTT 780

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CACTTGTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840  
 CCTGTGCCAG GTGCCTTGGC CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTC 900  
 TTTCAAGTGG ATCAGAAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960  
 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAATGAAA 1020  
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080  
 ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140  
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTAT 1200  
 CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTGCTCTGG ATTGGCTCA TACGTTGATA 1260  
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAGGAT TCATAATCAA TGCAGTGA 1320  
 ACAATTTAGA CTGATGCCCT CCCCATGGAT ACATCCATGT GCTGCTTTG ACAGAGAACA 1380  
 TCACGTAGTT TACGAAGACA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440  
 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGCTGTGA AAGTCATATC GGATGGCGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 GCAAAATGGC AGGCATAGTG GTGCCCAATG ACGGAACTG TCATCTGAAA AACAACTCT 1620  
 ACGTCAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680  
 ACAACAACAT TAAATGTCAT TTTGCAGTTC AAGGAAAACA ATTTCTTGG TATAAGGATC 1740  
 TTCTACCCCT CTGCCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACTCA 1800  
 ATAATTTGGT AGTGAAGCC TATCAGAAGC TCATTTTCAA AGTGAAGTT CAGGTGGA 1860  
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCATCTG TCCAGATGGG TCCAGAAA 1920  
 CAGGCATGGA AGGATGAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980  
 TTACAATGAA TAAATGATG GTCCACAGGAG GAAAAAACA TGCAATAATC AAACCTATTG 2040  
 GTTTTAATGA AACGCTAAA ATTCAATAC ACAGAACTG CAGCTGTGAG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAG TGTGTAGATG AAACTTTCT AGATTCCAAG TGTTTCCAGT 2160  
 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220  
 ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280  
 ACAAAATGAA TGTGGAAGAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGT 2340  
 CATATCACC TGAATATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520  
 GCACCGATCC CAGGAGCATC GGCCTCTTCT GTGAACACTG CCCACCTGT TATACAGCCT 2580  
 GCAAGGAAA CTGGAATTGT ATGCAATGCC TTCACTCTCA CAATTTGTCT CAGGCTATAC 2640  
 TTGATCAGTG CAAACCTCA TGTGCTCTCA TGAACAACA GCATTATGTC GACCAAACTT 2700  
 CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760  
 TCTGATTGG GTTGCTTAAA GTCTGTATCA TTAGACAGGT GATACTACAA TGAATAGTA 2820  
 ATAAATTAAT GTCTCATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATC 2880  
 TGCAAGTGT TGTGCAAGA GCAGTCACCT ACGGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATT 3000  
 TTAACACTT AATGGGAAAC TGAATTTGT AATAATTGCT CCTAAAGATT ATATTTTAA 3060  
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGTTGT ACATCGAAC 3120  
 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGTTTGA GCACCTTACT GTAATATATA 3240  
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCCTACGCTT CCAGAGAGA ACAATGCTGT GAGAGAGTT AGCATTGTGT 3360  
 CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 TATATTTCAA GTTGCCAAA CACTTCAACA GTTGGTGGT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT TTTGCTGTTT TCACCTTTTC AAGAGGTGAA CAGATAACAC CTTAATCTTA 3540  
 AAAGATTATT GCTTTTAAA GTGTGTAGTT TTATGATGT GTGTTTATGG TTTGCTTATT 3600  
 TTTGCAAGAT GATACATAAT TCCAGCATTC TCTCTCTTT GCCTTTATGT TTTGTTTCT 3660  
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780  
 GAATGTTAA

55 A127 Protein sequence:  
 Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 60 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane  
 65

1 11 21 31 41 51  
 70 MCGSALAPFT AAFVCLQND RGPASPLMAA WVPSLVILGL QGEDNRCASS NAASCARCLA 60  
 LGPECGWCQV EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120  
 GEVSIQLRPG ABANFMLKVH PLKCYVDLY YLVDVSASME NNIEKLNSVG NDLSRKMAFF 180  
 SRDFRLGPGS YDVKTVSPYI SIHPRIHNO CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240  
 VHRQKISGNI DPEGGFDAM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300  
 VPNDGNCHLK NNIVYKSTM EHPSLGQLSE KLIDNNINVI FAVGQKQFHW YKDLLPLLP 360  
 75 TIAGEIESKA ANLNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420  
 NVTSDEVLFP NVIVTMKKCD VTGGKNYAI KPIGPNETAK IHIHRNCSCQ CEDNRGPKGK 480  
 CVDETFLDSK CFQDCENKCH FDEDFSSSES CKSHKDQPV C SGRGVCVCGK CSCHKIKLKG 540  
 VYGKVCEDD FSCPYHKGNL CAGHECEAG RCQCFSGWEG DRQCPCPSAA QHCVNKSGQV 600  
 80 CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660  
 CALMBQHYV DQTSFCFSSP SYLRIFITF IVTFILGLKL VLIIRQVILQ WNSNKIKSSS 720  
 DYRVASAKID KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

A128 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942  
 Probeset Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTCTGTAA 60
CTCGCGGTCA GGATGGTTTT CTCTGTGTCAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTACTAGA CGTTCAAGAT ATTCTTGTC ATCATTGTTC TTATGTGCTG TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
GTCAAGTTTTG CCCCCTCTCT CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
AGCTTACTCC CTTCACACGA AACAGAAAAA ACTAAAAATCA CTATAGTAAA AACCTTCAAT 360
GCTTCAGGCG TCAAAACCCA GAGAAATATC TGCAATTGTG CATCTATTGT CAATGACTCA 420
GCATTTTCTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCAGAAAT 480
CAACATATAA CGAATGGCAC CTTAACATGA GTCTGTCTCT TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AAACCTTGCA AACCTTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCCAAA GCACATTAAA TTGTACATTG ACATAAAAAA TGAATAATAC AATGAATGCA 660
TGTGTGCGAA TAGCCGCTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
TCTGTACGGA TACCCTGCCC TTCTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATT TTC CAGCCAA 840
TCCATCCGAG TGGTGCTCTG GGCCACTGTG CTTTCCGAGG TCCCCTTTC TACCTCTTTT 900
GCTGAGCCTC CAGATTATTG ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCCGAGCG TTCACTCTCC ATAGCTTCCA GCCCTGCCAT TGACATGCC 1020
CCACAGTCTG AAGCAGTCTC TTCCCTATG CCCCACACCC ATGCTCCGG CACCCCACT 1080
CCTGTGAAAG CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGGAATGT CAACACTACC 1140
AGCGCACCTC CTGTGTCAGC AGACATGCTC AACACCAGCA GTATTCTGA TCTTGAGAAC 1200
CAAGTGTGCG AGATGGAGAA GGCTCTGTCC TTGGGCGACC TGGAGCCTAA CCTGCAGGA 1260
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GCTCAAGATG TGCTGAAAGT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAACACG 1380
ACTATAAGTC TAACCTCCCC TTCCTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
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ATCAACACAA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTGT 2460
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TCCACCACAC TGCTAGTGAA TAATGATTGC TCAGTACACG CAAGCGGGAA TGGAAATGCT 2940
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TTCACTGAAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCGGT 3060
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AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
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TTATTAGGAA CATTTCAAAC CCGCTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGCAAT 4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560

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CTGACTTGTC TTTGCAATAT TTCTTTCTG ATTTATTAA TTTCTTGTA TTTATATGTT 4620  
 AAAATCAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

# A129 Protein sequence

Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60  
 PSSNEVETTS LNDVTLISLLP SNETEKTIT IVKTENASGV KPORNICNLS SICNDSAPFR 120  
 GEIMFYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAGS 180  
 TLNCTFTIKL NMTNNAACAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240  
 VCLADHFRGP PFSSSQSIPV VPRATVLSQV PKATSFAPPP DYSPVTHNVP SPIGSIQPLS 300  
 PQPSAPIASS PAIDMPQSE TISSPMPQTH VSGTTPPVKA SFSSPTVSAP ANVNTTSAPP 360  
 VQTDIVNTSS ISDLENQVLQ MEKALSLSGL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL 420  
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 NSIGTITLPS SLMMNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVSSSVANL 540  
 TVRNLTNRVT VLKHNINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600  
 SHLTSFGVLL DLSRTSVLPA QMMALTFITY IGCGLSSIFL SVTLVITYIAF EKIRRDYPSK 660  
 ILIQLCAALL LNLVFLDLS WIALYKMQGL CISVAVFLHY FLVVSFTWMG LEAFHMYLAL 720  
 VKVFNTYIRK YILKFCIVGW GVPVAVVTII LTISPDNYGL GSYGKFPNGS PDDFCWINNN 780  
 AVFYITVVG YFCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840  
 ITWGFAPFAW GGVNVTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE 900  
 NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGMASTER 960  
 NGVSFSVQNG DVCLHDFGCK QHMFNEKEDS CNKGKRMALR RTSKRGSLSHF IEQM

# A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Probeset Accession #: AA460530  
 Nucleic Acid Accession #: NM\_003667  
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GTGGGCGCAA CGGCGACCTC AGTCCCGGCC GCGCTTCTCC TCGCGGCCCA GCGCGTGGG 60  
 TCAGGAACGC GCGCTCTGGC GCTGCGAGCG CCGCTGAGT TCGAGAAGCC CACGGAGCGG 120  
 CGCCCGGCGC GCCACGGGCC GTAGCAGTCC GGTGCTGCTC TCGCGCCGCG TCGCGCTCGT 180  
 GGCCCGCTAC TTGCGGCACC ATGGACACCT CCGGCTCGG TGTGCTCCTG TCCTTGCTCG 240  
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 GCGCCACACA CTGTCAATTG GAGCCCGAGC GCAGGATGTT GCTCAGGGTG GACTGCTCCG 360  
 ACCTGGGGCT CTGCGAGCTG CCTTCAACCC TCAGGCTCTT CACTCTCTAC CTAGACCTCA 420  
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 ACAGTCTACT CCATACCAAT AGATCTTATG CTGCAGAATA ATCAGCTAAG ACAGTACCC ACAGAAGCTC 600  
 TGCAGAAATT GCGAAGCCTT CAATCCCTGC GTCTGGATGC TAACCAATC AGCTATGTGC 660  
 CCGCAAGCTG TTTAGTGGC CTGCATTCCC TGAGGCACTT GTGGCTGGAT GACAATGGT 720  
 TAACAGAAAT CCGCGTCCAG GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG 780  
 CCTGGAACAA AATACACCA ATACCAAGCT ATGCTTTGG AAACCTCTCC AGCTTGGTAG 840  
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 CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCATTTTGGT CTGTCCTCTG CTGGCCTTGA 2280  
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5 GAGACCTGGA GAATATTGG GACTGCTCTA TGGTAAACA CATTGCCCTG TTGCTCTTCA 2520  
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 10 AATGTTTTCA AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000  
 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

15 **A131 Protein sequence**  
 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 20 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 MDTSLRLGVL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLENPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120  
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLSALQA MTLALNKKIH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLETLD 240  
 30 LNYNNLDEFF TAIRTLNLK ELGFHSNNIR SIPEKAFVGN PSLLTIHFYD NPIQFVGRSA 300  
 FOHLEPELRL TINGASQITE FPDLTGTANL ESLLTGAQI SSLPQTVCNQ LPNLQVLDLS 360  
 YNLLDLEPSF SVCQKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHPNAPST 420  
 LPSLKLKLDL SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480  
 AFGVCENAYK ISNQNNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLDDE EDLKAHLSVQ 540  
 CSPSPGPFKP CEHLDDGWL I RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 35 AVNMLTGVS AVLAGVDAFT FGSEFARHGA WENGVGCHVI GFLSIFASE SVFLLTLAAL 660  
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGE 720  
 STMGYMVALI LINSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFNCILNC 780  
 PVAFLSPSSL INLTIFISPEV IKFILLVVVP LPACLNPLLY ILFNPHEKED LVSLRKQTYV 840  
 40 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSITYDL PPSVSPSPAY PVTESCHLSS 900  
 VAFVPC

45 **A132 DNA SEQUENCE**  
 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Probeset Accession #: U25128  
 Nucleic Acid Accession #: NM\_005048  
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
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5 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040  
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# 15 A133 PROTEIN SEQUENCE

Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Protein Accession #: NP\_005039.1  
 Signal sequence: 1-25  
 Pfam domain: 7tm\_2 [141-420]  
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419  
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 MAGLGASLHV GWLMLGSSCL LARAQLDSGD TITIEEQIVL VLKAKVQCEL NITACLQEGE 60  
 GNCFPEWDL ICWPRGTGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120  
 NYSDCLRLFIQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180  
 30 MHLFVSFMLR ATSFIVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240  
 VMFIYFLATN YYWILVEGLY LHNLIFFVAF SDTKYLWGF I LGWGFPAAF VAAWAVARAT 300  
 LADARCEWLS AGDIKIWIQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360  
 LAKSTLVVLV VFGVHIYIVF CLPHSFTGLG WEIRMHCELF FNSFGGFVS IICYCNGEV 420  
 QAEVKKMWSR WNLSDVDKRT PFCGSRRCGS VLTVTTHSTS SQSQVAASR MVLISGKAAK 480  
 35 IASRQPDHSI TLPGYVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPMESNPDE 540  
 GCQGETEDVL

# 40 A134 DNA sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251.  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
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 50 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGGCT GGATCCGCGC CCAGCAGCAG 240  
 CCGCGGCGCG CGCCAGCTGG CAGAGCTCCC GGGAGTGGCG CTGGGGGCGC GCAGGACCTT 300  
 CGCTTGGCTC CTGGAAGTTC CCGGGGAGAG GTCCGGTTGC CAGTGAACCC TCCAGAGGCT 360  
 TCCGAGCAGC AGCCCGGGGG GCCTTCTGAC TGCAATCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 55 GCTCCTGGAC CTAGGGCCCG GCGTCTGCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540  
 CCGCGCGGAA AGCGCGCGCG GACAGTCACT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600  
 CTTCTCGGAG ACCGCTCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAGC GGTGGTGCCA 660  
 TGTGGGGGCG TCGCGCTCGC TCGCTCTCCT CATCTCGGAA CGCCGCTTCG CTCTGCGAGC 720  
 TGCTGCTGCG TGCGCTGCTG CCGCGCGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGGC 780  
 60 TGGCTGGAGC CGCAGGGGCT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCSAGCGC 840  
 GCGCAGCCCA CCATCTGCTG CCGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCGAG 900  
 GCGCGCCTGG ACCAGGGGGG CTGGGACAAAT GACCGCCAGC AGGGCGCTGG CGAGCGTGGC 960  
 CCGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGCGC AGGGTGGCGC CCACCGGTG AGGGCTGGC AGCGGTGCTC CCTGAAGGC 1080  
 65 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC 1140  
 CCGCGGATTC CATCTCTGCC ACGCGGCGGC CCTCTCCGCC TGCAGCGGCC CGCTTGGCCC 1200  
 ATCTACGTGC CGTCTCTCAT TGTGGCTCC GTGTTTGTGC CTTTATCAT CTTGGGGTCC 1260  
 CTGGTGGCAG CTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCA GCAGAGCCGA 1320  
 GCGCCAGGGG GTACCGCTT GATGGAGACC ATCCCATGA TCCCACTGC CAGCACTCC 1380  
 70 CCGGGGTGCT CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440  
 GGGGCGCGGG CGCCCCCAAC AAGGTACAGC ACCAACTGTT GCTTGCCTGA AGGGACCATG 1500  
 AACCAAGCTG ATGTCAACAT GCCCAAGAAAT TTCTCTGTGC TGAAGTGA CAAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG CAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620  
 CAGACTCTG TGCCCTGACC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680  
 75 AGGCAGATTG AGTCCCTCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTGAG GTGGAGTCC GCACATGTGC GTGGATTTA TGGCAGGATT CCTTTGGATG 1860  
 GCTTCATTG CCCCCAGACT GTATGAAAC ATCTCCGAAT TAGCAITTC GGATATGTTT 1920  
 CATCCAGGGT ATCATTGATT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 80 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATC TTGTTATTAT TATTTCTTTT 2100  
 TTGTTGTTGA CTGCAAGGTA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTCTT 2160  
 TTTTCTTTT TTTTCTTTAA TCAGACAGGG TCTTGTCTG TGGCCAGGC TGGAGTGCAG 2220  
 TGGTCCGATC TCGGCTCACT GCAACTCAG CCTCTGGAT TCAGGCAACA CTCTGCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGATTTTT 2340

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TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC 2460
TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
ATTCTAAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
GGCACACCTT AATTTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
GGGCCTAITT TGTCCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAAT CATCCCCTTC 2820
TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCTC 3000
GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCTTA GATCTGATAA 3060
AAAAATTTTC TTGCTTCTAGT TATAAAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTT 3180
GCAGATCAAT AGGCTTTTTA TACTCTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
GATTGTAAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCCAC ACTGTTCTTG 3300
ATTTCTCTC TCCTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCTAAATAT 3360
CAAATTTCAAG TGAATTTATT TTGTGTCTCT TTACTTATAT AAAAAAAGAT AACTTTAAG 3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT 3480
GTATGTATG GTCTCTTACA CATTATATG TATAGATATC TATCGATCAT CTTTCTATTC 3540
TGTTTCTATG CTGAATTAAT TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAAATA AAAAAAATA AAAAAAATA

```

**A135 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

35  
40  
45

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1 11 21 31 41 51
| | | | |
MLSGFLMSPS TOHRAOYTPG GKKLFWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
GEAEKGNRGE PPAWIRAQQQ PRPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPPEA 120
SGRQPRGPSD CIPRFPASASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAARESSG 180
PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVVP CGALAARPSP HPGTPLRSCS 240
CCWLKRRRG RGPSEYCHG WLDAQGVWRI GFQCPFERFDG GDATICCGSC ALRYCCSSAE 300
ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPPV RAWQRCSPG 360
SPKGRQLLRA FPGLLPRARR RGFPPSPRGG PSPLQRPALP IYVPELIVGS VFVAFIILGS 420
LVAACCCRCL RPKQDPQQR APGGNRLMET IPMIPSASTS RGSRRQSSST AASSSSSANS 480
GARAPPTRS TNCCLPBGTM NNYYNMPMTN FSVLNCQQAT QIVPHQGGYL HPPYVGYTVQ 540
HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMPAV TV

```

**A136 DNA SEQUENCE**

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55  
60  
65  
70  
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```

1 11 21 31 41 51
| | | | |
ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60
GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
CAGCAAAAGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
TCCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAAGT CAACAATGTG 240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAAT TGTGAACGTG 540
ACAGCCCTGG AATCCCTCTG GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAAACTTC 600
AGCTACAATT CTTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
ACCATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCTGT CAATGTGGTT 720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGA 780
AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840
GCCACAGACC TTCAGTGATC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
GCTGTGACAT GCAGGGCCGT CGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
CCTGTGAGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
TTGCAGGGAC CAGCCAGGT TGAATGCACC ACTCAAGGCG AGTGGACACA GCAAAATCCA 1080
GTTTGTGAAG CTTTCAAGT CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
CTTCTAGTGT CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
GGTTTGTGTT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
GTGAGGTGTG CTCATTCCTC TATTGGAGAA TTCACCTACA AGTCTCTTGT TGCCTTCAGC 1380
TGTGAGGAGG GATTGTGAAT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA 1440
TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGGA 1500
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTGT 1560
CCTGAAGGAT GGAGCTCAAA TGGCTCTGCA GCTGGGACAT GTGAGGCCAC AGGACACTGG 1620
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
CTTCTGCTGC CTGGACTCTC CCTCTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740

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TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800  
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5 A137 Protein sequence:  
Gene name: Selectin E (endothelial adhesion molecule 1)  
Unigene number: Hs.89546  
Probeset Accession #: M24736  
Protein Accession #: NP\_000441  
10 Signal sequence: 1-22  
Transmembrane domains: 555-573  
C-lectin domain: 23-139  
Cellular Localization: plasma membrane

15  
1 11 21 31 41 51  
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKKEIEYLN 60  
SILSYSPSYW WIGIRKVVNV WVVVGTQKPL TEEAKNWPAG EPNNRQKDED CVEIYIKREK 120  
20 DVGMMNDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180  
TALESPEHGS LVCSEPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240  
ECDAVTNPAN GFVECFQNPQ SPFWNTTCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300  
AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNPTCEEGFM LQGPQVVECT TQGWTOQIP 360  
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420  
25 EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAPS CEEGFELYGS TQLECTSQGQ 480  
WTEEVPSQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKAKKFVP ASSCQSLESD 600  
GSYQKPSYIL

30 A138 DNA SEQUENCE:  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
35 Nucleic Acid Accession #: AA487468  
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60  
CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGCTCAGAG TTTCTTCCAA CCTTGCCATT 120  
GCAATAAAAA AGSAAAAGAG GCCTCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
ACTTGGGTAC AAACATTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
45 ATGGTTATTC ATCACCTGGA GGATGTCAA TACTCTCAAG CACTAAGAA AGTATTGCC 300  
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
GAAACCACTG ATAAGAAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAAT CATGTTTGTA 420  
GACCTTCTT TAAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540  
50 GAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT 600  
GAAGAAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAAT 660  
TTACTATTTA GTTTTITTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTITTTAA 720  
TCTGAAAAA AAAAAAATAA AAAAAAATAA

55 A139 Protein sequence:  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
60 Protein Accession #: none found  
Signal sequence: 1-23  
Transmembrane domains: none found  
Cellular Localization: secreted

65 1 11 21 31 41 51  
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQYEE GLFYAQKSKK 60  
FLAVIHLEED QYSSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNS PDGQYVPRIM 120  
70 FVDPSTLVRA DIAGRYNRL YTYEPRDLPL LIENMKKALR LIQSEL

75 A140 DNA SEQUENCE  
Gene name: TMPRSS3a  
Unigene number: Hs.298241  
Probeset Accession #: AI538613  
Nucleic Acid Accession #: AB038157  
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
ACCGGGCACC GGACGGCTCG GGTACTTTG GGTCTTAATTA GGTATGCCCC GTGTGAGCCA 60  
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGTGGC CTACTATCTC TTCCGTGGTG 120  
CCATCTACAT TTTTGGGACT CGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
AGAGGTCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240

5 TCATTCGGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTGCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCAATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAAAATGT TGCCTGTGCC CAATCGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 10 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGGT TACCTTGCG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCAGCCCTCT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGAATTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 15 CTAGTTTCCC TGTGGGACAA TCCAGCCCA TCCACITGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTACAGTCCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGGAAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTGCC TGAACCAAGC GGCGTCCCT TTGATTTCCT ACAAGATCTG CAACCAAGG 1320  
 20 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGTACCT GACGGGTGGC 1380  
 GTGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCGTG TCACTCTCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTGT AGGTGATGAA GACAGCCCGA 1620  
 25 TCCTCCCTG GACTCCCGTG TAGSAACTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGGC CCGSAAAGAG CACCTTCCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800  
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 TTGCTCAGC TTCCCCGACA GCTGGGACCA CAGGTGCCCG CCACACACC CAACTAATTT 1920  
 30 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGTCTCT AAACCCCTGA 1980  
 CCTCAATGA TGTGCTGCT TCAGCTCTCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040  
 AGCCTAGCC TCACGCTCTT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTCT 2160  
 35 ACAGATAAG CAGTTATGTG ACCTCACGTG CAAGCCACC AACAGCCAT CAGAAAAAGC 2220  
 GCACCAGCCC AGAAGTGACG AACTGCAGTC ACTGCAGTT TTTCTCTCTA GGGACCCAGAA 2280  
 CCACACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTTGTAGC ATTGGTGTCT TGACGTATTA 2400  
 TTGTCTTTG ATTCCAATA ATATGTTTCC TTCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAA

40 A141 Protein sequence:  
 Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 45 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

50  
 1 11 21 31 41 51  
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFPF IIVIGIIALI 60  
 55 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLVQV 120  
 TAASWTKMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEQPFREERFV SIDHLLPDDK 180  
 VTALHSHSVV REGCASGRHV TLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240  
 LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGEDTGA GDASPLVSHA 360  
 60 AVPLISNKIC NHRDVGII SPSMLCAGYL TGGVDSQGD SGGPLVQER RLWKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

65 A142 DNA SEQUENCE  
 Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

70  
 1 11 21 31 41 51  
 CCAACAGAT TTGCAGATCA AGGAGAACC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60  
 75 CTGAGATCTT TGCATAGCT ACATCTCTAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120  
 CGGTGCTTCC TATTGCTGAG CTGCTGGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180  
 AGACCCAGCT GTGCTCTGG ATGTTTTTAC CACAAGTCCA ATTGCTATGG TTAATCTCAG 240  
 AAGCTGAGGA ACTGGTCTGA TGCAGAGCTC GAGTGTCACT CTTACGGAAG CAGGAGCCAC 300  
 CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360  
 80 CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA CAGTGGCAG 420  
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480  
 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540  
 AACCAAGGCC AACACTTCTC GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600  
 AACTCTCTCA CCAGCCCGCT CCTCTTCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660  
 TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAGGGGCC CTACTACACT GGCTTTTTTA 720



GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780  
 CCCC GCCATC CCTTTCACCA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA 840  
 GCAGCTTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900  
 AAAGATTGA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960  
 ACACCCCTCT GCCTCTCTCT CATGCTCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020  
 TTTTCTCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080  
 TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

**A143 Protein sequence:**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

1 11 21 31 41 51  
 MASRSMRLLL LLSCLAKTV LGDIIMRPSG APGWYFHKSN CYGYFRKLNN WSDAELEQCS 60  
 YNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120  
 KSMGGNKHCA EMSNNNFLT WSSNECNKRO HFLCKYRP

**A144 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51  
 GGGGAACACC GGGCCGCCGT CGCGGCAGCT GCTTCAACCC TCTCTCTGCA GCCATGGGGC 60  
 TCCCTCGTGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGGCGCG 120  
 CCTCGAGACC GTGCCCGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGAGGCGG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCGATCCAAA CGTATCTTAC 360  
 GAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCGTGAATAA GGCAGGGGTC 420  
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGGGCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540  
 AGACAGGCTG GTTGTGTGTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660  
 TCATGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGGA 720  
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840  
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900  
 CAGTGGGCTT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020  
 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCCTGAG AATGCACTGG 1080  
 GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCACATCA CCAGGTGGC 1140  
 GTGCCACCTA CCTTATCATG GGGGCTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200  
 CTGAGACCTA CGCTGCTATC CTGACAAACA GGAAGGGTTT GGATTTGAG GCCAAAAACC 1260  
 AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCGCAACCT 1320  
 CCACAGCCAC CATAGTGGTC CAGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC 1380  
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GGAGCCTGTG TGTGTCTACA 1440  
 CTGCAGAGA CCTTGACAAG GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500  
 CAGGTTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGAAC 1560  
 GTGAGGATGA CGAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCACCACTT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAAAG 1680  
 ACCATGGCCC AGTCCCTGAG CCCGCTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740  
 ACGTGTCTGA CATCAGGAC AAGGACCTGT CTCCTCCACAC CTCCTCTTC CAGGCCACG 1800  
 TCACAGATGA CTACAGATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTCT CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAGAGCAG CTGACCGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGGAAGC CTGCCCTGGA CCTGGAAGG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGAGGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGCTTCT TACTATGGCG 2160  
 AAGAGGGGGG TGGGGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AATCGGCAA CTTTATATTT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTGACTATG 2400  
 AGGCGAGCGG CTCGAGAGCC GGTCCCTTGA GCTCCCTCAC CTCCTCCGCC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AOCAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGTGGCGG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AAGTCAGGC 2580  
 CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTCA 2640  
 GGAAGTGGCC GTAGCAACTT GGGCGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCCT TCTCAGGATG AGGAATGTGG GCAGTTTGA TTCAGCACTG AAAACCTGCT 2760  
 CACCTGGGCC AGGGTTGCTT CAGAGGCCAA GTTTCAGGAA GCCTCTTACC TGCCGTAATA 2820  
 TGCTCAACCC TGTGTCTCTG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940

TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG 3000  
 TCCTGCATT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTG TGCCTAGGTT GCCCCTATT TTTATTTTC CCGTTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTT TATTAAGAA A

#### A145 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 MGLPRGPLAS LLLQLVCWLQ CAASEPCRAV PREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDWV VAPISVPENG 120  
 KGFPFQRLNQ LKSNKDRDRTK IFYSITGPGA DSPPEGVFAV EKETGWLILLN KPLDREELAK 180  
 YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSGST TAVAVVEILD ANDNAPMFDP QXEAHVPEIN AVGHEVQRLT VTDLADPNPSP 360  
 AWRATYILIMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVE VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMPD DSGQVTAAGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLLID 540  
 VNDHGFPVEP RQITICNQSP VRHVLNITDK DLSPTSFPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFLF LVLALLVRKK RKIKEPLLLP EDDTRDNVVF YGEEGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

#### A146 DNA SEQUENCE:

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Nucleic Acid Accession #: NM\_003318  
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGAATTCCTT TTTTITTTTT TTTGAGATGG AGTTTCACCT TGTTTGCCCA GGCTGGAGTG 60  
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCTCCCGG GGTTCAGCGG ATTCTCCTGC 120  
 CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180  
 CTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240  
 AACTCAGGTG CAGCTCTGCG CTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAACCTG 300  
 TGCTGGCTG ATTCTTTTTT TGTGTGTGGA TTTTGAAC AGGCTCTCCC TTGGTGGCCC 360  
 AGGCTGGAGT GCAGTGGTGC GATCTGGCT CACTATAACC TCCACCTCCT GGTTCCAAGT 420  
 GATCTCCCA CTCTAGCTCT CTGAGTAGCT GTGATTACAG CGGTGCACCA CCACACCCGG 480  
 CTAATTTTTG TATTTTTATT AGAGACAGGG TTTCAACATG TTGGCCAGGC TGTCTCTCAA 540  
 CTCTGGACT CAGGGGATCC GCCTGCCTCC ACTTCCCAA GTCCCGAGAT TACAGGTGTG 600  
 AGTCACCATG CCTGACCTTA TAATCTTAA GTCATTTTTT CTGGTCCATT TCTTCCTTAG 660  
 GGTCTCTACA ACAATCTGCG ATTAGCGGT ACAATAATCC TTAACCTCAT GATTACAAA 720  
 AGGAAGATGA AGTGATTTCAT GATTTAGAAA GGGGAAGTAG TAAGCCCAT GCACACTCCT 780  
 GGATGATGAT CCTAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAA 840  
 TTTGGTTTAA ATTAATTATC TAAATATCTA AAACATTTT TGGATACATT GTTGATGTGA 900  
 ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCGCCAG 960  
 TGCAGTTTTT TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT 1020  
 CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080  
 AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAAC GTTAACCCAA 1140  
 TTATGATGAT GGCACCAAC CCAGAGGACT GGTGAGTTT GTTGCTCAA CTAGAGAAAA 1200  
 ACAGTGTTC GCTAAGTAT GCTCTTTTAA ATAAATGAT TGGTCTGTAC AGTCAAGCAA 1260  
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGTAGA ATTCAAGTGA 1320  
 GATTGTGCTA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG 1380  
 CCAAGAGCAA CTGCAAGAAA TTTGCTTTT TGCATATATC TTTTGCACAA TTTGAACCTG 1440  
 CACAAGGTAA TGTCAAAAA AGTAACAAC TTTCTCAAAA AGCTGTAGAA CGTGGAGCAG 1500  
 TACCACTAGA AATGCTGGA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560  
 TTTCAAGAGA GGAAGAAGAA AATTATACAG CATCTACGGT ATTAAGTGC CAAGAATCAT 1620  
 TTTCCGGTTC ACTTGGGCAT TTACAGAATA GGAACAACAG TGTGATTC AGAGGACAGA 1680  
 CTACTAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740  
 ACCGGAATTC ATGAGACAAA ACTAACAAAA CTAACAGTC ATGCCCATTT GGAAGAGTCC 1800  
 CAGTTAACTT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGTACCTT 1860  
 GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGTTGTG CTTGATCTA 1920  
 AACCAAGTGG AATGATTTC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980  
 TCAAGGAACC TCTGGTGTCA GATGAAAGA GTTCTGAAC TATTATTACT GATTCAATAA 2040  
 CCTGAAGAA TAAACCGGAA TCAAGTCTTC TAGCTAAATT AGAAGAACT AAAGAGTATC 2100  
 AAGAACCAGA GGTCCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160  
 GTATTAAACA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCGGAG TTAGCCCGAA 2220  
 AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC 2280  
 AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGT AAGACACCAA 2340

GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT 2400  
 TTCCACCTGC TTGTGAGTTG TCAACACCTT ATGGCCCAACC TGCCTGTTC CAGCAGCAAC 2460  
 AGCATCAAT ACTTGCCACT CCACCTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520  
 5 ATGAATGCAT TTCGGTTAAA GGAAGAATTT ATTCATATT AAAGCAGATA GGAAGTGGAG 2580  
 GTTCAAGCAA GGTATTTTTC GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640  
 TGAACCTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700  
 TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG 2760  
 ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2820  
 10 AGAAAAATC CATTGATCCA TGGGAACGCA AGAGTACTG GAAAAATATG TTAGAGGCAG 2880  
 TTCACACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCACT AACTTTCTGA 2940  
 TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAATG CAACAGATA 3000  
 CAACAAGTGT TGTAAAGAT TCTCAGGTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060  
 TCAAGATAT GTCTTCTCC AGAGAGAATG GGAAATCTAA GTCAAGATA AGCCCCAAA 3120  
 15 GTGATGTTG GTCTTAGGA TGTATTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180  
 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG 3240  
 AATTTCCGA TATTCCAGAG AAGATCTTC AAGATGTGT AAAGTGTGT TTAAGAAAGG 3300  
 ACCCAAAACA GAGGATATCC ATTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360  
 CTCATCCAGT TAACCAATG GCCAAGGGA CCACTGAAGA AATGAAATAT GTTCTGGGCC 3420  
 20 AACTTGTTG TCTGAATCT CTAACCTCCA TTTTGAAGC TGCTAAACT TTATATGAAC 3480  
 ACTATAGTGG TGGTGAAAGT CATAATCTT CATCTCCAA GACTTTTGA AAAAAAGGG 3540  
 GAAAAAATG AATTGCAATG ATTCTAATG TCAGATAGGA GGTATAAAT ATATTGGACT 3600  
 GTTATCTCT TGAATCCCTG TGAATCTA CATTTGAAGA CAACATCACT CTGAAGTGT 3660  
 ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3720  
 25 TTATGGCACT GTATATATTG TAGACTTGT TTCTCTGTTT TATGCTCTTG TGAATCTAC 3780  
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATCTA AAAAATCTTG 3840  
 TAAATAAAGT TTTGTGCTA AATGA

**A147 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51  
 MNKVRDIKNK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPDWL SLLKLEKNS 60  
 VPLSDALLNK LIGRYQAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120  
 ANCKKFAFVH ISFAQFELS GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLS 180  
 45 EEEKNLNSAS TVLTAQESFS GSLGHLQNRN NSCDSRQOTT KARFLYGENM PPQDAEIGYR 240  
 NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPVSGSKP 300  
 SGNDSCELRN LKSVNLSHFH EPLVSDKSS ELIITDSITL KNKTESSLLA KLEBTKKEYQE 360  
 PEVPESNQKQ WQAKRKSECI NQNPAAASNNH WQIPELARKV NTEQKHTTFF QPVFVSQKQS 420  
 PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFF PACQLSTPYG QPACFQQQQH 480  
 50 QILATPLQNL QVLASSANE CISVKGRISY ILKQIGSGGS SKVFQVINEK KQIYAIKYVN 540  
 LEEADNQTLQ SYRNEIAYLN KLQHQHSDKII RLYDYEITDQ YIYMVMECGN IDLNSWLKKK 600  
 KSIDFWERKS YWKNMLEAVH TIHQHGIHVS DLKPANFLIV DGMLKLIDFG IANQMOPDPT 660  
 SVVDSQVGT VNYMPEPAIK DMSSSRENGK SKSKIIPKSD VWSLGCILYI MTYGTPTFPQ 720  
 IINQISKLHA IIDPNHEIEF PDIEPKDLQD VLKCKLKRDP KORISIPELL AHPYVQIQTH 780  
 55 FVNQMAKGT EEMKYVLQQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK 840  
 K

**A148 DNA SEQUENCE**

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTCTTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTCTGA TGAATGGACA 120  
 70 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCTGTGT TATTTTITTT 180  
 TCTAATTTCT TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240  
 TACCTGTTGG CTAATTTAGC TGCTGCGGAT TTCTTCTGCT GAATTCGCTA TGTATTCTCTG 300  
 ATGTTTAAAC CAGGCCCACT TTCAAAAAC TTGACTGTCA ACCGCTGGTT TCTCCGTCAG 360  
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGTTTAT CGCCGTGGAG 420  
 75 AGGCACATGT CAATCATGAG GATGCGGTC CATAGCAACC TGACCAAAA GAGGGTGACA 480  
 CTGCTCATTT TGCTTGTCTG GGCATCGGCC ATTTTATAGG GGGCGGTCCC CACTGCGGC 540  
 TGAATTGCC CTCTGCAACAT CTCTGCTGCT TCTTCCCTGG CCCCATTITA CAGCAGGAGT 600  
 TACCTGTTT TCTGGACAGT GTCCAACTCT ATGGCCCTTC TCATCATGGT TGTGGGTAC 660  
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGCTCCGCA TACAAGTGGG 720  
 80 TCCATCAGCC GCCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780  
 GCGTTTGTGG TATGCTGGAC CCGGCGCTCG GTGGTCTGCT TCCTCGACGG CTTGAACCTGC 840  
 AGGCAGTGT GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900  
 GTCGTGAACC CCATCATCTA CTCTCAACAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960  
 ATGATCTGCT GCTTCTCTCA GGAGAACCAC GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020  
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAACTCTG GATGCCTCTC GGGCCACCCA GGTGATGACT 1140  
GTCTTAGG

5 A149 Protein sequence:  
Gene name: endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor, 7  
Unigene number: Hs.258583  
Probeset Accession #: NM\_012152  
Protein Accession #: NP\_036284  
10 Signal sequence: none found  
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
Cellular Localization: plasma membrane

15 1 11 21 31 41 51  
MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFF CLFIFPNSNL VIAAVIKNRK 60  
FHEFPFYLLA NLAAADFFPAG IAYVPLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120  
LVIAVERHMS IMRMVRHNSL TKKRVTLLIL LVWAIAlFMS AVPTLGNCL CNISACSSLA 180  
20 PIYSRSYLVF WTVSNLMAFL IMVVYLRIY VYVKKRTNVL SPHTSGSISR RRTPMKLMKT 240  
VMTVLGAFVW CWTPLGLVLL LDGLNCRQCG VQHVKNRFL LALLNSVNP IYYSYKDEDM 300  
YGTMKMKICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

## 25 Prostate

A150 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.293616  
30 Probeset Accession #: AW043782  
Nucleic Acid Accession #: none found  
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51  
AGCAACGAGC CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GCGCGCTGTG 60  
CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120  
GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180  
40 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
GTGAAATGT GGGCAACCT TCTTCCCTTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG 300  
CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
AAACCCCTCG CTTTGCTCCA CGGCCGCTCA CCACTGCAAG AACGGCCTCT GTATTGACAA 420  
GAGCTTCATC TGCATGGAG AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
45 AAGTTCTCAA GAACCCGGCA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
TTACCCGAGC ATCACCCTAT CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
CTGCTGGCA CTGCTCTTGC ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCGCT 660  
GCACCGGCTG CAGCACCTCG TGCTGCTGTC CCGCTCGGTG GTCTCGGACC ACCCCACCA 720  
CTGCAACGTC ACCTACAAAG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
50 GAATGCGTCG GAAGTAGGCT CCCCACCTCT CTACTCCGAG GCCTTCTGGT ACCAGAGGCC 840  
TGCTGTGATG GACCTTCCCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
CGACCTGCCC CCTTACCGCT CCGGTTCGGG GAGTGCCAAAC AGTGCCAGCT CCCAGGCAGC 960  
CAGCAGGCTC CTGAGCGTGG AAGACACAGC CCACAGCCCG GGGCAGCCTG GCCCCAGGGA 1020  
GGGCAACGTC GAGCCGAGGG ACTCTGAGCC CAGCCAGGSC ACTGAAGAAG TATAAGTCCC 1080  
55 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140  
TGCTCATGGG AAGCTCTTTA AGCAGCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
AACTATCTCT CATTGCCCTT CCTCCCCAG ACTTCAGAGA TGTTTTCTCG GGTCTCTCAGT 1260  
TGACATGATC TGTGTGCGT CTTTTCTGTC AGGTCACTCT TCCCTTGGGA CCGGAGATCA 1320  
CACCTCATCT TTTACATTA TTCTGTTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380  
60 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGAGGAGA 1440  
CGCTGGAGCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTGGGGA TTTGGGTTAG 1500  
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCAACCCCC CAAAAAATT CCAATTGAGC 1560  
ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAGC TTCAGCAGAG TCAGTGGCCA 1620  
AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTCCG AACGTTATTT TGGTTTGTG 1680  
65 AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTGG CCAAGAAGTG 1740  
CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG 1800  
GAGCCCTCC CTAGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920  
ACCTGCCGTG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980  
70 GTATGTCCCT GTGGCCACA CCCAGCCTGT CTTGCTCATC CATGCAGCCT CAACACTGGC 2040  
CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTTAACT GTGCATTGGG ACTTGAGGAC 2100  
ACTGTCTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
GGTCAGGCTC AGGCTCTTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
75 AGACAATTGG GAGTCAAGAT TTTCCATTGG GATCTATTTT AAATCTTTTA GAAATGCATT 2340  
TGAAACAGTG TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400  
AGCTGTCTCT TTTTGTGTTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460  
ACACCTTGGC CCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520  
ACATTGTGTC ATTTGTGAC TTTGAGTTA TTAATTATCA AGTTCTTGA GGAAGCAGAA 2580  
80 AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640  
TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAACGTT 2700  
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGTGAA CAGGTAGAG 2760  
CCACTCCGGG CAGCTGTAC CCATTGAGAA CTCTTCTCG CAGCTGAAGA AATGTTCACT 2820

AACCTGTTTG ACGCTAATTA AACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTGAG 2880  
 TGATCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTACAGAA 2940  
 AAGCTAGCCA CTGGTATTTT GTTTGTGTTA AAAAAAAGA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTTRA AATAGCACTT GAGTATTTT 3060  
 5 CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTTCATCT CTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180  
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTGTAGT 3300  
 10 AGATAAGGGA TGCTACTATA TGCTTTTITA AACAAACAG GCACATTTT ATTATAGATT 3360  
 TGATTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAAACCAG 3540  
 AATAAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTA GCATTAAATT 3600  
 15 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTTACCTT GAAATTGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTGT GTGTCGTTGC TTTTGTGTT GTGGTTAGGC TTGGTTTGT TTTTAAATT 3780  
 TTATACTTTC TAATAAATT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840  
 AAMMAAAAC ANYWTTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAAC CCACTTGGGG 3900  
 20 TGGGGCGGG GGGCCACGT AGGTACGGCG ACCACGCGG CCACAAACGG ACCCCAGAAG 3960  
 GAAACCTCG CCAAGAAAAA GSTGGCGAGA ATTCCTCACA CCAGAAAAA ACGCGCGGG 4020  
 GGAACCGCA GAGTGTGCG TAAACACAC CGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGCC AAGGAACCC GATAGAGTAC G

25 A151 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 30 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60  
 40 EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSP ICDGQNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHQRKR NMLMLPVHR LQHPVLLSRL VVLDHPHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPWA YDLPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASQAASS LLSVEDTSHS PQQPGQEGT AEPRDSEPSQ GTZEV

45 A152 DNA SEQUENCE  
 Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 50 Probeset Accession #: T48536  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 GTCATATTGA ACATTCACGA TACCTATCAT TACTCGATGC TGGTTGATAAC AGCAAGATGG 60  
 CTTTGAACCT AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAGAACCT GGATACCAAC 120  
 CGGAAACACC CTATCCCGCA CAGCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180  
 CTCAGTACTA CCGTCCCCC GTGCCCCAGT ACGCCCGAG GGTCTGACG CAGGCTTCCA 240  
 ACCCGTCTGT CTGCACGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAGACTA 300  
 60 AGAAAGCACT GTGCATCACC TTGACCCCTG GACCTTCCTT CSTGGGAGCT GCGCTGGCCG 360  
 CTGGCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCGACT 420  
 CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480  
 GGGAGGACGA GAATCGGTGT GTTCGCCCTT ACGGACCAAA CTTCATCCTT CAGATGTACT 540  
 CATCTCAGAG GAAGTCTCG CACCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 65 GGGCGGCTGT CAGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG 660  
 ATGACAGCGG ATCCACCAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720  
 ATAAAAAAT GTACCAAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780  
 TAGCTCGCG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840  
 CGCTCCCGG GGCCTGGCCC TGGCAGGTCA GCCTGCAAGT CCAGAAGCTC CACGTGTGCG 900  
 70 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCGC CCACTGCGTG GAAAAACCTC 960  
 TTAACAAATC ATGGCAATTG ACGGCATTG CGGGGATTTT GAGACAACTT TTCAATGTTCT 1020  
 ATGAGACCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAGACCA 1080  
 AGAACAAATG CATTGCGCTG ATGAAGCTGC AGAAGCTCTT GACTTTCAAC GACCTAGTGA 1140  
 AACCAGTGT TCTGCCCAAC CCAGGCATGA TGCTGCAGCG AGAACAGCTC TGCTGGATT 1200  
 75 CCGGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGCTGAAC GCTGCCAAGG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAC CTGATCACAC 1320  
 CAGCCATGAT CTGTGCGCGG TTCCTGCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGT 1380  
 GAGGCGCTCT GGTCACTTCG AACACAAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440  
 80 GTTCTGCGG GGCCTGCGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTACAGG 1500  
 ACTGGATTGA TCGACAAATG AAGGCAACG GCTAATCCAC ATGGTCTTCG TCCTTGACGT 1560  
 CGTTTACAGA GAAACAAATG GGGCTGGTTT TGCTTCCCG TGCAATGATT ACTCTTAGAG 1620  
 ATGATTACGA GGTCACTTCA TTTTATTAAC ACAGTGAAC TGCTTGGCTT TGGCACTCTC 1680  
 TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCAGGCC TGCTCTCCTT AACCCCTTGT 1740

CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800  
 GTTGGAGGCT GCCCCCATTT AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGGG 1860  
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920  
 GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGTGGTAGT 1980  
 TCCCCAGCCT ACTTCACAAG GGGATTITTC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040  
 GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCATGGGTG GTGACGTGGT AGTCACCTGT 2100  
 AAGGGGAACA GAAACATTTT TGTCTTATG GGGTGAAGAT ATAGACAGTG CCCTTGGTGC 2160  
 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGAGGTG TCCACCTGCA 2220  
 CATTGGGTGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCTCTC CTGACCTGTC 2280  
 TCCTAGCACC CTGGAGAGTG AATGCCCTTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340  
 ATGTGGGCTT CTTGAGGCTT GATAGTCATT GGAATTTAG GTCCATGGGG GAAATCAAGG 2400  
 ATGCTCAGTT TAAGGTACAC TGTTCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460  
 CTGAGTTCAA AGCCATCTT

**A153 Protein sequence:**

Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 Probeset Accession #: T48536  
 Protein Accession #: NP\_005647.1  
 Signal sequence: none found  
 Transmembrane domains: 85-107  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60  
 SNPVVCTQPK SPSTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120  
 DSSGTCTNPS NWCDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VCQDDWNENY 180  
 GRAACRDMGY KNNFYSSQGI VDDSGSTFSM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240  
 CLACGVNLS SRQSRIVGGE SALPGANPWQ VSLHVQNVHV CGGSIITPEW IVTAAHCEVK 300  
 PLNNPWHWTA FAGILRQSFM FYGAGYQVQK VLSHPNYDSK TKNDIALMK LQKPLTFNDL 360  
 VKPVCLFNP MMLQPEQLCW ISGNATPEEK GRTSEVLNAA KVLLETQRC NSRYVYDNL 420  
 TPAMICAGFL QGNVDSQCGD SGGPLVTSNN NIWWLIGDTS WSGGCAKAYR PGVYGNVMVF 480  
 TDWIYRQMK NG

**A154 DNA SEQUENCE**

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039

Unigene number: Hs.129179  
 Probeset Accession #: AI694767  
 Nucleic Acid Accession #: AI694767  
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CAGAGAGGCT GTATTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60  
 GGGGTCACAC ATTCTCTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCACAGTTC 120  
 AGCTTCTTCA TGATGGTGA TCCCAATGGC AATGAATCCA GTGCTACATA CTTTCATCTA 180  
 ATAGGCTTCC CTGGTTTAGA AGAGGCTCAG TTCTGTGTGG CCTTCCCATT GTGCTCCCTC 240  
 TACCTTATG CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGGGAC TGAGCACAGC 300  
 CTGCATGAGC CCATGTATAT ATTCTTTGCG ATGCTTTGAG GCATTGACAT CCTCATCTCC 360  
 ACCTCATCCA TGCCCAAAAT GCTGGCCATC TTCGTGTTCA ATTCCACTAC CATCCAGTIT 420  
 GATGCTGTGC TGCTACAGAT GTTGGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480  
 CTGCTGGCCA TGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGGG CCATGCCACA 540  
 GTACTTATG TCGCTCGTGT CACCAAAATT GGTGTGGCTG CTGTGGTGGG GGGGGCTGCA 600  
 CTGATGGCAC CCTTCTCTGT CTTTCATCAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660  
 TCCCATTCCT ACTGCTTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720  
 AATGTGCTCT ATGGCTTAT CGTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780  
 TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTGTGGGT TGACACGTGA AGCCAGGGCC 840  
 AAGGCATTG GCACCTTGGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900  
 ATTGGATTGT CCATGGTGCA TCGCTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCATC 960  
 TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020  
 ACAAGGAGA TTCGACAGCG CATCCTTCGA CTTTTCATG TGGCCACACA CGCTTCAGAG 1080  
 CCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTGAGAT CCTCTGATTC AGATTTTAAT 1140  
 GTTAACATTT TGAAGACAG TATTCAGAAA AAAAATTTCC TTAATAAAAA TACAACCTAG 1200  
 ATCCTTCAA TATGAACTG GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTCTT 1260  
 GTTTCTTGC ACCATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320  
 TTTTCATTTT TACATGAGT CCAATCTAA ACTGCTTCTA CTGATGGTTT ACAGCATTCT 1380  
 GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA 1440  
 TAAACACAGA ATATAATAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500  
 ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560  
 AAATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620  
 AGAGTACATT TACCTAGGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680  
 ATGGACCCCT TTTTCTCTAT TTAATTTTCT TATCAACCCCT TTAATTAGGC AAAGATATTA 1740  
 TTAGTACCCT CATTGTAGCG ATGGGAAAAAT TGATGTTTCA TGGGGATCAG TGAATTAAT 1800  
 GGGGTATAC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860  
 GGAAGAACTG TTAAGAGAG CAACAGGGTA GTGGGTAGA GATTTCAGA GTCTTACATT 1920  
 TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGTATTAG GAATTTCTCG 1980  
 GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGTCTGG TCCAATTGCC 2040  
 AATTACCTGT GCTCTGGAAG AAGTGATTTT TAGGTTCAAC ATTATGGAAG ATTCTTATTC 2100  
 AGAAAGCTG CATAGGCTT ATAGCAAGTT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160  
 TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGA TGGCAGGTGT 2220  
 TGAAGATAAC ATTGGCTCTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGG AATCTTCAGG 2280

ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGGACACGGG ACTTTGAGAC CGGGAAGCA 2340  
 ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400  
 ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAACTC AAATTACATA 2460  
 TACTAAAACA TGTGATCATA TATGTGGTAA GTTTCATTTT CTTTTCATAT CCTCAGGTTC 2520  
 CCTGATATGG ATTCCTATNA CATGCTTTCA TCCCCTTTTG TAATGGATAT CATATTTGGA 2580  
 AATGCCTATT TAATACTTGT ATTTGCTGCT GGACTGTAG CCCATGAGGG CACTGTTTAT 2640  
 TATTGAATGT CATCTCTGTT CATCATTGAC TGCTCTTTGC TCATCATTTGA ATCCCCCAGC 2700  
 AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACGGG TTATTTTTC TCAAACTGA 2760  
 TTCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTTCCTTTGAG TTGGGTATTA 2820  
 TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAGGTGAC ATGTGCAATT TTTATACCTG 2880  
 GCTCATAAAA CCTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTTGGGAAGC 2940  
 TATGTGTTAC ACAGAGTTAA TTAACCNAA AGGCCTGGNA ATTTTGTGN AANNAACTG 3000  
 TGGCCNAGAG GCCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCCCTTT GTANTTTGGT 3060  
 AAGGAGGCCA GTTGGATAAG TGAAAAATAA AGTACTATTG TGTC

**A155 PROTEIN SEQUENCE**

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039  
 Unigene number: Hs.129179  
 Protein Accession #: not available  
 Signal sequence: none found  
 Pfam domain: 7tm\_1 [43-293]  
 Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MVDPNNGESS ATYFILIGLP GLEEAQFWLA FPLCSLYLIA VLGNLTIIYI VRTEHSLHEP 60  
 MYIFLMLSG IDILISTSSM PKMLAIFWFN STTIQFDACL LQMPAIHSLS GMESTVLLAM 120  
 AFDYVAICH PLRHATVLT PLRTKIGVAA VVRGAALMAP LPVFIKQLPF CRSNLSHSY 180  
 CLHQDVMKLA CDDIRNVVY GLIVIIISAIG LDSLLISFSY LLILKTVLGL TREAAKAFG 240  
 TCVSHVCAVF IFYVPPFGLS MVHRFSKRDR SPLPVILANI YLLVPPVLNP IVYGVKTKEI 300  
 RQRILRLPHV ATHASEP

**A156 DNA SEQUENCE**

Gene name: vasoactive intestinal peptide receptor 1  
 Unigene number: Hs.198726  
 Probeset Accession #: X77777  
 Nucleic Acid Accession #: NM\_004624.1  
 Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

TCGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCCGCC TCACTCATGC 60  
 CTCTCTCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGTTGGCGG GTTAGCGGG 120  
 TGGTGGTGGC GGGGGCGGG GCTCGCTCTC GGGGAGCGCG GGGCGGATCT CGCGGCGCAG 180  
 GCGGCGGCGG CGGAGGTGGG GTGCGCGCGC GGAGGCGGCT CGAGCTTCGT GCTGCGGCGT 240  
 CGCTCTTGGG CTCTCTCGTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCGAGC 300  
 ACAAGCAGTG CCTGGAGGAG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360  
 GGGACAACCT CACCTGCTGG CCAGCCACCC CTCGGGGCCA GGTAGTTGTC TTGGCCTGTC 420  
 CCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCCGCAA TGTAAAGCCG AGCTGCACCG 480  
 ACGAAGCCTG GACGCACCTG GAGCCTGGCC CGTACCCCAT TGCTGTGGT TTGGATGACA 540  
 AGGCAGCGAG TTTGGATGAG CAGCAGACCA TGTCTACGG TTCTGTGAAG ACGGCTACA 600  
 CCATTGGCTA CGGCTGTGCC CTGGCCACCC TTCTGGTGGC CACAGCTATC CTGAGCCTGT 660  
 TCAGGAAGCT CCATGTCACG CGGAAGTACA TCCATGATCA CCTCTTCATA TCCTTCATCC 720  
 TGAGGGCTCG CGCTGTCTTC ATCAAAGACT TGGCCCTCTT CGACAGCGGG GAGTGGGACC 780  
 AGTGTCCGA GGGCTGGGTG GGCTGTAAAG CAGCCATGGT CTTTTCCTAA TATTGTGTCA 840  
 TGGCTAACTT CTCTGGCTGG CTGGTGGAGG GCCTCTACCT GTACACCTCG CTGCGGCTCT 900  
 CCTCTTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960  
 GCACATTCAC CATGGTGTGG ACCATCGCCA GGATCCATTT TGAGGATTAT GGTCTGTCTA 1020  
 GGTGTGGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCCTCACTT 1080  
 CCATCTTGGT AAACCTCATC CTGTTTATTT GCATCATCGC AATCCTGCTT CAGAAACTGC 1140  
 GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACCT AAGGCTAGCC AGGTCCACAC 1200  
 TCCTGCTGAT CCCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CGGACAATT 1260  
 TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TGCTGCTGGG GTCTTTCAGG GGTTTTGTGG 1320  
 TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380  
 GGCCTGGCA CCTGCGGGG GTCTGCTGGT GGAACCCCAA ATACCGGCAC CGGTGGGAG 1440  
 GCAGCAACGG CGCCACGTGC AGCACGACG TTTCCATGCT GACCCGCGTC AGCCAGGTG 1500  
 CCGCGCGCTC CTCACGCTTC CAAGCGAAG TCTCCCTGGT CTGACCACCA GATCCGAGC 1560  
 CCAAGCGGCC CCTCCGCCCC CTTCCTCACTC GCAGCAGAGC CGGGGAGAG AGGCTGCCCC 1620  
 GGGCGCGCCA CGCCCGGGCC TGGGCTGGGA GGCTGCCCCC GGGCCCTGGG TCTCTGGTCC 1680  
 GGACACTCCT AGAGAAAGCA GGCCTAGAGC CTGCTGGAGG CGTTCTAGC AAGTGAAGAG 1740  
 GATGGGAGCT CCTCTCTGG AGGATGCAGG TGGAACTCAG TCATTAGACT CCTCTCCAA 1800  
 AGGCCCCCTA CGCCAATCAA GGGCAAAAG TCTACATACT TTCATCTGA CTCTGCCCC 1860  
 TGCTGGCTCT TCTGCCAAT TGGAGGAAG CAACCGGTGG ATCCTCAAA AACACTGGTG 1920  
 TGACTGAGG GCAGAAAGGT TCTGCCCGGG AAGGTCAACA GCACCAACAC CAGGTAGTG 1980  
 CCTGAAATTT CACCATGCT GTCAAGTTC TTTGGTTAA GCATTACCAC TCAGGCATT 2040  
 GACTGAAGAT GCAGCTCACT ACCTATTCT CTCTTAACG TTAGTTATCA GCTTTTAA 2100  
 GTGGGTATT TGGAGTTT TGTTTGAGA GCACACCTAT CTTAGTGGT CCCCACGAA 2160  
 GTGAGCTGC CCTCGGTGA GTCTGGTGG AGGACGCTGC AACCCAAGGA CTGAGGAGT 2220  
 CTGAAGCTC TGGGAAATGA GAAGGCAGCC ACCAGCAAT GCTAGGTCTC GGACTAAGCC 2280  
 TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGT GGACTCTGTC ACACAGCCA 2340  
 TTCTTATCT TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTTGTCCACC 2400  
 CACCTATGTG CCAACTGTTG TAACTAGGCT CAGAGATGTG CACCATGGG CTCTGACAGA 2460

5  
AAGCAGATCC TCACCTGCT ACACATACAG GATTGAACT CAGATCTGTC TGATAGGAAT 2520  
GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACGAGCCAG ATCCTCTTGG 2580  
TTATTTGTTT ACCACTTGTA TTATTAATGC CATTATCCCT GAATTCCTCT TGCCACCCCA 2640  
CCCTCCCTGG AGTGTGGCTG AGGAGGCCTC CATCTCATGT ATCATCTGGA TAGGAGCCTG 2700  
CTGGTCACAG CCTCTCTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760  
CCTCTGCCAG AAGATCCCCT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820  
GGAAAAAAA AAAA

10 A157 Protein sequence:  
Gene name: vasoactive intestinal peptide receptor 1  
Unigene number: Hs.198726  
Probeset Accession #: X77777  
Protein Accession #: JC2195  
Signal sequence: none found  
15 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430  
Cellular Localization: plasma membrane

20  
1 11 21 31 41 51  
MPPFPLLSLR RLGGWSAVT RLVVAAAGAR SRGGRGGRG AGGGGRGGVA RRRRLRLRAA 60  
RSLGSSSLQE ECDYVMIEV QHKQCLEEAQ LENETIGCSK MWDNLTCWPA TPRGQVVVLA 120  
CPLIPKLFSS IQGRNVRSC TDEGWHLEP GPYPACGLD DKAAASLDEQ TMFYGSVKTG 180  
25 YTIYGLSLA TLLVATAILS LFRKLHCTRN YIHMFLFISF ILRAAVFIK DLALFDSGES 240  
DQCSGSEVGC KAAMVFFQYC VMANFFWLLV EGLYLYTLA VSFPSERKYF WGYILIGWGV 300  
PSTFTMWIT ARIHFEDYGL LRCWDTINSS LWWIKGPIL TSILVNFLF ICIIRILLQK 360  
LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFPD NFKPEVKMVF ELVVGSFQGF 420  
VVAILYCFN GEVQALRRK WRRWHLQGV LWNPKYRPS GSGNATCST QVSMLTRVSP 480  
GARRSSSFQA EVSLV

30 A158 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.29383  
Probeset Accession #: AW207206  
35 Nucleic Acid Accession #: AL133619  
Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

40  
1 11 21 31 41 51  
ATGAGCGGTG CGGGGGTGGC GGCTGGGAGC CGGCCCCCCA GCTCGCGGAC CCGGGGCTCT 60  
CGGGGCGGGC GCCAGCGGCC CTCTGTGGGC GTCCAGTCTT TGAGGCGGCA GAGCCCGCAG 120  
CTCAGGCAGA GCGAGCCGCA GAAACGGAAC CTGGACCTGG AGAAAGCCCT GCAGTTCCTG 180  
CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240  
45 GAAACAAGG GTGAGCGGCG GCGGGGCCCT AGGCCCGCCC TGCCCTCCCA GGCACACTCA 300  
ACACTGCGCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360  
GGGGGAACAC AGGAGCGGGA GCGCCCTCCAG ACTGTCTCTG CCCACCTGGC TGCACTGGCC 420  
CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC GCCTACTCTT 480  
AGCGGTGGCT GGAACATGTT ATGCAGCCAA GCACAGCAG TGCTGTCTCT GGGGAAGCCA 540  
50 GGGCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGCT GCTCCCAGA CCTCCTCTCT 600  
CCAAGTAGAG CTGAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660  
CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
ATGCTGGGGG CCGAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
GCAGCAACCA TGGGACAAA GGGAGGAAGC AGAGTCTCTT TTCTTGCCA CTGTCTCAAG 840  
55 GCACTTCCCC ATCCTGACAG CCGCCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGTGTGA 960  
TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCTTA GGGCTCTCCC TTCCAGGGA 1020  
GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGSCAA CTCCAGTGAG 1080  
CTGTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTCAGTGC TGGGGAOGCT 1140  
60 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTCGGGACCT GCTGTTCAT GTGTCCCAAG 1200  
CCCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTTT CCAGGGCCTC TGCTCCCTTG 1260  
GGGCTCGCT GGGCTGCTAT CAACGAGTGG TGGGTAGAGC CCGGAGGACC CAGCCCTGCC 1320  
AGGTGAAGG AGGCTCTCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG CGCTCTTGGG 1380  
GGGCTAGAG CCGACACTGT GCGCTCTCTT GCAGACAGCC TCTCATGTC AAGCTTCCAG 1440  
65 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCGGCC 1500  
TCCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCAGA AGGCCAGCTT GGAAGAGGAG 1560  
CCCTACTTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAGGGCA GGCCAGAAAG 1620  
GAGAAAGCAG AGGCTCTTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680  
AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCTGTC CCCTTCCCTT GOGAAAGCCC 1740  
70 ACCACACTTA GGCAGTGGGA AGTGTCTATC CGCGAGCTGT GGAATACCAA CCTCTGCAG 1800  
ACCAAGAGC TGCGGCACCT CAAGTCTCTC CTGGAAGGGA GCCAGAGGCC CCAGCAGGCC 1860  
CCGAGGAGAG CTAGCTTTCC CAGGAGCCAA GAAGCCAGC ATTTCCCAA GGTCTCCACC 1920  
AAGAGCTCT CCAAGAAATG CTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980  
CTGAGCAGA CCGGAAGAA CAACCTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCA 2040  
75 AAACGGGCC TGCATCGCTC AGTGCTTTGA

80 A159 Protein sequence:  
Gene name: ESTs  
Unigene number: Hs.29383  
Probeset Accession #: AW207206  
Protein Accession #: T43457  
Signal sequence: none found  
Transmembrane domains: 303-322  
Cellular Localization: not determined



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1      11      21      31      41      51
5      |      |      |      |      |      |
MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPQAH S TLPLPQHRNT AINSSTRILGS 120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180
GPEVIAGROV ATCCSPDLPP PSRAEMGRNP WDSFPCPARSL PQIAAVARPR ISSPMALSPH 240
MLGAQGIWTH SIQGSPLPAIW AATMTGKGS RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300
10     AHFPLSLGLG LTSQGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVVEGGP FPSRCGNSSE 360
LFWAKCGPSR QPQPCSGADA DRTREEAMLS LGTCCSMCPK PSCFPDGPSPG NHLRSASAPL 420
GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPPGKRGRLA GGSADTVRSP ADSLSMSSFQ 480
SVKSISNSAN SQSKARPQPG SPNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGOARK 540
EKAESANAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELMWNLLQ 600
15     TQELRHLKSL LEGSQRQPAQ PEEASFPRDQ EATHFPKYST KSLSKKCLSP PVAERAILFA 660
LKQTPKNMFA ERQKRLQAMQ KRRLHRSVL

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# A160 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated

Unigene number: Hs.79136

Probeset Accession #: U41060

Nucleic Acid Accession #: NM\_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
30     |      |      |      |      |      |
CTCGTGCCGA ATTCGGCAGC AGACCGCGTG TTGCGGCGCTG GTAGAGATT TCTCGAAGACA 60
CCAGTGGGCC CGTGTGGAA CAAACCTGCG CGCGTGGCCG GGCCTGGGA CAACGAGGCC 120
GCGGAGACGA AGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCC 180
TCTCTGTGAC AATCCCTT CATGAATAA AAGCAGCTGC TTTCCCCAG ACCACTGAGA 240
AAATTAGTCC GAATTGGGAA TCTGGCATT ATGTTGACTT GGCAATTTC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAATAA TTCTTTGTCA GTTGAAGGGT 360
35     TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCAAGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540
CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTCAG 600
40     GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCACCTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTTC 780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACTAC AAAGAGCCGG GTGAGCCGGC 840
TGGCTGGTAG GAAAACAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
45     GAAACACAAA TGAAATCTCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
TCAACCAAA TGAATGCTGA TCTGTCTGA TTCATACAAG TGAAAGAAG GCTGAAATCC 1080
CTCCAAAGAC CTATTCAAT CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCATCA 1140
TCAGTTCTCT GTCTCTGCTG GGGGTATCT TAGTGCTCT CATGAATCGG GTGTTTTC 1200
50     AATTTCTCCT GAGTTTCTTT GTGGCACTGG COGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
CAATGCAAA TGAAGAGAGA CCACCTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380
GTGCCTATTT TGATTCACG TGAAGGGTCT TAACAGCTCT AGGAGGCCGT TATTTCTATG 1440
TTCTTGTGTA ACATGCTCTC ACAAATTTAA AGATAAGAAG AAAAAGAATC 1500
55     AGAAGAAACC TGAAATGAT GATGATGTGG AGATTAAGAA CGAGTTGTCC AAGTATGAAT 1560
CTCAACTTTT ACAAATGAT GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTC 1620
GAGCAGACTC GAAAGAGACC TCCCACTTTG ATTCTCAGCA GCGTGCATCT TTGGAAGAAG 1680
AAGAGGTCTAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
GGTCAAGAAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
60     TCACCAACCA TCATGACTAC CATCATATTC TCATCATCA CCACCACCA AACCACCATC 1860
CTCAGCTGCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT 1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATTT CAGCGATGCC CTAGCAATTG 1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGCT GTGTTCTGTC 2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100
65     AGCAGGCTGT CCTTTATAAT GCATTGTGAC CCATGCTGGC GTATCTTGA ATGGCAACAG 2160
GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGT GATATTGCA CTACTGCTG 2220
GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
GTGACCAATG ATGTAGCGCG TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
GTTTGTGAAT TATGTTACTT ATTCCATAT TTGAACATAA AATCGTGTTC CGTATAAATT 2400
70     TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGTTCAT 2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATT 2520
TGTATTGAA TATGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTTAAGT 2580
TATTTCTAT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640
TAAACAAGAG ATTTGGCATG ACATGTTCTG TAGTGTTCAG GGAAAAATGT CTTAATGCT 2700
75     TTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG 2760
TGTTTAGGAA TAAGAAATGT CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
AGCAAGAGAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAA TATAAAAAGG 2940
CAGAATTAGC ATAGAGTACA TCCATTAAAC ATTTTGTCA GGATTATTTC CGTAAAAAC 3000
80     GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTAAAC TTTGTATAAT ACAGAAATCT 3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120
TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TAGTATCAC CAGACTGGGT 3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGGTTC ACCTGGTTTA 3240
CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAGTAC ACCTAAGTA 3300
TCATTGTATT CGATTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATGTT 3360

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GAGCAATGTG CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420  
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

# 5 A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated  
Unigene number: Hs.79136  
Protein Accession #: NP\_036451  
Signal sequence: 1-21  
Pfam domain: Zip[591-743]  
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
MARKLSVILI LTFALSVTNP LHELKAAAPP QTTEKISPNW ESGINVDLAI STROYHLQOL 60  
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHSDHS DHEHSDHER HSDHEHSDH 120  
EHHSDDHSDH HNHHAASGKN KRKALCPDHD SDSSGKDPN SQKGGAHRPE HASGRNVKD 180  
SVSASEVTST VYNTVSEGT PLETIETPRP GKLFPKDVSS STPPSVTSKS RVSRLAGRKT 240  
NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGGMGIQV PLNATEFNYL CPAIINQIDA 300  
RSLIHTSEK KAEIIPPKTYS LQIANVGGFI AISIISPLSL LGVILVPLMN RVFFKPLLSF 360  
LVALAVGTLG GDAFLHLLPH SHASHHSHS HEEPAMEMKR GLFSLHSSQ NIEESAYFDS 420  
TWKGLTALGG LYFMFLVEHV LTLIKQPKDK KKNQKKPEN DDDVEIKQL SKYESQLSTN 480  
EEKVDTDDRT EGYLRADSQE PSHFDSQQA VLEEEVEMIA HAHPEVYNE YVPRGCKNKC 540  
HSHFHTLQO SDDLHSHHH YHHILHSHH QNHHPHSHS RYSREELKDA GVATLAWMVI 600  
MGDGLHNFSD GLAIGAAFE GLSSGLSTSV AVFCHLPHE LGDFAVLLKA GMTVKQAVLY 660  
NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720  
RWGYFFLQNA GMLLGGFIML LISIFEKIV FRINF

# 30 A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGC GGAGA CCGCGGCGCT 60  
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120  
GTGAAGGAA AGGAAGATCA TTTATGCTCT TGTGTGATAA GGTCAGACT TCTGCTGATT 180  
CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300  
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360  
TTGCGTTTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480  
GGTTCGCTAG GACTAGAAGG CTCGATTTT CAGTGTGCGG ACCTCCCAT TCCTCATCAA 540  
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600  
TCGCTCCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCCTTACTT 660  
ATATCTGTGA TTTGCTCTGT TTTGCTCTGT GTCCTTATCA TATTATTGTT TACTTCCGG 720  
TATAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780  
ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
TCAGGCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900  
ATTGGAAGAG TCGCTGATGG GGAAGTTTGG ATGGGAAGT GGCCTGGCGA AAGGTAGCT 960  
GTGAAGTGT TCTGTACCA AGAGGAAGCC AGCTGGTCCA GAGAGACAGA AATATATCAG 1020  
ACAGTGTGA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGACAA 1080  
GGGTCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTATGAT 1140  
TATCTGAAGT CCACACCTCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200  
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260  
CATCGAGATC TGAAGGATGA AAACATTCTG GTGAAGAAA ATGGAACTTG CTGTATTGCT 1320  
GACCTGGGCC TGGCTGTATA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
ACTCGAGTGG GCACCAAAAG CTATATGCTT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440  
AATCATTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTTGGGAG 1500  
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560  
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620  
CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGTG TAAGGCAGAT GGGAAAACCTC 1680  
ATGACAGAA GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740  
ACACTTGCCA AAATGTCAGA GTCCGAGGAC ATTAACTCT GATAGGAGAG GAAAAGTAAG 1800  
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
TAAGCATCCA CAGTACAGC CTTGAACATC GTCTGCTTC CCACTGGGTT CAGACCTCAC 1920  
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
TCTGTTTGTA GCGGAGAAA CGTGGGTA ACTTGTTCAA GATATGATGC AT

# 75 A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.72472 / Hs.87223  
Probeset Accession #: AA250737 / U89326  
Protein Accession #: NP\_001194  
Signal sequence: 1-13  
Transmembrane domains: 128-144  
PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
 5 MLLRSAGKLN VGTKKEDGES TAPTTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60  
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKOLHPTL PPLKNRDFVD 120  
 GPIHRRALLI SVTVCSLLLV LIILPCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
 EQSSSSGSGS GLPLLQRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 240  
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YRENGSLYDY LKSTTLDAKS 300  
 10 MLKLAIVSVS GLCHLHTEIF STQKPAIAH RDLKSKNIV KKNGTCCIAH LGLAVKFISD 360  
 TNEVDIPNPT RVGTKRYMPP EVLDESINRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420  
 EEQQLPYHDL VPSDPSYEDM REIVCIKKLR PSPFNRRSSD ECLRQMGKLM TECWAHPAS 480  
 RLTALRVKKT LAKMSSESQDI KL

A164 DNA sequence

15 Gene name: ESTs  
 Unigene number: Hs.157601  
 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 20 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 25 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60  
 TTTTATTTCG AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACTTC 120  
 OCTGGCGGTA GTTCTCCGA CCTCAGCCGG GTCCGGTGTG GCGGCCCTCT CCCAGGAGAG 180  
 ACAAACAGGT GTCCACGCTG SCAGCCGCGC CCCGGGCGCC OCTCCTGTGA TCCCGTAGCG 240  
 CCCCTGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCGCGGGCAC CGAGCGCTGG 300  
 30 TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCTTTCC TGTGTCTGGA GCGCGTCTGT 360  
 GTTTTCTCTG TTTCCAGAGT GCGCCCATCT CTCCCTTCCC AGGAAGTCCA TGTAAAGCAA 420  
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480  
 ATCATGTTTC TGTAGATGCG GTCTAACAGC GTCGGGAAAG GGAGCTTTGA AAGGTCCRAAG 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600  
 GCATTCAGT GCAGTTCAC TCCTCATCTG GAATTCCTCT TGGATTCAAT TTCAACCCAA 660  
 35 CAGGAAGTGA AGGCAAGAAAT CAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720  
 CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCTGGAG GCAGAAATGC TTCTGTGCC 780  
 CAGATCTCTA TCATCTGTC TGATGGGAAG TCCAGGGGG ATGTGGCACT GCCATCCAAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGG TCAGGTTTCC CAGGTGGGAG 900  
 40 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGG TGCTGTGGC TGAGCAGGTG 960  
 GAGGATGCCA CCAACGGGCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCACGGGCC 1020  
 ACGCCAGATG GGAAGGCTCA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGTCGCG 1080  
 GAGTTCGCTG GCAATGCCCC ATGCTGAGGA GSATCGCGGC GSACCCCTGC GGTGCTGGCT 1140  
 GCACACTGCT CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGTC CACTGCTAC 1200  
 45 AGGACCACTT GCGCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260  
 CAGGAAGGAC TGGACGGCTA CCAATGCTCT TGCCCGCTGG CCTTGGAGG GGAGGCTAAC 1320  
 TGTGCTCTGA TGTGGACAC CTCTGCTCTG GGAATGCAGG GTGCACTCC TCTTCTGCT GGACAGCTCT 1380  
 GCGGGCACCA CTCTGGAAGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTGTGCGG 1440  
 GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGAGCTG 1500  
 50 TCGTGGCGGG TGCTGTGGG GAGTACCCAG GATGTGCTG ACCTGGTCTG GAGCTCGAT 1560  
 GGCATTCCTT TCGTGTGGG CCCACCCCTG ACGGGCAGTG CCTTGGCGCA GCGCGCAGAG 1620  
 CGTGGCTCTG GAGGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGTTTGT 1680  
 CTCAGTGAAT CACACTCCGA GGATGAGGTT GCGGGCCAG CGCTCAAGC AAGGGCGCGA 1740  
 GAGCTGCTCC TGCTGGGTGT AGGCAGTGA GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800  
 55 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1860  
 GAGCTGAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1920  
 CTGCTCTTCA TGTGGACAC CTCTGCTCTA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980  
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGCGC 2040  
 CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCACCCCG 2100  
 60 GCTGCGATGC TCGGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160  
 ACGCCCTGTC TGACATCTTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220  
 GTCCCAAGAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCTT 2280  
 GCCCAGAAGC TGAGSAAACA TGGCATCTCT GTCTGTGTCG TGGCGTGGG GCCTGTCTTA 2340  
 AGTGAGGGTC TCGGAGGGCT TGCAGGTCCC CGGATTCCC TGATCCAGT GGCAGCTTAC 2400  
 65 CCGGACTGTC GGTACCAACA GACGTGCTC ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG 2460  
 CCACTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520  
 GGGAGCTACC GCTGCAAGT TCGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580  
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATT TTAGAGGCC CCTGAGGCAC 2640  
 ATGGCTCCCG TGCAGGAGG CAGCAGCCGT ACCCTCCCA GCACTACAG AGAAGGCCCTG 2700  
 70 GGCAGTGAAG TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760  
 TTCCCGCCGT GGCAGGAGC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 ATGCTGCTTA GAGCAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT 2880  
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940  
 CTGCCACCTT TCCCTTGAGG ATAAACRAG GTCCTGAAG ACTTAAATTT AGCGGCTGA 3000  
 75 CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060  
 AGGCCCTTAC TAGAGCATCC TTGGAAGCGC GAAGGCCACG GCCTTTCAAG ATGGAAGGCA 3120  
 CGAGCTTTTC CACTTCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAGGGGG 3180  
 CTTGAGGGAC GTTGTGACT TCTTGGCGAC TGCCTTTGT GTGTGGAAGA GACTTGAAGA 3240  
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGA GGGGCTGAGT 3300  
 80 TGTGATGGG CCCAGGCTG GAGGGCCAG TAAATCGTT CTGAGTCGTG AGCAGTGTCC 3360  
 ACCTGAAGG TCTTC

A165 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QGEVKARIKR 120
MVFKGSRRTT ELALKYLLHR GLPGGRNASV PQILLIVTDG KSQGDVALPS KQLKERVTV 180
PAVGVRFPFW EELHALASEP RGQHVLLAQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSMK RVFLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVFKRFV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVNSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT GQDRPRRVV LLETSHSEDE VAGPARHARA RELLLLVGVS 480
EAVRAELEEI TGSPKHMVMY SDPQDLFNOI PELQGLCSR QRPGCRTQAL DLVFMLDISA 540
SVGPENFAQM QSFVRSCALQ FEVNPVDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARF GVPKAVVLT GGRGAEDAAV PAQLRNNGI 660
SVLVVGVGVF LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETFLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

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A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Probeset Accession #: AA011176  
 Nucleic Acid Accession #: AF272890  
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCGCG GCCCGGGCTT CTGGGGTGTG CCCCAACCAC GGCCAGCCCG TGCCACACCC 60
CCCGCCCCCG GCGTCCGCGAG CTGCGCATGG GCGCGGGGGT GCTCGTCTCG GCGCGCTCCG 120
AGCCCGGTAA CCGTGTCTCG GCGCGACCGC TCCCGGACGG CGCGGCCACC GCGCGCGCGC 180
TGCTGTGTCC CCGCTGCGCG CCCGCTCGT TGCTGCTTCC CGCCAGCGAA AGCCCGGAGC 240
CGCTGTCTCA GCAGTGAACA GCGGGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGTCTA 300
TGCTGGCGGG CAATGTCTGT GTGATCGTGG CCATCGCCAA GACGCGCCGG CTGCAGACGC 360
TCACCAACTC TTTCATCATG TCCCTGGCCA GCGCGGACCT GGTGATGGGG CTGCTGGTGG 420
TGCGGTTCGG GGCCACCATC GTGGTGTGGG GCGCGTGGGA GTACGGCTCC TTCTTCTGCG 480
AGCTGTGAGC CTCAGTGGAG GTGCTGTGGG TGACGGCCAG CATCGAGACC CTGTGTGTGA 540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCGAGAG CTGCTGACGC 600
GCGCGCGGGC GCGCGGCGCT GTGTGACCGG TGTGGGCCAT CTCGCGCCCT GTGTCTCTCC 660
TGCCCATCCT CATGCACTGG TGGCGGGGCG AGAGCGAAGA GCGCGCGCGC TGCTACAAGC 720
ACCCCAAGTG CTGCACTTTC GTCAACAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT 780
CCTTCTACGT GCCCTGTGCG ATCATGGCCT TCGTGTACCT GCGGGTGTTC GCGAGGCCCC 840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCTCGCGCGC CCAGCGCGGC 900
CGCCCTCGCC CTGCGCTCGC CCGCTCCCCG CGCCCGCGCC GCGCGCGCGA CCGCGCGGCT 960
CGCGCGCGCG CGCGCGCCAC GCGCGGCTGG CCAACGGGGG TGCGGGTAAG CGCGCGGCTT 1020
CGCGCTGTGT GCGCTACGCG GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
TCCTTACGCT CTGCTGGCTG CCTTCTTCC TGGCCACGTT GGTGAAGGCC TTCCACCGCG 1140
AGCTGTGTCC CGACCGCTTC TTGCTTCTT TCAACTGGCT GGGCTACGCC AACTCGGCTT 1200
TCAACCCCAT CATCTACTGC CGCAGCCCGC ACTTCCGCAA GGCCTTCCAG GGAAGTGTCT 1260
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CGCGCTGTCT GCGCGGCGCC GGACCCCGCG CATGCGCGCG GCGCGGCTCG GACGACGAGC 1380
ACGACGATGT CGTCGGGGCC ACGCGCGCGG CGCGGCTGCT GGAGCCCTGG GCGCGCTGCA 1440
ACGCGGGGCG GCGCGGCGGAC AGCGACTCGA GCCTGGACGA GCGGTGCGCG CCGGCTTTCG 1500
CCTCGGAATC CAAGGTGTAG GCGCGGCGCG GGGGCGCGGA CTCGGGCGAC GCGCTTCCAG 1560
GGGAACGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAAGTCTG AGCCCACAAT 1620
CCTGCTCTGA ATCATCCGAG GCAAGAGAA AAGCCACGGA CCGTGCACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGGAGAG TGGCTTGTG ATGTTCTCTG TGT

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A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Protein Accession #: AA011176  
 Signal sequence: none found  
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248  
 Pfam domain: 7tm\_1 [75-377]  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVLGA SEFGLNLSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG 60
MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMLGL VVFPGATIVV 120

```

WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLI TRARARGLVC 180  
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 AFVYLRLVPRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAATAP 300  
 LANGRAKRR PSRLVALREQ KALKTLGIIM GVFTLCWLFP FLANVVKAFH RELVPRDLFV 360  
 FFWNLGYANS AFNPIIYCRS PDKRKAFOGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420  
 PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAAASD SSLDEPCRPC FASESKV

**A168 DNA sequence**

Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GCGTCCGCG CACACCTCCC CGGCGCGCG CGGCCACCG CCGCACTCCG CCGCCTCTGC 60  
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 CCGGTCCGGG CCGTGC CGGCGCGCAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240  
 ATGACTGCCA TGCCGACGCC CTGTGT CAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360  
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420  
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480  
 AGAACAAATG CCGCTGCCAG CATACCTGTG TCAACGTCT GGGAGCTAT GAGTGTCTGT 540  
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 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT TGTCGAAGGAG GCCCAAGGG 660  
 GCAGCGTCCG CTGTGAGTGT AGGCCCTGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 TCTTGACCTG TAAOCATGGG AACGCTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 GCGCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840  
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 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG 960  
 ACCGACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCTCTGT GGATTCACCTC 1020  
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 AATTATTAAAC AGATGAGAAG TCTTGCCAAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200  
 GTGACCAACG CTGCAATCAAC CACCTTGGCA CATTGCTTTG TGCTTGCAAC CGAGGGTACA 1260  
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 AGCTCCACTG CATATAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT 1440  
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 GTCACTCTGG CATTCACTTC TCTTCAGATG TCACCAACAT CAGGCAAGT GTAACCTTTA 1560  
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 TGAGCTGCTG CGTAAAGGCA ACCGAGAAGC GGCTCCGTAA AGCCATCCG ACCTCAGAA 1860  
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 GCGCAAGACC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2160  
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 GTGCCCTGGG CAGCTTCCAG CCTGAAGCTG GTGCAACTTC CTGCTTCCCT TGCGAGGAG 2280  
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 ACTTTGATGG CTCACCAAC ATAAACCCAG GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520  
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 GAACCTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300  
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CCGGCTGGCT GAGCTGACT 3360  
 TTGCTCAGC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTCC TCAAGGAGTC 3420  
 TGTAGTGAAG AGGAGGCCAC AGAATAAGCT GCTTATCTG AAACCTCAGC TTCTCTAGC 3480  
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540  
 CAAGAGGGGA GGAAGAGGAG CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG 3600  
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGTATC CAGGAACCTG 3660  
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 AGCACTTCTG GAGACAT

**A169 Protein sequence**

Gene name: CEGP1  
 Unigene number: Hs.222399

Probeset Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like\_domains [49-84,132-167,177-213,286-321,407-442] CUB\_domain [809-918]  
 Cellular Localization: may be secreted

10 1 11 21 31 41 51  
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 LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNR CTCFDGFMIA 120  
 HDGHNCLDVO ECLENNNGCQ HTCYNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSOMNK 180  
 DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGCOHSCDD TADGPECSCH 240  
 15 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300  
 STGVHSCSPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSPDCGCK KGFLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCOQVCVN 420  
 TVGSYECQCH PGYKLHNKK DCVEVKGLLP TSVSPRVSLH CGKSGGSDGC FLRCHSGIHL 480  
 20 SSDVTIIRTS VTFKLNEGKC SLKNAELFPE GLRPALEPKH SSVKESFRYV NLTCSSGKQV 540  
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 FHLQLSGMNL DVAKKPPRST ERQAESCQVG QGHAEQCVS CRAGTYIDGA RERCILCPNG 660  
 TFQNEEQMT CEPCEPRGNS GALKTPFAWN MSECGGLQCP GEYSADGFAP CQLCALGTFO 720  
 PEAGRTSCFP CGGLATKHG GATSFQDCET RVQCSFGHFY NTTHRCIRC PVGTQPEFG 780  
 25 KNCVSCFPN TTTDFDGSIN ITQCKNRRCG GELGDFTYGI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPEIFLPIED DQGDYLVMRK TSSNSVTTY ETCQTYERPI AFTSRSKLW 900  
 IQFKSNEGNS ARGQVPYVT YDEYQELIE DIVRDGRLYA SENHQEILWD KKLIALFDV 960  
 LAHPQNYFKY TAQESREMP RSFIRLLRSK VSRFLRPYK

30 A170 DNA sequence  
 Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Nucleic Acid Accession #: AF007170  
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

35 1 11 21 31 41 51  
 AAGGAGGCGG CTTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60  
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 40 AGCTACCTCA AGCCCAAGAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180  
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 75 TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCCTCAGA GGACCTGAGG AATGCTGGG 2220  
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 AGTAGAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCGAG 2460  
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 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Protein Accession #: AAC39582  
 Signal sequence: none  
 Transmembrane domains: 210-226  
 Cellular Localization: plasma membrane

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 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAPNLT LSMLPTRLIR 180  
 LLEFVGFSNG KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TPLTFVLGTG NVNIEEAELK 240  
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECC E AQHWHKQFHH MCYWELMWCF 300  
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 KLKIAGKSLP TEKFAIRKSR RYFSSNPISL PVPALMMYI WNGYAVIGKQ PKLTDGILEI 420  
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# Al72 DNA sequence

Gene name: EST  
 Unigene number: Hs.200102  
 Probeset Accession #: AL117406  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
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	AAGATGTGTG	TCTCGGAAGC	TCCITTACAC	ATGGAAGGCA	CAAGTTGTCC	CCAGGGGTGG	3300
5	CCACAGCATG	GGGAATCAT	ATTTCAGGAT	TATCACATGA	AATACAGAGA	CAACACACCC	3360
	ACCGTGTTC	ACGGCATCAA	CCTGACCATC	CGCGGCCACG	AAGTGGTGGG	CATCGTGGGA	3420
	AGGACGGGCT	CTGGGAAGTC	CTCCTGGGC	ATGGCTCTCT	TCCGCTTGGT	GGAGCCCATG	3480
	GCAGGCGGGA	TTCTATTGA	CGCGTGGAC	ATTTGCAGCA	TCCGCTTGGG	GGAGCTTGGG	3540
	TCCAAGCTCT	CAGTGATCCC	TCAAGATCCA	GTGCTGCTCT	CAGGAACCAT	CAGATTCAAC	3600
10	CTAGATCCCT	TTGACCGTCA	CACTGACCAG	CAGATCTGGG	ATGCCTTGGG	GAGGACATTC	3660
	CTGACCAAGG	CCATCTCAAA	GTTCGCCAAA	AAGCTGCATA	CAGATGTGGT	GGAAAACGGT	3720
	GGAAACTTCT	CTGTGGGGGA	GAGGCAGCTG	CTCTGCATTG	CCAGGGCTGT	GCTTCGCAAC	3780
	TCCAAGATCA	TCCTTATCGA	TGAAGCCACA	GCCTCCATTG	ACATGGAGAC	AGACACCTTG	3840
	ATCCAGCGCA	CAATCGGTGA	AGCCTCCAG	GGCTGCACCG	TGCTGCTCAT	TGCCACCGT	3900
15	GTCAACCACTG	TGCTGAAGTG	TGACCACATC	CTGGTTATGG	GCAATGGGAA	GGTGGTAGAA	3960
	TTTGATCGCG	CGGAGGTACT	GCGGAAGAAG	CTGGGTTCAT	TGTTGCGAGC	CCTCATGGCC	4020
	ACAGCCACTT	CTTCACTGAG	ATAAGGAGAT	GTGGAGACTT	CATGGAGGCT	GGCAGCTGAG	4080
	CTCAGAGGTT	CACACAGGTT	CAGCTTCGAG	GCCACAGCTG	TGCGACCTTC	TTGTTTGGAG	4140
	ATGAGAGATT	CTCTGGGAG	CAGGGGTAAA	TGTAGGGGGG	GTGGGGATTG	CTGGATGGAA	4200
20	ACCTGGAAT	AGGCTACTTG	ATGGCTCTCA	AGACCTTAGA	ACCCAGAAAC	CATCTAAGAC	4260
	ATGGGATTC	GTGATCATGT	GTTTCTCCTT	TTAACTTACA	TGCTGAATAA	TTTTATAATA	4320
	AGGTAAAGC	TTATAGTTT	CTGATCTGTG	TTAGAAGTGY	TGCAATGCT	GTACTGACTT	4380
	TGTAATATAT	AAACTAAGG	AAACTCAAA	AAAAAAAAA	AAAAAAA		
25	<u>A173 Protein sequence</u>						
	Gene name:	EST					
	Unigene number:	Hs.200102					
	Probeset Accession #:	AL117406					
	Protein Accession #:	none found					
	Signal sequence:	none found					
30	Transmembrane domains:	169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034					
	PFAM domains:	ABC transporter [502-673], ABC membrane region [163-432, 771-1060]					
	ATP-binding domains:	[508-516, 1139-1147]					
35	Cellular Localization:	plasma membrane					
	1	11	21	31	41	51	
	MTRKRTYVWP	NSSGGLVNRG	IDIGDDMVSG	LIYKTYTLQD	GPWSQQRNP	EAPGRAAVPP	60
40	WGYDAALRT	MIPFRPKPRF	PAPQPLDNAG	LPSYLTVSWL	TPLMIQSLRS	RIDENTIPPL	120
	SVHDASDKNV	QRLHRLWEEB	VSRRIEKAS	VLLVLMRFQR	TRLIFDALLG	ICFCIASVLG	180
	PILITPKILE	YSBEQLGNVV	HGVGLCFALF	LSECVKSLSF	SSSWINQRT	AIRPRAAVSS	240
	FAFEKLIQFK	SVIHITSGEA	ISFFTGDVNY	LFEGVCYGPL	VLITCASLVI	CSISSYFIIG	300
	YTAFTAILCY	LLVFPLAVFM	TRMAVKAQHH	TSEVSDQIRI	VTSEVLTCIK	LKMYTWKFP	360
45	FAKIEGMES	LTPCKSPGDG	MAFSMLASIN	LLRLSVFFVP	IAVKGLTSNK	SAVMRFKCFP	420
	LQESPVFVYQ	TLQDPSKALV	FEEATLSWQQ	TCPGVINGAL	ELERNHASE	GMTRPRDALG	480
	PEEENSLGP	ELAKINLVVS	KGMMLGVCGN	TGSGKSSLLS	AILEEMHLE	GSVGVQSSLA	540
	YVPOQANIVS	GNIRENIMG	GAYDKARYLQ	VHCCSLNRD	LELLPFGDMT	EIGERGLNLS	600
	GQKQRIQLA	RAYVSDRQIY	LLDDPLSAVD	AHVGHIPFEE	CIKTLRGKT	VVLVTHQLQY	660
50	LEFCQIILL	ENKICENGT	HSELMQKKGK	YAQLIQMHK	EATSDMLQDT	AKIAEKPKVE	720
	SQALATSLLE	SLNGNAVPEH	QLTQEEEMEE	GSLSWRVYHH	YIQAAGGYMV	SCIIFPFVVL	780
	IFVLITFSFW	WLSYNLEQGS	GTNSSRESNG	TMADLGNLAD	NPQLSFYQLV	YGLNALLLIC	840
	VGVCSSGIET	KVTRKASTAL	HNKLFNKVFR	CPMSFFDTIP	IGRLLNCFAG	DLEQLDQLLP	900
	IFSEQPLVLS	LMVIALLLIV	SVLSPYILLM	GAILMVICFI	YMMFKKAIK	VFKRLNYSR	960
55	SPLFSLHLS	LQGLSSIHVY	GKTEDFISQF	KRLTDAQNNY	LLFLSSTRN	MALRLEIMTN	1020
	LVTLAVALEP	AFGISSTPYS	PKVMVAVNIV	QLASSFPQATA	RIGLETEAQF	TAVERILQYM	1080
	KMCVSEAPLV	AGGSCPCQGW	PQHGEIIFQD	YHMYKRDNT	TVLHGINTLI	RGHEVVGIVG	1140
	RTSGSKSLG	MAFLRIVPEM	AGRILIDGVD	ICSIGLEDLR	SKLSVTPQDP	VLLSGTIRFN	1200
60	LDPFDRHTIQ	QIMDALERTF	LTKAISKFPK	KLHTDQVVEG	GNFSVGERQL	LCIARAVLRN	1260
	SKILIDEAT	ASIDMETDTL	IQTIREAFQ	GCTVLVIAHR	VTVLNCQDI	LVMGNGKVVE	1320
	FDRPEVLRKK	PGSLFAALMA	TATSSLR				
65	<u>A174 DNA sequence</u>						
	Gene name:	ESTs					
	Unigene number:	Hs.128899					
	Probeset Accession #:	AA983251					
	Nucleic Acid Accession #:	AA983251					
	Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)					
70	1	11	21	31	41	51	
	ATGCTGTCTG	GCTTCTTGAT	GAGTCCCACT	ACCCAGCACA	GAGCACAGTA	CACTCCCGGA	60
	GGAAAGAAAC	TTCCGTGGGA	GGCTTCCATC	GGTGCGCACA	CCTCCCGAGG	GCGAGGCAGC	120
75	GACCGGGAGA	GGGAGAGCCG	GCCGGAGGCT	GCCGGGCTCC	TGTGGGACCG	CGCTGCAGCC	180
	GGGAGGCGG	AGAAGGGGAA	CCGGGGCGAG	CCGCCCGCCT	GGATCCGCGC	CCAGCAGCAG	240
	CGCGGGCCG	CGCCAGCTGG	GCAAGCTCCC	GGGACTGCGG	CTGGGGGCGC	GCAGGACCTT	300
	CGCTGCGCT	CTGACGCTTC	CCGGGGGAGG	GTCCGGTTCG	CAGTGAAACC	TCCAGAGGCT	360
	TCCGAGGAC	AGCCCGGGG	GCCTTCTGAC	TGCATCCCGA	GATTTCATC	AGCGAGTGCA	420
80	ACTCATAAGG	CAGTCCCTAA	GGGACCCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCTCTGAC	CTAGGGCCCG	CGCTCGTGGC	CTCCTGGGCG	TCCGCGCAGA	GGGAGTGGC	540
	CGCGCGGAA	AGCGCCGGG	GACAGTCAGT	GACGAGGCC	GGGGGTGCGC	GGGGCCACGA	600
	CTTCTCGGAG	ACCGCTCTCG	GCTCTCTGGA	GACGCGCTGT	CGCGCGCCAG	GGTGGTGCCA	660
	TGTGGCGGCG	TGCGGCTCG	TCCGCTCTCT	CATCCTGGAA	CGCGGCTTCC	CTCCTGCAGC	720
	TGCTGCTGGC	TGCGTGTGCTG	GCGCGGGGGG	CGAGGGCCCA	GCGCGAGTA	CTGCCAGGC	780



5 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 GGCGACGCCA CCATCTGCTG CGGCAGCTGC CGCTTGGCGT ACTGCTGCTC CAGCGCCGAG 900  
 GCGCGCTTGG ACCAGGGCGG CTGCGACAAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960  
 CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGCG AGGGTGGCGC CCCACCGGTG AGGGCTTGGC AGCGGTGCTC CCCTGAAGGC 1080  
 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TCCCGGGGCG TGCTGCCCGG TGCCAGACGC 1140  
 CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCG TGCAGCGGCC GCGCTTGCCC 1200  
 ATCTACGTGC CGTTCCTCAT TGTTGGCTCC GTGTTGTGCG CCTTATCAT CTGGGGGTCC 1260  
 CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCTTAAGC AGGATCCCCA GCAGAGCCGA 1320  
 GCGCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC 1380  
 CGGGGGTGTG CTTCAGGCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCAACTCC 1440  
 GGGGCGCGGG CGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCAGGA AGGGACCATG 1500  
 AACAACTGT ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACGTCA GCAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620  
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGS AGGCGCTGCA GCCTGGCTAC 1680  
 AGGCAGATTG AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
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 GATTCTCGAG GTGGAAGTCC GCACATGTG GTGGTATTTA TGGCACTGAT CCTTGTGATG 1860  
 GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920  
 CATCCAGGTT ATCAATGATT TATGATGGAA AACCGGCTCT AGCTGGAGAT GACTGTGATG 1980  
 TTGCTGATGG GTGCTAGACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTCTTTT 2100  
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTT 2160  
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 TGGTGGGATC TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCTGCTCTC 2280  
 AGCCTCCCAAC GTGGCTGGGA TTACAGGTGC CTGCCCCAT GGCTAATTTT TTGATTTTTT 2340  
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 TCTGCTGTCT TCAGCTTCCC AAAGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGGCC 2460  
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 GGGCTATTTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700  
 TTAAAGAGAG ACTGAAATTA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760  
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 TGGTTATGGT TTGGCGTTTC CTCTGTTTG GTTTTCAGAG CCCATGTCT ATATAGTCTC 3000  
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTCTGCTCA GATCTGATA 3060  
 AAAAATTTTC TTGTCTTAGT TATAAAATTT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCTCCA GCCATAAACC GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT 3180  
 GCAGATCATA AGCTTTTITA TACTCTTGT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240  
 GATTGTAAAG AGAAAGGCTT TTCAAGCAAG GATTGCCITT CTCTCCAC ACTGTTCTTG 3300  
 ATTTCTCTC TCCTTCAGGC CTCAACAGGC ACTGATTCA TTGCCAATGT TCCAATAT 3360  
 CAAATTCAG TGAATTTATT TGTGTGTTCT TTAATTATAT AAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTGTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480  
 GTATGGTATG GTCTCTACA CATTATGTC TATAGATATC TATCGATCAT CTCTCTATTC 3540  
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGAAAAAATA AAAAAAATA AAAAAAATA

**Al75 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MLGFLMSPS TOHRAQYTPG GKLEWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKGNRGE PPWIRAOQQ PRPPPAQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPEA 120  
 SGRQPRGPD CIPRPPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEAGSG 180  
 PRGKRRGTVS DEARGSPGPR LIGDRPALSG DALAPRVVP CGALAARPS HPGTPLRSCS 240  
 CCLWRCWRRG RGPSEYCHG WLDAGGVWRI GFQCPERFDG GDATICOCSG ALRYCCSSAE 300  
 ARLDQGCCDN DRQAGAGEPG RADKDGPRRL GRASCLRGTO GDGEGAPFPV RAWQRCSPFG 360  
 SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420  
 LVAACCCRL RPKQDPQQR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480  
 GARAPPTRSQ TNCLPBGTM NNIVVNMPTN FSVLNCQQAT QIVPHQGYL HPPYVGYTVQ 540  
 HDSVPMTAVP PFMGLQPGY RQIQSPFFHT NSEQRMYPV TV

**Al76 DNA SEQUENCE**

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300  
 10 TGTGCCAGCC GGGCCCTGCC CCCGTCTCTC TCCGGGCCCC CCTGCCCTGC CCTGACGTCC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGCG TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAACTCG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGGCC CCAGGSCCAG CCTGGCACTC 600  
 15 AGCCCTTCGA GGGTGGGGCC CCCATGCGAC CCACCTCTCT TGGCTGGAGA CCCCCGGCAG 660  
 GCGCAGGCAC AGTCCCGGAG TGGGGCGCTT CTGCGCGCCC TTGCCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC GGTGTGTCCT CGCACCGAGC GCTTGACTCC GTTTKGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGAG CTACTACTGG CGCTGTCTAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCAGCGG TGCCGCCCTG 900  
 20 GGTCCCATCT TCAGGGAAAG GCATGCCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
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 CAGGAGGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTCTGC TGGCTGGGGA GCCCAGGGA TAGCGGTGG ACTTCAGGTT 1140  
 CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 25 GGCTCGATG TGCTTCCCA AGACCTGGGG GTGATGGCTT TCCCCCTCTT GGCCGGGACG 1260  
 TTGCCCCAGG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCACGTCC TAGGCAAAAGC CTGTTTCCCC CGACTCAGGA TTTCGAAGGC 1380  
 CTGGGGTCTG GGTCAACCCC CTTTGTCTCT ACGCCAGGCC TGTCCCGAGG TTTCAGCTGG 1440  
 GAGAGGCCAC CTCCTCTCAG CAAGGAAAC GAGAACCCCC AGGTACAGG AGGAGGCTGG 1500  
 30 GGCAAGTCCC CTGGGTGTCT ACTCCCTCAG CCCCCTGCCA GGCCCACTCC CGCTGGTGCT 1560  
 GGAGTAGCGA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTCACCA 1620  
 GAACGAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGCGCAG GGCCCTCGAT GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1740  
 CCGGATGCGG GGTCACTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACITTTGT 1800  
 35 ACACGTGCCC ACAAGGCCAC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860  
 CCTTCCGAGG GCGCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGGCCA GCATGCAGCT 1980  
 GCCCTCCTG CTTGAGAGAT GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCCTG 2040  
 ACCTCCTGGG CAGGAAAGGG TGCAGTCTCT GAGGGCCTGT GCCCACAGC CCCAGCACCC 2100  
 40 AGGTGGAGTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160  
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 45 AAAGAAATAG GTCTCTCCAG TTTCAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460  
 CACGAGGGGA GAATTTAAGG GCGCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520  
 GCAGACCCCT GCTGGAGGCT GCGCTAGGAC GCTGGGGCGG TCAGTCTCCG TGCAAGGATG 2580  
 GAGCAGGCTC CTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640  
 50 GCGTGACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700  
 CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCACACCA GGCCTCAGGA 2760  
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 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 55 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTCTCG GAAACATGAA AAAAAA

## A177 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs. 2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51  
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 GCGGAACACC GGGCCGCGCT CGCGGAGCT GCTTCAACCC TCTCTCTGCA GCCATGGGGC 60  
 TCCCTCGTGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGGCGCG 120  
 65 CTTCCGAGCC GTGCCGGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCTT GGGCTGCCCT GGGCAAGAGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCAATCCAAA CGTATCTTAC 360  
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAGGGGTC 420  
 70 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTGGCT GTAGAGAAGG 540  
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 75 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
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 CCAATGGGCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
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 80 ACAATGCTCC CATGTTTGAC CCCCAGAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080  
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 5 ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
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 10 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
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 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA 2100  
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 15 AGGCCAGGCG GAGGTGGTTC CTCCGCAATG ACGTGGCACC AACCATATC CCGACACCCA 2280  
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 AGGCCAGCGG CTCCGACGCG GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460  
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 20 ACGTGGCGG GAGGAGACAG TAGGCGGCTT GCCTGCGAGG CTGGGGACCA AACGTCAGGC 2580  
 CACAGAGCAT CTGCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTC 2640  
 GGAAGTGGCC GTAGCAACTT GGCAGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCCT TCCAGTATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC ATGGGTGCTT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 25 TGCTCAACCC TGTGTCTCTG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940  
 TCAGAAAGCT AGAGAAAGTT CTCAAAAGT GCAGCCACGA GCTGCTGGGC CCACTGGCGG 3000  
 TCTGTGATTT CTGGTTTCCA GACCCCAATG CTTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 30 ATACTGAGTG TGCCTAGGTT GCCCTTATT TTTTATTTTC CTTGTGCGT TGCTATAGAT 3120  
 GAAGGTGAG GACATCTGT TATATGTACT AGAAGTTTTT TATTAAGAA A

**A178 Protein sequence:**

35 Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675  
 40 Cellular localization: plasma membrane

1 11 21 31 41 51  
 45 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLA GGAQEPEGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120  
 KGFPFQRLNQ LKSNKORDTK IFYSITGPGA DSPPEGVFAV EKETGMLLIN KPLDREELAK 180  
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKPTQDTF RGSVLEGLVP GTSVMQVTAT 240  
 50 DEDDAIYTYN GVVAIVHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMDDGSGST TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVQRLT VTDLDAFNPS 360  
 AWRAATYLMG GDDGDHFTIT THPESNQGIL TRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLLTLD 540  
 55 VMDHGFVPEP RQITICNQSP VRHVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFL LVLALLVRKK RKIKEPLLLP EDDTRDNVFP YGEBGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKLA DMYGGGEDD

**A179 DNA SEQUENCE**

60 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Nucleic Acid Accession #: NM\_012152  
 65 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 70 CTCTTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAGCACA TGGACTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120  
 GGAAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCGCTGT TATTTTTTTT 180  
 TCTAATCTC TGGTCATGCG GGCAGTGATC AAAAAACAGAA AATTTCATT CCCTCTCTAC 240  
 TACCTGTGGG CTAATTTAGC TGCTGCGGAT TTCTTCTGCTG GAATTGCCCTA TGTATTCTCTG 300  
 75 ATGTTTAAAC CAGGCCCACT TTCAAAAACCT TTGACTGTCA ACCGCTGGIT TCTCCGTCAG 360  
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420  
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480  
 CTGCTCATTT TGCTGTCTCG GGCCATCGCC ATTTTATGAG GGGCGGTCCC CACACTGGGC 540  
 80 TGGAAATGCC TCTGCACAT CTCTGCCTGC TCTTCCCTGG CCCCCTTTTA CAGCAGGAGT 600  
 TACCTTGTTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGGTGAC 660  
 CTGCGGATCT ACGTGTAGCT CAAGAGGAAA ACCAAGCTCT TGTCTCCGCA TACAAGTGGG 720  
 TCCATCAGCC GCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

5 GCCTTTGTGG TATGCTGGAC CCCGGGCGCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840  
 AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900  
 GTCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960  
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGCGGTC CCTCTCGCAT CCCCTCCACA 1020  
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080  
 GTCTGCAATA AAAGCATCTC CTAAACTCTG GATGCCTCTC GGCCCAACCA GGTGATGACT 1140  
 GTCTTAGG

10 A180 Protein sequence:  
 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Protein Accession #: NP\_036284  
 15 Signal sequence: none found  
 Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51  
 MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60  
 FHPPFYLLA NLAAADFFAG IAYVPLMFNT GPVSKTLTVN RWPLRQGLLD SSLTASLTNL 120  
 25 LVIAVERHMS IMRMVHSNL TKKRVLLIL LVWAIATFVG AVPTLWGNCL CNISACSSLA 180  
 PYRSRYLVF WTVSNLMAPL IMVVYLRIY VYVKRKTNVL SPHTSGSISR RRTFPMKLMKT 240  
 VMTVLGAFVV CWTPLGLVLL LDGLNCRQCG VQHVKRWFL LALINSVVNP IYYSYKDEDM 300  
 YGTMKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

30 A181 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.162859  
 Probeset Accession #: AA569531  
 Nucleic Acid Accession #: AA569531  
 35 Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 40 ATGACCTACA GTTACTCAIT TTTCAGGCCT GAGTTGATCG TTAATCATCT TAATTATGTT 60  
 CATTCTGAAG CCAACAGGAG AACCAAGACC AAACTTTTAT TGCTCTGCTT TTCATTCTCT 120  
 GATGAAACCT CTGGACATAG CACACATCTT CCTTGTATTAT CTCTCTCAAA GGAGTTGGGA 180  
 GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240  
 CAGCTATACC TGTGGGACAT GGGTGGTTTT ACAATATTTA AGAAGCTGTG GATGAGCCTC 300  
 ATACCCAGAG GAAACAAACG CTCGCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360  
 45 AAGCAGAAGC AAGTTTCAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420  
 CTCTCTTCAT TCTGGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTGGGGCA 480  
 GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTCTTCA 540  
 GCTACGTTGT CCCAGCACTT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600  
 AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTATC TACTGAGCTG CTACCATATC 660  
 50 CCACTACTCT CTTCATGTT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720  
 TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTCTT GCCAATCATC 780  
 ACATGAGGAT GAACAATGAA ACCGATTGTA AACCAGGATT GTCTGATTCC AACATCTCTG 840  
 GGTCTCTTTT CACTCTGATA TGCTGCAATT AAAAGCCAT TTCTAAGACT GT

55 A182 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.162859  
 Probeset Accession #: AA569531  
 Protein Accession #: none found  
 60 Signal sequence: 1-46  
 Transmembrane domains: none found  
 Cellular Localization: not determined

65 1 11 21 31 41 51  
 MTYSYSFFRP ELIVNHLNIV HSEANRRXT KTLLSLLSFL DETSGLSTHL PCLSLSKECG 60  
 VLHLDIHGKK EDMRITQOSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF 120  
 70 KQKQSSKIQE ERRRESAGPN LSSFWFVGNA GRGDRPQIWA GSKQPSG

75 A183 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.179809  
 Probeset Accession #: N95796  
 Nucleic Acid Accession #: XM\_050197  
 Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCCGGGTGAC 60  
 AGCCGCGGCG CTCGGCCAGG ATCTGAGTGA TGAGACGTGT CCCCACTGAG GTGCCCCACA 120  
 GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAGGGCT GGCAGAAATG 180  
 GCGCCTGGC TGATTCTTCT GCACTTGGCG GCAGCAAGGA GGAGAGGCG CAGCTTCTGG 240  
 AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCTGAGC CCTACCGGCC 300

5 TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCGCCTGC TGGGACCCG GAAAGCCCAG 360  
 CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCCG AGGCATCACC 420  
 TATGTGCCCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGCTG 480  
 GGCATTGGTC CAGTGTCTGG CCTGGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCAC 540  
 TGGCGTGGAG GCTATGGCCG CCGCCGSCCC TTCATCTGGG CACTGTCCTT GGGCATCCTG 600  
 CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCGGATCCC 660  
 AGGCCCTGG AGCTGGCACT GCTCATCTG GCGGTGGGGC TGCTGGACTT CTGTGGCCAG 720  
 GTGTGCTTCA CTCCACTGGA GGCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780  
 CGCCAGGCT ACTCTGTCTA TGCCTTCATG ATCAGTCTTG GGGCTGCCT GGGTACCTC 840  
 10 CTGCTGCCA TTGACTGGGA CACCAGTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900  
 TGCCTCTTTG GCCTGCTCAC CCTCATCTTC CTCACCTGG TAGCAGCCAC ACTGTGGTG 960  
 GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTCCGC CCCCTCCTTG 1020  
 TCGCCCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080  
 CCGCGCTGC ACCAGCTGTG CTGCGCATG CCGCGCACCC TGGCGCGCT CTCTGTGGCT 1140  
 15 GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCAGCTGT TTTACACGSA TTTCTGTGGC 1200  
 GAGGGGCTGT ACCAGGGCTG GCCCAGAGCT GAGCCGGGCA CCGAGGCCCC GAGACACTAT 1260  
 GATGAAGGGG TTGGATGGG CAGCCTGGGG CTGTTCTGTC AGTGCCCAT CTCCCTGGTC 1320  
 TTCTCTCTG TACTGACCG GCTGGTGCA CGATTGCGCA CTGAGCAGT CTATTGGCC 1380  
 20 AGTGTGGCAG CTTTCCCTGT GGCTGCCGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440  
 GTGACAGCT CAGCCGGCTT CACCGGGTTC ACCTTCTCAG CCTGCGAGT CTGCCCCTAC 1500  
 ACACCTGCTT GCCTGTACCA CCGGAGAGA CAGGTGTTC TGGCCAAATA CCGAGGGGAC 1560  
 ACTGGAGGTG CTAGCAGTGA GGACAGCCTG ATGACAGCT TCTGCCAGG CCTAAGCCT 1620  
 GGAGCTCCTT TCCCTAATG ACAGTGGGT GCTGGAGGCA GTGGCTGCT CCCACCTCCA 1680  
 CCGCGCTCT CCGGGCCCTC TGCCTGTGAT GTCTCCGTAC GTGTGTGTGT GGTGAGGCC 1740  
 25 ACAGAGGCA GGGTGGTTCC GGGCCGGGGC ATCTGCCTGG ACCTGCCAT CTGGATAGT 1800  
 GCCTTCTGCT GTGCCAGGT GGCCCATCC CTGTTTATGG GCTCCATTG CCAGCTCAGC 1860  
 CAGTCTGTCA CTGCTATAT GGTGTCTGCC GCAGGCTGG GTCTGTGCTG CATTACTTT 1920  
 GCTACACAGG TACTATTGTA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACTTCC 1980  
 30 AGCATTGG GGTGAGGGC CTGCTCACT GGTCCACAG TCCCGCTCC TGTAGCCCC 2040  
 ATGGGGTGC CCGGCTGGCC GCCAGTTTCT GTTGTGCCA AAGTAATGT GCTCTCTGCT 2100  
 GCCACCTGT GCTGCTAGG TCGTAGCTG CACAGCTGGG GGCTGGGGG TCCCTCTCCT 2160  
 CTCTCCCGAG TCTTAGGGC TGCCTGACTG GAGGCTTCC AAGGGGTTT CAGTCTGGAC 2220  
 TTATACAGG AGGCCAGAG GGTCCATGC ACTGGAATGC GGGGACTCT CAGGTGGATT 2280  
 35 ACCAGGCTC AGGGTAACA GCTAGCCTC TAGTTGAGC ACACCTAGG AAGGGTTTT 2340  
 GGGAGCTGAA TAAACTCAGT CACCTGGTT CCCATCTCTA AGCCCCTTA CCTGCAGCTT 2400  
 CGTTTAATGT AGCTCTTGA TGGAGTTTC TAGGATGAAA CACTCTCCA TGGGATTGTA 2460  
 ACATATGAAA GTTATTGTA GGGGAAGAGT CCTGAGGGG AACACACAAG AACAGGTCC 2520  
 40 CCTAGCCCC ACAGGCACTG GTCTTTTTC CTNGANTCCA CCCCCCCT CTTTACCCTT 2580  
 TT

**A184 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.179809  
 45 Probeset Accession #: N95796  
 Protein Accession #: XP\_050197  
 Signal sequence: none  
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401  
 50 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 55 MVQLRWVSR LRRHKAQLLL VNLTFGLEV CLAAGITYVP PLLLEVGVVE KPMIMVLGIG 60  
 PVLGLVCPVL LGSASDHWG RYRRRPFIW ALSLGILLSL FLIPRAGMLA GLLCPDFRPL 120  
 ELALLILGV LLDPCGVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGCLGYLLPA 180  
 IDWDSALAP YLGTQECLEF GLLTLIFLTC VAATLLVAEE AALGPTPEAE GLSAPLSLPH 240  
 CPCRRLAPL RNLGALLPRL HQLCCRPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL 300  
 60 YQGVPRAEFG TEARRHYDEG VRMSLGLFL QCAISLVPSL VMDRLVQRFQ TRAVYLASVA 360  
 AFPVAAAGAT LSHSVAVVTA SAALTGFTEF ALQILPYTLA SLYHREKQVF LFKYRGDTGS 420  
 ASSEDSLMTS FLPGPKPGAP FPNHVGAGG SGLLPPFPAL CGASACDVSV RVVVGEPTEA 480  
 RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSTVQLSQSV TAYMVSAGL GLVAIYFATQ 540  
 VVFDKSDLAQ YSA

**A185 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.11260  
 70 Probeset Accession #: R73640  
 Nucleic Acid Accession #: AK002126  
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 75 ATGGTTCCGC GGGGGCTGCT TGCCTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60  
 TGCTGTGCTA TCTCTGTCTT GTACATGTTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG 120  
 CTGGCACTGC CCAGGGCCAA CAGCCCAACG GGAAGGAGG GGTACCAGGC CGTCTCTCAG 180  
 GAGTGGGAGG AGCAGCACCG CACTACGCTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240  
 80 AAGAGGAGC TGCAAGGAGG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300  
 GCTGCTGGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCTGGCC 360  
 TTCTGCACT CGCAGGTGGA CAAGCAGAG GTGAATGCTG GGTCAAGCT GGCCACAGAG 420  
 TATGACAGC TGCCTTTTGA TAGCTTTACT CTACAGAGG TGTACCAGCT GGAGACTGGC 480  
 CTTACCGCC ACCCCAGGGA GAAGCCTGTG AGGAAGGACA AGCGGATGA GTTGGTGGAA 540  
 GCCATTGAAT CAGCCTTGA GACCTGAAC AATCTCTGAG AGAACAGCCC CAATCACCGT 600

CCTTACACGG CCTCTGATT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660  
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAACGGCT CATCTTATTT 720  
 CGACCATTCG GCCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780  
 ATCAATGTTA TCGTGCCTCT AGCAAAAAGG GTGGACAAGT TCGGCAGATT CATGCAGAAAT 840  
 TTCAGGGAGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACTGTTGT TTACTTTGGG 900  
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTTGAAAACA CTTCCAAAGC TGCCAACTTC 960  
 AGGAACCTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAAGG ACTTGATGTT 1020  
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTTCTCTTT TCTGTGATGT GGACATCTAC 1080  
 TTCACATCTG AATTCTCTAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140  
 TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGTATGCACTC 1200  
 CCTCCCTTGG AACACGACGCT GGTCAATAAG AAGGAACTG GATTTTGGAG AGACTTTGGA 1260  
 TTGGGATGA CGTGTGAGTA TCGGTGAGAC TTCAATCAATA TAGGTGGGTT TGTCTGGAC 1320  
 ATCAAAGGCT GGGGCGGAGA GGATGTGCAC CTTTATCGCA AGTATCTCCA CAGCAACCTC 1380  
 ATAGTGGTAC GGACGCTGT GCGAGGACTC TTCACCTCT GGCATGAGAA GCGCTGCATG 1440  
 GACGAGCTGA CCCCAGAGCA GTACAAGATG TGCATGCAGT CCAAGGCCAT GAACGAGGCA 1500  
 TCCCACGGCC AGCTGGGCAT GCTGTGTTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAAA 1560  
 CAGAACAGA AGACAAGTAG CAAAAAACA TGA

20 A186 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.11260  
 Probeset Accession #: R73640  
 Protein Accession #: NP\_060841  
 25 Signal sequence: 1-26  
 Transmembrane domains: none found  
 Cellular Localization: not determined

30 1 11 21 31 41 51  
 MVRRLAWI SRVVLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60  
 EWEQHRNYV SSLKQRIQAL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTQADLLA 120  
 FLHSQVKAE VNAGVKLATE YAAVPDSFT LQKVQLEBTG LTRHPEEKPV RKDKRDELVE 180  
 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILE 240  
 35 RPFGRIMVK NEKLNMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300  
 KEEINEVKGI LENTSKAANF RNFTFIQLNG EFSRGKGLDV GARFWKGSNV LLFFCDVDYI 360  
 FTSEFLNTR LNTQPGKVPF YPVLFSSQYNP GIIYGHDAV PPLEQQLVIK KETGFWRDFG 420  
 FGMTQYRSL FINIGGFOLD IKGWGGEDVH LYRKYLHSLN IIVRTPVRGL FHLWHEKRCM 480  
 40 DELTPEQYKM CMQSKAMNEA SHQQLGMLVF RHEIEAHLRK QKQKTSKKT

45 A187 DNA SEQUENCE  
 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCCTCAAG CTGATCTTCA GAATCGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTCTAGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTITTA 240  
 55 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360  
 CCAGAAATGCC ATTTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTGCCCGC AGACTTGGTT 420  
 CCAGGTGATA CAGTTTGCCT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTIT 480  
 60 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540  
 AAGGTGACAG CTCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCSAG AAGTAACATT 600  
 GCCTTATGGG GAACACTGGT CAGATGTGGC AAGCRAAAG GTGTTGTCTAT TGGAAACAGGA 660  
 GAAATTTCTG AATTGGGGA GGTITTTAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780  
 65 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAG ATATCTCGGA AATGTTTACT 840  
 ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTGT GGTCAACAGT 900  
 ACGTAGCTC TTGGTGTATT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960  
 ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTCG AACACTGACG 1020  
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTACT 1080  
 70 GGAGTTGGCT ATAACTAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATT 1140  
 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGTGTAATT 1200  
 AGAAACAATA CTCTAATGGG GAAGCCAAAC GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260  
 ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320  
 GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
 75 TGTITTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500  
 ATGGGCTCAG CGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGTGACT GGGCAGCTG 1560  
 ACATTTCTTG GCTTGGTGGG AATCAATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620  
 ACACAAAGT TTGCCTCAG AGTATCAATA AAAATGATTA CTGGAGATT CACAGGAGACT 1680  
 80 GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAAA CTTCCAGTCT AGTCTCAGGA 1740  
 GAAGAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAA GGTTCAGTA 1800  
 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860  
 TCAGTTGATG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920  
 ATTGGAGTTG GATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980  
 CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGTTAA AGGGATTTAT 2040

5 AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100  
 ATCTCATTTG CTACATTAAAT GAACTTTTCT ATCTCTCTCA ATGCCATGCA GATTTTGTGG 2160  
 ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACCC AGTGGATAAA 2220  
 GATGTCAATC GTAAACCTCC TCGCAACTGG AAGACACGCA TTTTGACTAA AAACCTTGATA 2280  
 CTTAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340  
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400  
 TTTTGTGACA TGTTCAATGC ACTAAGTTCC AGATCCCGA CCAAGTCTGT GTTTGAGATT 2460  
 GGACTCTGCA GTAATAGAAT GTTTGTCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520  
 10 CTAGTTAATT ACTTCTCCCT GCITCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
 GATCTGTGTG TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640  
 AAGGTTGAAA GGAGCAGGGA AAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700  
 CTGAAGTAT GA

# A188 Protein sequence:

15 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 20 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

25 1 11 21 31 41 51  
 MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI 60  
 SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQYRSEK SLEELSKLVP 120  
 30 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDSLIDES SLTGETTPCS 180  
 KVTAPQPAAT NGDLASRSNI AFMGTLVRCG KAKGVVIGTG ENSEFGEVFK MQAEEAPKT 240  
 PLQKSMDLGL KQLSFYSFGI IGIIMLVGWL LGRDILEMFT ISVSLAVAAI PEGPLIVTV 300  
 TLALGVNRMV KRAIVKLLP IVETLGCCNV ICSDRTKTLT KNEMTVTHIF TSDGLHAEVT 360  
 CVGVNQFGEV IVDGVDVHGF YNPVSRIVE AGVCNDNAVI RNNTLMGKPT EGALIALAMK 420  
 35 MGLDGLQODY IRKAEYFPSS EQKMAVKCV HRTQQRPEI CFMKGAYEQV IKYCTTYQSK 480  
 GQTLTLTQQQ RDVIYQEKAR MGSAGLRVLA LASGPELQQL TFLGLVGIID PPRTVKKEAV 540  
 TLLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEDAMDVQQ LSQIVPKVAV 600  
 FYRASPRHOM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGTGT DVCKEADMI 660  
 LVDDDFQTIM LAIEEGKIY NNKNFVRFP LSTSIALLTL ISLATLMNFP NPLNAMQILW 720  
 40 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLEFVFW 780  
 ELRDNVITPR DTTMTFTCFV PFDMPNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840  
 LVIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSREKIQ KHSVSTSSSF 900  
 LEV

# A189 DNA SEQUENCE

45 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 50 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 55 ATGGGCTACC AGAGGCAGGA GCCTGTCTAT CCGCCGCGA GAGGATTGCC TTATTCAATG 60  
 AAGCAAGCTG GGTTCCTTTT GGAATATATG CTTTATTCT GGGTTTCATA TGTACAGAC 120  
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180  
 TTGGTCAATA AAACITTCGG CTTTCCAGGG TATCTGTCTC TCTCTGTCTT TCAGTTTTTG 240  
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300  
 60 TTTCAAGAA TCCAGGAGT TGATCCTGAA AACGTGTTA TTGGTGCCCA CTTCAATTAT 360  
 GGACTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT 420  
 GGAAAGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAA TGTAAATGGCA 480  
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540  
 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTCAT TTATTTGCCA CCATAACTCC 600  
 65 TTCTTAGITT ACAGTTCTCT AGAAGAACC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660  
 ATGTCCATCG TGATTCTCTG ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720  
 TTTACTGGCT TCACCAAGG GGACTTATTT GAAATTAAT GCAGAAATGA TGACCTGGTA 780  
 ACATTGTGAA GATTTTGTGA TGGTGTCACT GTCAATTTGA CATACCTAT GGAATGCTTT 840  
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTITTCAC 900  
 70 ATTGTGTAA CAGTGATGCT CATCACTGTA GCCACGCTTG TGTCAATGCT GATGATTGTC 960  
 CTCGGGATAG TCTAGAACT CAATGGTGTG CTCGTGCA CCCCCCTCAT TTTTATCATT 1020  
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080  
 TCTTGTGACA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGATTCTGT CATGGCTATT 1140  
 ACAAAATCTC AAGACTGCAC CCATGGGCAG GAAATGTCT ACTGCTTTC TGACAATTC 1200  
 75 TCTCTCACA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260  
 ATTAGTATCT TCAACTCGA GTAA

# A190 Protein sequence:

80 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 | | | | |  
 MGYQRQEPVI PPQRGLPYSM KQAGFPILGIL LLFWVSIVTD FSLVLLIKGG ALSGTDITYQS 60  
 LVNKTGFEFG YLLLSVLQFL YPFIAMISYN IAGDTLSKV QRIPGVDPD NVFIGRHFII 120  
 GLSTVTFTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK 180  
 10 PNAIQAVGVM SFAFICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFC IFFATCGYLT 240  
 FTGFTQGLDF ENYCRNDLV TFGRFCYGVV VILTYPMECF VTREIVANVF PGNLSSVVFH 300  
 IVTVMVITV ATLVSLIDC LGIVLELNGV LCATPLIFII PSACYLKSE EPRTHSDKIM 360  
 SCVMLPIGAV VMVGFVMAI TNDQCTHGQ EMFYCFDNF SLTNTSESHV QQTQLSTLN 420  
 ISIFQLE

**A191 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 25 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGT TTTCCCTTGT TTTATTGATA 60  
 AAAGGAGGGG CCTCTCTCGG AACAGATACC TACCACTCTT TGGTCAATAA AACITTCGGC 120  
 TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180  
 AGTTACAATA TAATAGCTGG AGATACITTTG AGCAAAGTTT TCAAAGAAT CCCAGGAGTT 240  
 GATCCTGAAA ACGTGTITAT TGGTCGCCAC TTCATTATTG GACTTTCCAC AGTTACCTTT 300  
 30 ACTCTGCCCT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGCTCT CCTCATCTCT 360  
 ACAGGTTTAA CAATCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420  
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAGC CCAATGCCAT TCAAGCGGTC 480  
 GGGGTTATGT CTTTTCGATT TATTTCGCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540  
 GAAGAACCA CAGTAGCTAA GTGGTCCGCG CTTATCCATA TGTCCATCGT GATTTCGTGA 600  
 35 TTTATCTGTA TATCTTTGCG TACATGTGGA TACTTGACAT TTACTGGCTT CACCAAGGGG 660  
 GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTGTTTAT 720  
 GGTGTCACTG TCATTTTGAC ATACCTATG GAATGCTTTG TGACAGAGA GGTAAATGCC 780  
 AATGTGTTTT TTGTTGGGAA TCCTTCATCG GTTTTCCACA TTGTGTAAAC AGTATGGTTC 840  
 ATCACTGTAG CCACGCTTGT GTCACTGCTG ATTGATTGCC TCGGGATAGT TCTAGAAGTC 900  
 40 AATGGTGTGC TCTGTGCAAC TCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
 CTGTCTGAAG AACCAAGGAC ACACTCCGAT AAGATTATGT CTGTGTGTCAT GCTTCCCAT 1020  
 GGTGCTGTGG TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
 CATGGGCAGG AAATGTTCTA CTGCTTTCTT GACAATTTCT CTCTACAAA TACCTCAGAG 1140  
 45 TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200  
 TAA

**A192 Protein sequence:**

Gene name: ESTs  
 50 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: 1-26  
 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351  
 55 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 60 MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLSVL QFLYPFIAMI 60  
 SYNIIAGDTL SKVFQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLLS 120  
 TGLTTLILGI VMARAIISLG HIKPTEDAVV FAKFNIAQAV GVMSFAPICH HNSFLVYSSL 180  
 EEPTVAKWSR LIHMSIVISV PICIFFATCG YLTPTGFTQG DLFENYCRND DLVTFGRFCY 240  
 65 GVTVILTYPM ECFVTREIVIA NVFPGGNLSS VFHIVTVMV ITVATLVSLI IDCIGIVLEL 300  
 NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360  
 HGQEMFYCFP DNFLNTISE SHVQQTQLS TLNISIFQLE

**A193 DNA SEQUENCE**

Gene name: ESTs  
 70 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 75 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGG TCAATAAAAC TTTCCGCTTT 60  
 CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120  
 80 TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180  
 CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240  
 CTGCTTTTAT CCTGTAGCCG AAATATAGCA AAGCTTGGAA AGGCTCCTCT CATCTCTACA 300  
 GGTTTAAACA CTCTGATCTT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360  
 ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGTCCGGG 420



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GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480  
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540  
 ATCTGTATAT TCITTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600  
 TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660  
 GTCACGTGCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720  
 GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780  
 ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840  
 GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTTCCAT CAGCCTGITA TCTGAACTG 900  
 TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGCTT GTGTCATGCT TCCCATTGGT 960  
 GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020  
 GGGCAGGAAA TGTTCTACTG CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080  
 CATGTTTCAG AGACAACACA ACTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

# A194 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGYQRQEPVI PPQVNTKFGF PGVLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIIPGVD 60  
 PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLKGVSLIST GLITLILGIV MARAISLGP 120  
 IPKTEDAWVF AKPNAIQAVG VMSFAPICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVP 180  
 ICIFATCGY LFTFTGTQGD LFENYCRNDD LVTFRFCYGY VTVILTYPM ECFVTREVIAN 240  
 VFQGNLSSV FHIIVTVMWI TVATLVSLLI DCLGIVLELN GVLCAATPLIF IIPSACYLKL 300  
 SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360  
 HVQQTQLST LNISIFQLE

# A195 DNA SEQUENCE:

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51  
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGAG GAGATTAGA TGACAGAGAA 60  
 ACCCTTGTTC CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120  
 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180  
 GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGSTTTCAT ATGTTACAGA CTTTTCCTTT 240  
 GTTTTATTGA TAAAGAGAGG GGCCCTCTCT GGAACAGATA CCTACCAATC TTGGTCAAT 300  
 AAAACTTTGG GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTTC GTATCCTTTT 360  
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAGA 420  
 ATCCAGGAG TTGATCCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480  
 ACAGTTACCT TTAATCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC 540  
 TCCTCATCT CTACAGGTTT AACAACCTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600  
 TCACTGGGTC CACACATACC AAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC 660  
 ATTCAAGCGG TCGGGGTTAT GTCITTTGCA TTTATTTGCC ACCATACTC CTCTTAGTT 720  
 TACAGTTCTC TAGAAGAAC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCATC 780  
 GTGATTTCTG TATTATCTG TATATTCTTT GCTACATGTC GATACCTGAC ATTTACTGGC 840  
 TTCAACCAAG GGGACTTATT TGAAAAATAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900  
 AGATTTTGT ATGGTGTGAC TGTCAATTTG ACATACCTTA TGGAAATGCT TGTGACAAGA 960  
 GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTCCA CATTGTTGTA 1020  
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATGATTG CCTCGGGATA 1080  
 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140  
 TGTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200  
 ATGCTTCCA TTGGTGTCTG GGTGATGGTT TTTGGATTG TCATGGCTAT TACAAATACT 1260  
 CAAGACTGCA CCCATGGGCA GGAATGTTC TACTGCTTC CTGACAATT CTCTCTACA 1320  
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380  
 TTTCAATGA

# A196 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60

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GFPLGILLLF WVSVYTFPSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPP 120  
 IAMISYNIIA GDTLSKVQFR IPGVDPENVF IGRHFIIIGLS TVTFTLPLSL YRNIKLGKV 180  
 SLISTGLTTL ILGLVMARAI SLGPHIPKTE DAWVFAKPNIA IQAVGVMSFA FICHNSFLV 240  
 YSSLEETPA KWSRLIHMSI VISVPICIFF ATCGYLTFGT FTQGDLFENY CRNDDLVTFG 300  
 RFCYGVTVIL TYMECFVTR EVIANVFPG NLSSVFHIV TVMVITVATL VSLLDCLGI 360  
 VLELNGVLCA TPLIFIIPSA CYLKLSEEP THSDKIMSCV MLPIGAVMV FGFVMAITNT 420  
 QDCTHGQEMF YCFPDNPSLT NTSSEHVQQT TQLSTLNISI FQ

**A197 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Nucleic Acid Accession #: NM\_017636  
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

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ATGAGGAGT CTTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCACG 60  
 GAGAAGCCCA CCGATGCCCTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACACG 120  
 AATTTCCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTCAACACG 180  
 ACATGGGGCT TCGTGCCGCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGGCCC 240  
 GTCTCCAGA CTTGGCTGCA GGACCTGCTG CGTCTGGGGC TGGTGGGGG TCGCCAGAGC 300  
 ACAGAGGCTT GGATTGTGAC TGGGGGTCTG CACACGGGCA TCGGCCGCA TGTGTGTGTG 360  
 GCTGTACGGG ACCATCAGAT GGGCAGCACT GGGGGCACCA AGGTGGTGGC CATGGGTGTG 420  
 GCGCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCCAGGG CTCGTTCCTT 480  
 GCGAGGTACC GTTGGCGCGG TGACCCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAAC 540  
 TACTCGGCTT TCTTCTGTGT GGAAGACGGC ACACACGGCT GCCTGGGGGG CGAGAACCGC 600  
 TTCCGCTTGC GCCTGGAGTC CTACATCTCA CAGCAGAAGA CCGCGGTGGG AGGGACTGGA 660  
 ATTGACATCC CTGTCTCTGT CCTCTGTATT GATGGTGTAT AGAAGATGTT GACGCGAATA 720  
 GAGAAGCCCA CCGAGGGTCA GCTCCCATGT CTCTCGTGG CTGGCTCAGG GGGAGCTGGG 780  
 GACTGCTGCG CGGAGACCTT GGAAGACACT CTGGCCCGAG GGAGTGGGGG AGCCAGGCAA 840  
 GCGCAAGCCC GAGATGGAAT CAGGCGTTTC TTTCCCAAAG GCGACCTTGA GGTCTGCAG 900  
 GCGCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTGTA CAGTCTATT TCTGAGGAT 960  
 GGGTCTGAGG AATTCTGAGC CATAGTTTTC AAGGCCCTTG TGAAGGCTTG TGGGAGCTCG 1020  
 GAGGCTCAGG CCTACCTGGA TGAGCTGCGT TTGGCTGTGG CTTGGAACCG CGTGGACATT 1080  
 GCGCAGAGTG AACTCTTTTC GGGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140  
 CTCATGGAGC CCTCTGTGAA TGACCGGCTT GAGTTCGTGC GCTTGTCTAT TTCCCAAGGC 1200  
 CTCAGCTGCG GCCACTTCTT GACCCCGATG CGCTGGCCCC AACTCTACAG CGCGCGCCCC 1260  
 TCCAACCTGC TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACAGCGCAGG CACCAAGGCC 1320  
 CCAGCCCTAA AAGGGGGAGC TGCGGAGCTC CGGCCCTCTG ACGTGGGCA TGTGTGTAGG 1380  
 ATGCTGCTGG GGAAGATGTG CGCGCGAGG TACCCCTCCG GGGGGCGCTG GGACCTCAC 1440  
 CCAGGCCAGG GCTTCGAGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTCGCGCTC 1500  
 TCGCTGAGTG CTGCGCTGGG GCAGGCCCCC TGGAGCGACC TGCTTCTTTG GCACTGTGTG 1560  
 CTGAACAGGG CACAGTGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620  
 GCTCTTGGG GCTTCTGTGT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGTGTAGGAG 1680  
 GCAGCAGGA GGAAGACCTT GCGTTCAGG TTTGAGGGGA TGGGCGTGA CCTCTTTGGC 1740  
 GAGTGTCTAT GAGCAGTGA GGTGAGGGCT GCGCGCTCTC TCCTCGTCTG CTGCGCGCTC 1800  
 TGGGGGGATG CCACTTGCTT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTCTTTTGCC 1860  
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920  
 CCCATCTGGG CCTCTGTCTT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGCCTCATC 1980  
 ACCTTCAGGA AATCAGAGA GGAGCCACA CCGGAGGAGC TAGAGTTTGA CATGATAGT 2040  
 GTCATTAATG GGAAGAGGCC GTTCGGGACG GCGGACCCAG CCGAGAAGAC GCCGCTGGGG 2100  
 GTCCCGCGCC AGTCCGGCCG TCCGGGTGTC TCGGGGGGCC GCTCGCGGGG GCGCGGCTGC 2160  
 CTACCGCGCT GGTTCACATT CTGGGGCGCG CGGTGACCA TCTTCATGGG CAACGTGGTC 2220  
 AGCTACCTGC TGTCTCTGCT GCCTTCTCTG CGGGTGTGTC TCGTGGATT TCCAGCGGGC 2280  
 CCGCCCGGCT CCTCGAGCT GCTGCTCTAT TTCTGGGCTT TCACTGCTCT GTGCGAGGAA 2340  
 CTGCGCCAGG GCTGAGCGG AGGCGGGGCG AGCCTCGCCA GCGGGGGCCC GGGGCTGGC 2400  
 CATGCTCTAC TGAGCCAGCG CCTGCGCCTC TACCTCGCGC ACAGCTGGAA CAGTGGGAC 2460  
 CTAGTGGCTC TCACCTGCTT CCTCTGGGCG GTGGGCTGCC GGCTGACCCC GGGTTGTAT 2520  
 CACCTGGGCC GCATGTCTCT CTGCATCGAC TTCTATGTTT TCACGTGGCG GCTGCTTAC 2580  
 ATCTTCACGG TCAACAAACA GCTGGGGCCC AAGATCGTCA TCGTGGGCAA GATGATGAAG 2640  
 GAGTGTCTCT TCTTCTCTCT CTCTCTCGG GTGTGGCTGG TAGCCTATGG CGTGGCCAG 2700  
 GAGGGGCTTC TGAGGCCAGG GGACAGTGAC TTCCCAAGTA TCCTGCGCGG CGTCTTCTAC 2760  
 CGTCCCTACC TGCAGATCTT CGGGCAGATT CCCCAGGAG ACATGGACGT GGCCTCATG 2820  
 GAGCACAGCA ACTGCTCTGT GAGGCCCGGC TTCTGGGCAC ACCCTCTTGG GGGCCAGGCG 2880  
 GGCACCTGCG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTGT CATCTTCTG 2940  
 CTGTTGGCCA ACATCTCTGT GGTCAACTTG CTCAATGGCA TGTTCAGTTA CACATTGGC 3000  
 AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGCGCGAGC GTTACCGCTT CATCGGGAA 3060  
 TTCACTCTCT GGGCCCGGCT GGGCCCGGCC TTTATCGTCA TCTCCACTT GCGGCTCTG 3120  
 CTCAGGCAAT TGTGACGGCG ACCCCGGAGC CCCCAGCGGT CCTCCCGGCG CCGAGCAT 3180  
 TTCGGGGTTT ACCTTTCTAA GGAAGCGGAG CGGAAGCTGC TAAAGTGGGA ATCGGTGCAT 3240  
 AAGGAGAAGT TCTGCTGGC ACGCGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG 3300  
 AAGCGCAGGT CCGAGAGAGT GGACTTGGCA CTGAACAGC TGGGACACAT CCGGAGTAC 3360  
 GAACAGCGCC TGAAGTGTCT GGAGCGGAG GTCCAGCAGT GTAGCCCGGT CCTGGGGTGG 3420  
 GTGGCCGAGG CCTGAGCGG CTCTGCTTGG CTGCCCCAG GTGGGCGGCC ACCCCCTGAC 3480  
 CTGCTGGGT CCAAGACTG A

**A198 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Protein Accession #: none found

Signal sequence: none found  
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995  
 Cellular Localization: plasma membrane

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|      |      |      |      |      |
MEDAFGAADV TVWDSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
TWGFRAPNLV VSVLGGSGGP VLQTLQDILL RRGVLRAAQS TGAWIVTGGI HTGIGRHHGV 120
AVRDHQMAST GGTKVAMGV APWGVVRNRD TLINPKGSFP ARYRWGRDPE DGVQFPPLDYN 180
YSAFPLVDDG THGCLGGENR FRLRLSYIS QKRTGVGGTG IDIPVLLLI DGDERMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLAELETD LAPGSGGARQ GEARDRIIRF FPKGLLEVLQ 300
AQVERIMTRK ELLTVYSSD GSEEFETIVL KALVKACGSS EASAYLDEL RAVAWNRVDI 360
AQSELEFRDI QWRSFHLEAS LMDALLNDRP EFVRLLSHG LSLGHFLTPM RLALYLSAAP 420
SNSLIRNLDD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQGFSGSMY LLSDKATSPL SLDAGLGQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540
ALGACLLLRV MARLEPDARE AARRKDLAFK FEGMGVDLFG ECTRSSEVRA ARLLLRRCPL 600
WGDATCLQLA MQADARAFPA QDGVQSLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI 660
TFRKSEEPRT RELEFDMDIS VINGEGPVT ADPAEKTPLG VPRQSGRPGC CGGRCGGRC 720
LRRWPHFWGA PVTIPMGNVV SYLLFLLLFS RVLLVDFQPA PPSLELLLY FWAFTLLCEE 780
LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLFG VGCRLTPGLY 840
HLGRTVLCID FMVFTVRLHL IFTVNKQLGP KIVIVSKMMK DVFFFLFPLG VWLVAYGVAT 900
EGLLRPRDSD FPSILRRVFP RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPGGAQA 960
GTCVSYANW LVVLLVIFL LVANILVNL LIAMFSYTPG KVQNSDLYW KAQRYRLIRE 1020
FHSRPAALFP FIVISHLRL LRQLCRPRS PQSSPALEH FRVYLSKAE RKLLTWESVH 1080
KENPLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQLKVLERE VQCSRVLGW 1140
VAEALSRSAL LPPGPPPPD LPSGKD
  
```

30  
 35

**A199 DNA SEQUENCE**  
 Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Nucleic Acid Accession #: AA054237  
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

40  
 45  
 50

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCTGGGG 60
CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CGACCCCGCG CGCCACAAG 120
GAGAGCTGCG AGCCGACCGC CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CCGCCTGATG 180
CGCTGTGCGC ACTTGCCTCGT CGCGGACTCG CCCCCTGCGG GCGCGCGGCT GCTCCCGGCG 240
GCGCGCGGGC GCGCGGACCC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC 300
GCCGAGTGGC GCGCGGCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCATCG ACOGGGACAT CGACCCCTC ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCTTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCTTGG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCTCATGAC AGGATATTT 660
TGCACCATTT CCTCTGTAC TTATGCGCGC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCGCTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA
  
```

55  
 60  
 65

**A200 Protein sequence:**  
 Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Protein Accession #: none found  
 Signal sequence: 1-18  
 Transmembrane domains: 179-201, 209-231, 257-279  
 Cellular Localization: plasma membrane

70

```

1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DFPDQKNRLM 60
PLSHLPLRDS PPLGRRLLP GPGRADPESW RSLGLGLD AECGRPLFAT YSGLWRKCYF 120
LGIDRDIDTL ILKGIAQRCT AIKYHPSQPI RLRLNIPNLT KTIQDEWHL LHLRRITAGF 180
LGMVAVLLC GCIVATVSFP WEESLTQHVA GLLPLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV
  
```

75  
 80

**A201 DNA SEQUENCE**  
 Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCGAC TGAATCGGAA AAAAAGTTTA AGTTTGGTAA AAGAGTTGGA TGCCITTCGG 60
AAGGTTCTCG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
  
```

5 TTTACAATA TGGCTTTATT AACATAATG GAATTCCTAG TATATCAAGA TACATGGATG 180  
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT 240  
 ACTGTTGCCA TGAAGTGTC AATGTTTGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300  
 GTTGCACTCG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360  
 10 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420  
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480  
 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATAAAA 540  
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600  
 CATTGGCAG CACITGTCAA CCATGAATCT TACAATTTT CTCTAGAAT AGATCATTG 660  
 15 TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAAGTGA AAAAATGTCT 720  
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAAACAA ACTACATACA 780  
 TATAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840  
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTTCTCTT 900  
 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGCCAGT TTTTGTGAAG ACTCTGTGGT 960  
 20 ATTGTTGGAG GAATCTTTTC AACACAGGC ATGTTACATG GAATTGGAAG ATTTATAGTT 1020  
 GAAATATTT GTGTCGTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCTTTT 1080  
 GAGGATGGCC ACACAGACAA CCACTTACCT CTTTTAGAAA ATAATACACA TTGA

20 **A202 Protein sequence:**  
 Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Protein Accession #: NP\_057654  
 25 Signal sequence: none found  
 Transmembrane domains: none found  
 Cellular Localization: nuclear

30 1 11 21 31 41 51  
 | | | | | |  
 MRRLNRKKTLLVSKELDAFPKVPESYVETSASGGTVSLIAFTTMALLTIM EFSVYQDTWM 60  
 KYEYEVDRDFSSKLRLINIDI TVAMKQYVGVADVLDAETM VASADGLVYEPTVFDLSPQQ 120  
 35 KEWQRLQLI QSRLEQEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180  
 VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGLVPAII NPLDGTEKIA 240  
 IDHNMQFYF ITVVPKLTHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300  
 MVTVEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKFIV EIICRFRLG SYKFPVNSVPP 360  
 EDGHTDNLHP LLENNTH

40 **A203 DNA SEQUENCE:**  
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 Probeset Accession #: S79876  
 45 Nucleic Acid Accession #: NM\_001935.1  
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 | | | | | |  
 CGCGCGTCTCG CGCGCGCCGCG GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC 60  
 GAGGAGACGCG CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGCTGCT 120  
 GCGCTTGTCA CCATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180  
 55 ACAGCTGACA GTGCAAAAC TTACACTCTA ACTGATTACT TAAAAATAC TTATAGACTG 240  
 AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAT 300  
 ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360  
 GATGAGTTTG GACATCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420  
 TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTTAT 480  
 60 GATTAAATAA AAGGCGAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540  
 ACATGCTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGA ACAAATGACAT TTATGTTAAA 600  
 ATTGAACCAA ATTTACCAAG TTACAGAAATC ACATGGACGG GGAAGAAGA TATAATATAT 660  
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCCACTC TGCTCTGTGG 720  
 TGGTCTCCAA ACGGCACTTT TTTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780  
 65 ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA 840  
 TATCCAAAGG CAGGAGCTGT GAATCCAATC GTAAAGTTCT TTGTTGTAAG TACAGACTCT 900  
 CTGAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGCTTTC TATGTTGATA 960  
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAGAATTTTC TTTGCACTGG 1020  
 CTGAGGAGGA TTCAGAACTA TTCGGTCAAT GATATTGTG ACTATGATGA ATCCAGTGGG 1080  
 70 AGATGGAACCT GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140  
 AGATTTAGGC CTTCAGAAC CATTTTTACC CTGATGGTA ATAGCTTCTA CAAGATCATC 1200  
 AGCAATGAAG AAGGTTACAG ACACATTGCG TATTTCACAA TAGATAAAAA AGACTGCACA 1260  
 TTTATTACAA AAGGCACTCG GGAAGTCATC GGGATAGAAG CTCTAACAGG TGATTATCTA 1320  
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAATCCAA 1380  
 75 CTTATTGACT ATACAAAAGT GACATGCTCT AGTTGTGAGC TGAATCCOGA AAGGTGTCAG 1440  
 TACTATTCTG TGTCATTGAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCGGTCTCT 1500  
 GGTCTGCCCC TCTATCTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCTTGGA 1560  
 GACAAATCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAACTGGGAC 1620  
 TTTATTATTG TGAATGAAC AAAATTTTGG TATCAGATGA TCTTGCTTCC TCAATTTGAT 1680  
 80 AAATCCAGAA AATATCTCT ACTATTAGAT GTGTATGACG GCCCATGTAG TCAAAAAGCA 1740  
 GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800  
 GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860  
 AGAAGACTTG GAACATTGGA AGTTGAGAT CAAATTTGAAG CAGCCAGACA ATTTTCAAAA 1920  
 ATGGGATCTG TGGACAAACA ACGAATTGCA ATTTGGGGCT GGTCAATAGG AGGGTACGTA 1980  
 ACCTCAATGG TCCTGGGATC GGAAGTGGC GTGTTCAAGT GTGGAATAGC CGTGGCGCT 2040

5 GTATCCCGGT GGGAGTACTA TGA CT CAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100  
 CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAAAAATTTT 2160  
 AAACAGTTTG AGTACTCTCT TATTTCATGA ACAGCAGATG ATAAACGTTCA CTTTCAGCAG 2220  
 TCAGCTCAGA TCTCCAAGC CCGGTGCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280  
 ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340  
 AGCCACTTCA TAAACAAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400  
 AAGCTTATTA AAACCTATT TTGTTTTCAT TATCTCAAAA CTGCACGTGC AAGATGATGA 2460  
 10 TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520  
 ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCAACA GAATTATTACC TTACAGAAAGT 2580  
 TTGAATTATC CGGTCGGGTT TATTGTTTAA AAATCATTTC TGCATCAGCT GCTGAAACAA 2640  
 CAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700  
 TTCTAATCTG GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760  
 AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGATTAG GGAGAGAAGA TAGCAGGSCA 2820  
 TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTCAG CTCCCCTCGG 2880  
 15 AGAAGAGCTG TTCACCACGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT 2940  
 CAGGAATACA AATATCGAAA GCCTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000  
 AAAGAAATGT AAGGGAACCT GCCAGCAACG CAGCCCCCAG GTGCCAGTTA TGGCTATAGG 3060  
 TGCTACAAAA CACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATAA 3120  
 20 TACTGATGTT CCTAGTGAAG GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180  
 CTGTTAAAG ATGAAATAT TTGTATCACA AATCTTAACT TGAAGGAGTC TTGTCATCAA 3240  
 TTTTCTTAT TTCTTTCTT TGAGTGTCTT AATTAAAGA ATATTTTAA TCCTTGGAC 3300  
 TCATTTTAAA AAATGGAACA TAAATACAA TGTATGTAT TATTATTCCT ATCTACATA 3360  
 CTATGGAATT TCTCCAGTC ATTTAATAA TGTGCCTCA TTTTTC

25 A204 Protein sequence:  
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 30 Probeset Accession #: S79876  
 Protein Accession #: NP\_001926.1  
 Signal sequence: none found  
 Transmembrane domains: 6-28  
 DPPIV\_N\_term domain: 43-557  
 35 Peptidase\_S9 domain: 558-635  
 Cellular Localization: plasma membrane

40 1 11 21 31 41 51  
 MKTPWKILLG LLGAAALVTI ITVPVLLLNK GTDDATADSR KTYTLTDYLK NTRYRLKLYSL 60  
 RWISDHEVLY KQENNILVFN AEYGNSSVPL ENSTFDEFHG SINDYSISPD GQFILLEYN 120  
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVINSFP GHKLAYVMNN DIYVKIEPNL 180  
 PSYRITWGK EDIYNGITD WYEEEVFSA YSALWWSPNG TFLAYAQFND TEVPLIEYSF 240  
 45 YSDESLQYPK TURVPYKPKG AVNPTVKPFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300  
 CDVTWATQER ISLQWLRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360  
 EPHFTLDGNS FYKISNEEG YRHICYFQID KKDCTPITKG TWEVIGIEAL TSDYLYIYSN 420  
 EYKGMPPGGRN LYKIQIDYD KVTCLSCLEL PERCQYYSVS FSKEAKYQQL RCGSPGLPLY 480  
 TLHSSVNDRG LRVLEDNSAL DKMLQNVQMP SKKLDPIILN ETKFWYQML PHFEDKSKKY 540  
 50 PLLLDVYVAG CSQKADTVFR LHWATYLAST ENIIVASFDG RSGGYQGDKI MHAINRRLGT 600  
 FEVEDQIEAA RQFSKMGFVD NKRIAINGWS YGGYVTSMWL GSGSGVFKOG IAVAPVSRWB 660  
 YYDSVYTERY MGLPTPEDNL DRYRNSTVMS RAENFKQVEY LLINGTADDN VHFQQAQIS 720  
 KALVDVGVDV QAMWYDDEH GIASSTAHQH IYTHMSHFIX QCPSLP

55 A205 DNA SEQUENCE  
 Gene name: predicted exon  
 Unigene number: none found  
 Probeset Accession #: none found  
 Nucleic Acid Accession #: none found  
 60 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51  
 ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAATGACA ATGCCATCAG AGTTGACAAC 60  
 AGAAGTGTA TTAAGTGCG TGCTAACCG TGTTCCTGCG ATGAGGCAGA AAGTGAATCC 120  
 AGAAACCCCTC AGGAGCTCTG GATGGGCTG CTCCTCTGA TGGGGTCTCT AGAAGCATGT 180  
 GTGGAAATGA GGCCTCTGTC AGCTGTGTC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240  
 CAGCCACAC TGGATGCTA A

70 A206 Protein sequence:  
 Gene name: predicted exon  
 Unigene number: none found  
 Probeset Accession #: none found  
 75 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 46-68  
 Cellular Localization: not determined

80 1 11 21 31 41 51  
 MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHEASES RNPQELWMGL LLLMGVLEAC 60  
 VEMRPLSVWS LRDDKEQSPH QPTLDV

Gene name:	ESTs
Unigene number:	Hs.222886
Probeset Accession #:	AI672225
Nucleic Acid Accession #:	none found
Coding sequence:	1-462 (underlined sequences correspond to start and stop codons)

10	1	11	21	31	41	51	
	ATGCCAAATG	CTGAGTTAGA	AGCAAAGAGC	CTTGAAGACA	GTAATAGTTT	AAAAACTGCT	60
	CTCATACTTG	CTGTATGTTG	TGGATCAGCA	AATATAGTCA	GCCTCTCTCT	CTGACAAAAT	120
	ATTGATGTAT	CTTCTCAGAA	CTCGACAGCA	CGCCACAGAG	GTATGCTGTT	TGAGTCATC	180
15	ATCATGTGGA	CCAGTTTTGT	GGAAGACAA	TCTTCCATGG	GCTGGGGGAA	GCTAGAGAGT	240
	TTTATGCTTA	TTGAAGAAGA	AATGAAGAAG	CACGGAACTA	CTCATGTGGG	ATTCCCAGAT	300
	AACCTGACTA	ATGGTGGCGC	TGCTGGCAAT	GGTGATGATG	GATTAATTCC	TCCAAGGAAG	360
	AGCAGAGATC	CTGAAAGCCA	CGAATTTTCT	GACACTGAGA	ATGAAGAGTA	TCCACGGTTT	420
20	GTCAAAGATC	AGATAGTTGT	AGCATTCGGG	CGTTATTTCT	GA		

Gene name:	ESTs
Unigene number:	HS.222886
Probeset Accession #:	AI672225
Protein Accession #:	none found
Signal sequence:	none found
Transmembrane domains:	16-38
Cellular Localization:	not determined

30  
1 11 21 31 41 51  
| | | | |  
MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLEQN IDVSSQDLDR RPESMLFLVI 60  
35  
1MWTSFVEDN LSMGWGKLED FMAIEEMKK HGSTHVGPE NLINGAAAGN GDDGLIPPRK 120  
SRTPESQQFP DTENEYYHRP VKDQIVDMR RYF

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1  
Unigene number: Hs.23796  
Probeset Accession #: NM\_014253  
Nucleic Acid Accession #:          NM\_014253  
Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

45	1	11	21	31	41	51	
	GACTGCTTGC	ATTAAAGGAC	TTCTCATCC	TTTTTTCAT	GAAACTGAGC	TTGCTTAATC	60
	AGAGATGGAG	CAAACTGACT	GCAAAACCTTA	CCAGCTCTCTA	CCAAAGATCTA	AGCATGAAT	120
	GGATCTAGCT	TACACCAGTT	CTTCTGTAGT	GAGTGAAGAT	GGAAGAAAC	CAGACGATC	180
50	ATACAACTCC	AGGGAGACCC	TGCACGAGTA	TAACCAGGAG	CTGAGGATGA	ATTACAATAG	240
	CCAGAGTAGA	AAGAGGAAAG	AGTACGAAAA	ATTACTACTCA	GAGATGTGAAT	TCCTGTGAAC	300
	CTCTCAACT	CTGTGCTCTG	GACTACAAAC	AGACATGCAC	AGCGTTTCTC	GGCATGTGCTA	360
	CCAGCTAGAG	ATGGGATCTG	ATGTGGACAC	AGAGACAGAA	GGTGCTGCGCT	CACCTGACCA	420
	TGCCTAGA	ATGTGGATAA	GGGGAATTGA	ATTACAGACAT	AGTTCTCTGT	TGTGCGCGC	480
55	GGCCAACTCT	GCATTTCCT	TGACTGACAC	TGACCATGAA	AGGAAGTCTG	ATGGGGAAAA	540
	TGGTTTCAA	TTCTCTCTCT	TTTGTGTGA	CATGGGCGCT	CRACTCGGGT	CTACTCAAGA	600
	TGTGACAGC	AGCCCAACA	ACAGGTTTCT	CTTCAGACCC	CTCCACCGGT	CACCTCGCGC	660
	TTCTCATGCC	TGCACATGCT	CCAGGAAGCC	ACCCCTGTGA	GGGGATCTCT	TTACGAGAG	720
60	ATCAATGACT	ACCGCAGCG	AGCCGAGCC	AGCTCTCCA	GCTCCCCAA	CACGACCGCA	780
	GGATTTCATC	CATCTGCATA	ACAGCTGGGT	CCTGAAACGC	AACATACCAT	TGGAGACCG	840
	GCATTCTCTG	TTCAAACGAT	GATCTGGTCT	CTCTGCGATC	TTCACTGCGC	CCAGTCAAGA	900
	CTACCCCTTG	ACATCCAATA	CCGTGTATC	GGCCCTCCCC	AGGCGTCTTC	CTCGAAGCAC	960
	CTTTTCCCGA	CTCGCTTTTA	CTTTTAAACA	ACCTTACAAG	TGCTGCAACT	GGAAAGTGAC	1020
65	AGCAATTGAG	GCCATGCAA	TCACAGTAG	TTTGGCCTTG	TTACTAGCCT	ATGTGATTGC	1080
	AGTGCAATTT	TTGCGCCTGA	CTTGGCAGTT	GCAACCAAGT	GAAAGGACAT	TGTATGCAAA	1140
	TGGAGTTAGC	AAGGGGAACA	GGGGGACCGA	GTCCTATGGAC	ACTACTTACT	CTCCAATTGG	1200
	AGGAAGAAGT	TCTGATAAAT	CAGAGAAAAA	AGTGTTCAG	AAGGGACGGG	CGATAGACAC	1260
	TGGAGAGATT	GACATTTGGT	CACAGGTCA	CGAGACCAAT	CCACCTGTTT	TATTTCTGGC	1320
70	TTTCCGAGTT	ACTATCCACT	ATTCCAATAT	TCTGAGATT	AATATTTCTT	TGACCAAGAA	1380
	CTCTCTGCTG	GGAAATTTAT	GCAAGAAAA	CACTCCAAC	ACCATATCTC	AGTTTGATTT	1440
	TGTAAAAACT	ATGGATGGCA	AAGACTGGT	CRAAGCAGGAC	TCCAAGCGCT	CTGATGATAC	1500
	ACAGCACTCC	CTCGGAACC	TGATCTTAAC	TTGCGTTCAG	GAGACAGGTT	TCATAGAGTA	1560
	TATGGATCAA	GGACCTTGGT	ATCTGGGAT	TTACAAATGAT	GGAAAAAAGA	TGGAGCAAGT	1620
75	ATTCTGTGTA	ACTACAGCAA	TTGAATAAT	GGATGACTGT	TCAACAAATT	GCATGGGAAA	1680
	TGGAGAGTGT	ATCTCTGGCC	ATTGTCAATG	TTTCCAGAGA	TTCTTGGAAC	CTGACTGTGC	1740
	TAGAGATTCC	TGCGCTGTGC	TGTGTGGTGG	GAATGGAGAA	TACGAGAAAG	TACGACTGTGT	1800
	CTGCGCGCAT	GGCTGGGAAG	GGCCAGAGTG	TGACGTTCCG	GAAAGACAAT	GCATTGATCC	1860
	AACATGCTTT	GGCCACGGCA	CTGTCATCAT	GGGAGCTGCG	ATCTGTGTGC	AGGATACAAA	1920
	AGGTAGCAAT	TGCGAGGAAG	AGGACTGCCT	AGAACCAATG	TGTTCCAACC	CTGCGATCTG	1980
80	TGTAAAAGGA	GAATGTCAT	GTTCTACTGG	CTGGGGAGGA	GTTAACTGTG	AAACACCACT	2040
	TCCTGTATGT	CRAAGAGCAT	GCTCAGGACA	CGGAACTTTG	CTTCTGGAGC	CTTGGAGTATG	2100
	CAGCTGTGAT	CCCAAGTGGGA	CAGGATCTGA	CTGCTCAACA	GAGCTGTGTA	CCATGGAGTG	2160
	TGGTAGCCAT	GGAGTCTGCT	CAGAGGGAAT	TGCGAGTGT	GAAAGAGGCT	GGGTAGGACC	2220
	AACATGTGGG	GAAAGCTCCT	GTCATTCTGA	TTGTACTGAG	CATGGCCAA	GCAAGAGGCT	2280

	AAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
	AAATGGTTGG	CACGTGTGTG	GTCAAGGTGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTGAT	2460
5	GGAAATGCTT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTAACC	ACTGTGTGGA	2520
	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCTT	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCAITTCAGC	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAATTC	TCATTGGCAA	GGACAGTACT	CATGTCAITC	CTCCTGAGGT	2700
	GTCAITTCAG	AGCAGGCGTG	CTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
10	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCACAGT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAGCTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CCTTTCTCTG	CTGAGAAGAG	AACACTCTGG	TTGCCCTTGA	ATCAGTTTAT	2940
	TGTGGTAGAG	AAAGTCACCA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCTC	GCGATATCTC	3000
	CAACTTTATC	AGCCCAAACC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
15	CTGTCCAGAG	AGGGGAACCTA	TTGTTCTGTA	GCTGCAGGTT	GTACAGGAGG	AAATTCCTCAT	3120
	TCCTCCAGC	TTTGTGAGGC	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAAACCT	3180
	GCTACGGATC	CTTCTGACAC	ATTCAAGAT	TCCCGTAGGC	ATGATAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGCTTA	3300
	CACATTGTCT	TGGAACAAGA	CCGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
20	TTTGGTATCT	TGCGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTCTCT	GGGAGCAAAG	3420
	GACAGTGGTT	TTCAAGGTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAAGTGG	AATCATACT	AAAGGGAATG	GAGAAAAAT	3540
	GTTCATTTCC	CAGCAGCCCC	CAGTCATATC	AACATAATG	GGTAATGGAC	ACCAAAGGAG	3600
	TGTAGCTGCG	ACCAACTGCA	ATGGCCCGAC	CCACAACAAC	AAACTCTTTG	CTCCTGTGCG	3660
25	CTTAGCTTCT	GGCCCTGATG	GCAGTGTGTA	TGTTGGGAC	TTCAATTTTG	TAAGGAGAAT	3720
	ATTTCCCTCG	GGAAACCTCG	TTAGTATTTT	GGAAATTAAG	ACAAGTCTGT	CTCACAATA	3780
	CTATCTGGCT	TGGAACCTCG	TGCTGAAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTACAAG	TTGAAATCTC	TTGTGGAGAC	GAAAGATCTG	TCCAAGAATT	TTGAAGTGGT	3900
	GGCAGGAAGT	GGTGATCAGT	GCCTTCCCTT	TGACCAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
30	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTGATAGGCG	ATGGATTAT	4020
	TTACTTTGTG	GATGGGACTA	TGATTCGCAA	AATGATGAG	AATGCTGTGA	TCACAACCTG	4080
	AATCGGCTCA	AATGGCTGCA	CTTCCACACA	ACCACTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTCAGTG	GATTAGAGT	GGCCAACAGA	CCTTGCGATA	AATCTATG	ACAATTCATT	4200
	GTATGTCTGT	GATAACAACA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTGCGATCAT	4260
35	CCAGGAGCGC	CCCAATCACT	GCCAGGTGCC	AGGCATCGAT	CATTTCCTGG	TCAGCAAGGT	4320
	AGCAATTCAC	TCCACTCTAG	AGTCAGOGAG	GGCCATCAGT	GTCTCCCA	GCGGGCTGCT	4380
	CTTCATAGCT	GAACACAGAG	AGAGGAAAGT	AAACCGCATT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATCGCTG	GTGCCCCAC	TGACTGTGAC	TGCAAAATTG	ATCCAAACTG	4500
	TGACTGTGTT	TCAGGTGATG	GTGGCTATGC	CAAAGATGCA	AAGATGAAAG	CCCTTCTCTC	4560
40	CTTAGCAGTG	TGCGCTGATG	GAACCTCTA	TGTGGCAGAC	CTCGAAATG	TTGGAATTGG	4620
	TACCATCAGC	AGGAACCAAG	CCCACTGAA	TGACATGAAC	ATTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACGTGTTT	ATAACTTCAC	CTACAATTCT	GARGGTGACT	TGGCGCGCAT	4740
	GATAACAAGG	GACTATGTTT	ATAACTTCAC	CTACAATTCT	GARGGTGACT	TGGCGCGCAT	4800
	TACCAGCAGC	AATGGCAATT	CAGTGACAT	TCGCCGTGAT	GCAGGCGGAA	TGCCGCTATG	4860
45	GCCTGTGGTG	CCTGGGCGAC	AAGTATACCT	GCTGACTATA	AGCAGCAATG	GAGTCTGAA	4920
	AAGAGTGTC	GCCCAAGGCT	ATAATCCGGC	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCGTGGTACC	AAAGTAAAG	AAATGGATG	GACAAACGTT	TATGAGTATG	ACCCGAGGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTGACG	AGCTTCCACA	GTGACCTGGA	5100
	GAAGCTGACA	AAAGTGGAGC	TAGATACCTT	CAACCGTGAA	AATGTCTCTA	TGTCAACCAA	5160
50	CTTGAACGCA	ACTAGTACCA	TATATATTTT	AAAACAAGAA	AATACTCAAA	GTACCTATCG	5220
	GGTGAATCCA	GATGGTTCCC	TGCGTGTGAC	TTTTGCCAGC	GGGATGGAGA	TGCGGCTCAG	5280
	CTCAGAGCCC	CACATCACTG	CAGGGGCGAGT	CAACCTTACC	CTGGGCAAT	GCAACATCTC	5340
	ATTGCCCGGA	GAGCACAATG	CAAACTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
	AGGCAATGTT	TGCGCTTTTG	AAAGGAGGCT	GAGGGCCAC	AACAGAAACC	TACTCTCCAT	5460
55	AGATTTTGAT	CATATAACCC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AATTCACCTT	5520
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	TGAAGTCAAC	ATCATATTT	CACCTTCGGG	ATTGGTGACG	TTTATTCAAA	GAGGAAACGTG	5640
	GAATGAAAAA	ATGGAATATG	ACCAGAGTGG	GAAATATTAT	TCAAGAACTT	GGGCTGATGG	5700
	GAAAAATTGG	AGCTATACCT	ACTTAGAAAA	ATCTGTGATG	CTTCTCTTAC	ACAGCCAGCG	5760
60	GGGTTACATC	TTTGAGTATG	ACCAATCAGA	TTGCCCTGCT	TCAGTTACCA	TGCCATGAT	5820
	GGTGGGCCAC	AGCTTACAAA	CCATGCTTTC	AGTGGGCTAC	TACCGTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAAG	CTATAGTCGA	GATGGCCGAT	TGCTACAGAC	5940
	CCTGCATCTG	GGGACAGGGC	GCAGAGTCTT	ATACAAGTAC	ACCAAGCAAG	CAAGGCTTTC	6000
	TGAGGTTCTC	TATGATACCA	CTCAGGTCAC	ATTAACATAT	GAAGAGTCTT	CTGAGGTGAT	6060
65	TAAGACAAATA	CACCTGATGC	ATGACGGATT	CATCTGCACA	ATCAGATACA	GGCAACAGG	6120
	ACCTCTTATT	GGAGCCGAGA	TTTTAGATT	CAGTGAAGAA	GGCCTTGTGA	ATGCAGCGTT	6180
	GCATACAGC	TACAACAATT	TCCGAGTCAC	AAGCATGCAA	GCTGTAATCA	ATGAAACCCC	6240
	TTTGCCCTATA	GATCTTTTACC	GATATGTTGA	TGCTCTGGC	AGAACAGAGC	AGTTTGGAAA	6300
	ATTCAAGTGA	ATTAAATTAG	ATTAAATCA	GGTCATAACT	ACTACAGTGA	TGAAACACAC	6360
70	CAAAATCTTC	AGTGCCAATG	GACAAGTCAT	TGAAGTCCAA	TATGAATCC	TAAAGGCAAT	6420
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	GGTAGGAGTA	GATGCAATA	TAAACAGGTA	CTTCTATGAA	TACGATGCTG	ATGGGCAACT	6540
	TCAGACTGTT	TCTGTAATG	ACAAACCCA	GTGGCGTTAT	AGTTACGATC	TGAATGGAGA	6600
	CATCAACCTC	TTAAGCCATG	GGAAGAGTGC	TGCTCTTACT	CCTCTCGAT	ATGACCTCG	6660
75	AGACCGCATC	ACCAGATTAG	GAGAAATTC	GTATAAAATG	GATGAAGATG	GCTTCTGTAG	6720
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	TAAGGCTTCT	GGCTGGAGCT	TGCAGTATTA	CTATGATGGG	CTTGGGCGAC	GTGTCGCGAG	6840
	TAAGTCCAGC	CTAGGGCAGC	ACCTTCAGTT	CTTTGTGAC	GCGACCGCGA	ACCCCATAG	6900
	AGTTACTCAT	TTGTACAACC	ACCAAGCTC	GGAGATTACA	TCTCTGTATT	ATGATCTCCA	6960
80	AGGTCACTTT	ATTGCCATGG	AGTTAAGCAG	TGGTGAAGAA	TATTATGTAG	CCTGTGATAA	7020
	TACAGGTACC	CCATGAGCTG	TGTTAGCAG	CCGAGGTGAG	GTCAATAAAG	AGATACCTATA	7080
	CACACCTTAT	GGGATATCT	ATCATGACAC	TTACCTGAC	TTTCAGGTCA	TAATTGGTTT	7140
	TCATGGAGGA	CTCTATGATT	TCCTTACTAA	ATTAGTGCAC	CTGGGGCAA	GGGATTATGA	7200
	TGTTGTGCT	GGCAGATGGA	CAACGGCCTA	TCATCACA	TGGAACAGT	TGAACCTCT	7260
	TCCTAAACCA	TTCAACCTCT	ACTCCTTTGA	AAATAACTAC	CCAGTTGGCA	AAATTCAAGA	7320

	TGTTGCAAG	TATACCACAG	ACATCAGAAG	TTGGTTGGAG	CTATTTGGTT	TCCAATTACA	7380
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	TCTACGGCTT	CAGACAAAAA	CTCAAGAGTG	GGATCCTGGA	AAGACTATCC	TGGGCATTCA	7500
5	GTGTGAACCT	CAGAAACAGC	TCAGGAATTT	CATTTCCTTG	GACCAACTAC	CTATGACTCC	7560
	CCGATACAA	TATGGACGGT	GCCTTGAAGG	AGGGAAGCAA	CCAAGGTTTG	CTGCTGTCCC	7620
	TTCTGTTTTT	GGCAAGGTA	TAAAAATTTG	CATCAAGGAT	GGCATAGTAA	CAGCTGATAT	7680
	TATAGGAGTA	GCCATGAAG	ATAGCAGGCG	GCTTGCTGCC	ATTCTCAATA	ATGCCCATTA	7740
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15	GGAAAAGCAG	CAGCTTTTGA	GCACCTGGCG	GGTACAAGGT	TACGATGGGT	ATTTTGTITT	8160
	GTCTGTGAG	CAGTATTTAG	AACTTTCTGA	CAGTGCCAAT	AATATTCAC	TTATGAGACA	8220
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	GTITTTAAAA	CATAAAATGG	TTTATTGTAT	TGGTTTTCTA	GATCAGAACT	CTGTATATGT	8340
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	TTGTGAGAG	CAGTTTCATC	CTTAACCTGT	GGCAGAACTT	ACGGGCTATT	TGAATAGGTT	8640
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	TGTGTAAC	AGACTGTATA	GCCGCTATTT	GCTCGTGTGT	ACATGATACC	AAAGCAGCTG	8940
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30	GCTGTATTGG	TATCATGTAA	ACATAGCTTT	TATTAACCTG	GGTAGGAATT	TCTCATTTAT	9060
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	AATCTCTAGG	AATCCTCGAG	TAAAACAAGC	CCCTTGGTGA	GCTGGAAGAT	TTGTGCCCAG	9720
	TGACAAAGAG	TGCAATTTGA	AAATGCTGTG	TAAATGTAA	TTACACACAA	TGAAATATCA	9780
	TGACAGCACA	ATGTGGCCCG	TAGAAAATTC	CCCTGAGCCA	GCTTCTGCAC	TTTCATCACC	9840
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	TTGAAATAT	GCAAAGTCAT	AAGCTCATGT	TAAGGTTTTT	CAAGAGTCTG	CCTCCTACTA	10020
	CACAAAGGAA	AGCAAGGCAA	AGGAAATGAC	CCTGGCAAA	AGTAGGGAAG	GGTGTATTCA	10080
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50	TAAATCCATC	TAAATTCATA	TTATTGGGTT	TTTTCTGAAT	CAGGCTGTGA	TTAATGGTAC	10260
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	GSAAATGCAC	TTTTTATTAC	TTACAGCTGT	GGTTTTAATA	CTGCTTGAA	CTATTATTAT	10740
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	CCTGTTTCT	TGAAGAAAT	CACATACACA	TAGCTGACCT	GACTAGTACT	TCAGCTCTTC	11940
	CACAGCCTTC	TATAAAGGTT	CTTCTTCTG	CAAGAAAAAC	AAAAACAAAC	AAAAACAAAC	12000
80	AAAAAAAAC	AAAAAAGCG	CAAAAAACAA	AAAAACAAA	AAAAGCAAG	TAAATTTTAA	12060
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	AGTTGTCATC	TTACATTATT	TGTCAAAGGA	AATGTGTTG	GCAATTAAAA	ATCTTCTCTT	12300
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AAAAATATT TACTTGATG AATCATGACA ACGTCTAAAT CTTTACTATT CTCTCGCAA 12420  
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**A210 Protein sequence:**

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1

Unigene number: Hs.23796

Probeset Accession #: NM\_014253

Protein Accession #: NP\_055068

Signal sequence: none found

Transmembrane domains: 318-340

Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MEQTDCKPYQ PLPKVKHEMD LAYTSSSDES EDGRKPRQSY NSRETLHEYN QELRMNYSQ 60  
 SRKRKEVEKS TQEMEFCEFS HTLCSGYQTD MHSVSRHGYQ LEMGSDVDTE TEGAASPDHA 120  
 LRMWIRGMKS EHSSCLSSRA NSALS LTDITD HERKSDGENG FKPSPVCCDM EAQAGSTQDV 180  
 QSSPHNQFTF RPLPPPPPPP HACTCARKPP PAADSLQRRS MTRSQPSPA APAPTSTQD 240  
 SVHLHNSWVL NSNIPLETRH SLFKHSGSGS AIFSAASQNY PLTSNTVYSP PPRPLPRSTF 300  
 SRPAFTFNKP YRCNCWKCTA LSATAITVTL ALLLAYVIAV HLFGLTQWLQ FVEGELYANG 360  
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 HSPRNLILTS LQETGFIEYM DQGPWYLAFY NDGKMEQVFP VLTIAEIMD DCSTNCGNG 540  
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 PDHITRTGKI YDHRKFTLR ILVDQTGRPI LWSFVSRYNE VNITYSPSGL VTFIQRGTWN 1860  
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 RGNDFEYNS NGLLQKAYNK ASGWTQVYYY DGLGRRVASK SSLQQLHQP VDATANPIRV 2280  
 THLYNHTSSE ITSLYYDLQ HLIAMELSSG EEEYVACDNT GTPLAVFSSR GQVIKEILYT 2340  
 PYGDIYHDTY PDFQVIGFH GGLYDFLTKL VHLGQRDYDV VAGRWTAYH HIWKQLNLLP 2400  
 KPNLYSPEN PVPVGIQDV AKYTTDIRSW LELPGFQLHN VLPGFPPKPEL ENLELYTELL 2460  
 RLQTKQEWAD KDGIVTADII GVANEDSRRL AAILNAHYL ENLHFTIEGR DTHYFIKLS 2520  
 VFGKGIKFAI KDGIVTADII GVANEDSRRL AAILNAHYL ENLHFTIEGR DTHYFIKLS 2580  
 LEEDLVLIQN TGGRRILENG VNVTVSQMST LLNGRTRRFA DIQLQHGCALC FNIRYGTIVE 2640  
 EEKNHVLEIA QRRAVAQAWT KEQRRLQEGE EGIRAWTEGE KQQLLSTGRV QYDGYFVLS 2700  
 VEQYLELSDS ANNIHFMRQS EIGRR

**A211 DNA SEQUENCE:**

Gene name: Solute carrier family 26, member 4

Unigene number: Hs.159275

Probeset Accession #: AF030880

Nucleic Acid Accession #: NM\_000441

Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTCAGCCTTC CCGGTTCCGG AAAGGGAAG AATGCAGGAG GGGTAGGATT TCTTCTCTGA 60  
 TAGGATCGGT TGGGAAAGAC CGCAGCCTGT GTGTGTCTTT CCCCCTGACC AAGGTGCTCG 120  
 TTGCTCCGTA AATAAAACGT CCCACTGCCT TCTGAGAGCG CATATAAGGC AGCGGAAGGG 180  
 TAGTCCGCGG GGCATTCCGG CGGGGGCGCG AGCAGAGACA GGTCTATGCA GCGCCAGGCG 240  
 GCAGGTGCGA GCCGCCGCG AGCTCCCGAGT ACAGCTGCAG CTACATGTGT TCGCGGCGCG 300  
 TCTACAGCGA GCTCGCTTTC CAGCAACAGC ACGAGCGCGC CTGTCAGGAG CGCAAGAGCG 360

5 TGCGGGAGAG CCTGGCCAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCTTT GGTGTGCTAA 420  
 AGACTCTTGT GCCCATCTTG GAGTGGCTCC CCAAAATACCG AGTCAAGGAA TGGCTGCTTA 480  
 GTGAGGTCAT TTGGGGAGTT AGTACTGGGC TAGTGGCCAC GCTCAAGGG ATGGCATATG 540  
 CCTACTAGC TGCAGTTCTT GTCGATATG GTCTCTACTC TGCTTTTTC CCTATCCTGA 600  
 CATACTTTAT CTITGGAACA TCAAGACATA TCTCAGTTGG ACCTTTTCCA GTGGTGAGTT 660  
 TAATGGTGGG ATCTGTGTGT CTGAGCATGG CCCCCGACGA ACACTTTCTC GTATCCAGCA 720  
 GCAATGGAAC TGTATTAAAT ACTACTATGA TAGACACTGC AGCTAGAGAT ACAGCTAGAG 780  
 TCCTGATTGC CAGTGCCCTG ACTCTGCTGG TTGGAATTAT ACAGTTGATA TTTGGTGGCT 840  
 10 TGCAGATTGG ATTCCATAGTG AGGTACTTGG CAGATCCTTT GGTGTGGTGG TCAACACAG 900  
 CTGCTGCCCT CCAAGTGCTG GTCTCACAGC TAAAGATTGT CCTCAATGTT TCAACCAAAA 960  
 ACTACAATGG AGTTCCTCTC ATTATCTATA CGCTGGTTGA GATTTTTCAA AATATTGGTG 1020  
 ATACCAATCT TGCTGATTTC ACTGCTGGAT TGCTCACCAT TGCTGCTGT ATGGCAGTTA 1080  
 AGGAATTAAT TGATCGTTT AGACACAAAA TCCAGTCCC TATTCTATA GAAGTAATTG 1140  
 15 TGACGATAAT TGCTACTGCC ATTTCCATATG GAGCCAACTT GGAAAAAAAT TACAATGCTG 1200  
 GCATTGTAA ATCCATCCCA AGGGGGTTTT TGCTCCTGA ACTTCCACCT GTGAGCTTGT 1260  
 TCTGGGAGG TCTGGCTGCA TCATTTTCCA TCGCTGTGGT GGCTTATGCT ATTGCAGTGT 1320  
 CAGTAGGAAA AGTATATGCC ACCAAGTATG ATTACACCAT CGATGGGAAC CAGGAATTCA 1380  
 TTGCTTTGGG GATCAGCAAC ATCTTCTCAG GATTCCTCTC TTGTTTGTG GCCCACTG 1440  
 20 CTCTTTCCCG CAGGCGCGTC CAGGAGAGCA CTGGAGGAAA GACACAGGTT GCTGGCATCA 1500  
 TCTCTGCTGC GATTGTGATG ATCGCCATTTC TTGCCCCGGG GAAGCTTCTG GAACCTTTCG 1560  
 AGAAGTCGGT GTTGGCAGCT GTTGTAAATG CCAACCTGAA AGGGATGTTT ATGCAGCTGT 1620  
 GTGACATTCC TCGTCTGTGG AGACAGAATA AGATTGATGC TGTATCTGG GTGTTTACGT 1680  
 GTATAGTGTG CATCGTTCTG GGGCTGGATC TCGGTTTACT AGCTGGCCTT ATATTGGAC 1740  
 25 TGTGACTGT GGTCTGTAGA GTTCAGTTTC CTCTTGGAA TGGCCTTGA AGCATCCCTA 1800  
 GCACAGATAT CTACAAAAGT ACCAAGAATT ACAAAAACAT TGAAGAACCT CAAGGAGTGA 1860  
 AGATTCTTAG ATTTTCCAGT CCTATTTTCT ATGGCAATGT CGATGGTTTT AAAAAATGTA 1920  
 TCAAGTCCAG AGTTGGATTG GATGCCATTA GAGTATATAA TAAAGGCTG AAAGCGCTGA 1980  
 GGAATAATCA GAAACTAATG AAAAGTGGAC AATTAAGAGC AACAAGAAT GGCATCATAA 2040  
 30 GTGATGCTGT TTCAACAAAT AATGCTTTTG AGCCTGATGA GGATATTGAA GATCTGGAGG 2100  
 AACTTGATAT CCCAACCAAG GAAATAGAGA TTCAAGTGGG TTGGAACCTC GAGCTTCCAG 2160  
 TCAAGTGAA CGTTCCCAAA GTGCCAATCC ATAGCCTTGT GCTTGACTGT GGAGCTATAT 2220  
 CTCTCTGGA CGTTGTGTGA GTGAGATCAC TGCGGGTGAT TGTCAAAGAA TTCCAAAGAA 2280  
 TTGATGTGAA TGTGTATTCT GCATCACTTC AAGATTATGT GATAGAAAAG CTGAGCAAT 2340  
 35 GCGGGTCTT TGACGACAC ATTAGAAAG ACACATTCTT TTTGACGGTC CATGATGCTA 2400  
 TACTCTATCT ACAGAACCAA GTGAAATCTC AAGAGGGTCA AGGTTCCATT TTAGAAACGA 2460  
 TCACCTCTAT TCAAGATTGT AAAGATACCC TTGAATTAAT AGAAACAGAG CTGACGGGAG 2520  
 AAGAATCTGA TGTCCAGGAT GAGGCTATGC GTACACTTGC ATCCTGAAAG TGGGTTCCGG 2580  
 AGGTCTCTAT GAGCAAGGAA TACAGACAA AACTTCTCTA ATGCATTGAC TATTCTTCTA 2640  
 40 GACTCAAAAC ACTCATCTTT TTTTCTATTA AGCCATTGAA AGAGAAGCAC TAAGACTGCT 2700  
 TCTAGGCTTT ATTTATAAAA TAAACACCTT ATCCCTAACA TGGGCAAAAT GGCTAGAATT 2760  
 ATTCAGACGA TTGGCAGGTC TCCAGGGTAA GCTGGTGTTA TAATACGCTG CTGATCTACA 2820  
 TCACAGATTG GCTAATAATG TTCAAGTGGG CCGTGGCATA TCTCTGTCA GTTAGAGTGA 2880  
 GTGCTGACCC AACAGCCTCT GTGGTCAAGC GAGTCAOGAA TGATTATCA TAAAGAAAAA 2940  
 45 TCAGTTTTTG ACTGACCTGG ATATCCATGA GCTGCACCTA TCACCATGTA AGGTCACATT 3000  
 TAGTAATATG TGAATAAAA TGATTAAATG ATTTATCAAT AAAAGCCTTT GAAAATACTT 3060  
 TGGATAATAA ATTTGAGTTT TAAAAATGCA AATTTGCTTA GTATCTAATA ATGAAGTGT 3120  
 ATTACATATA GCGGGAATTG AGGATCTCTT TGATCCTGGA AATGGTTTAC CTAAAAAGCTA 3180  
 CAGAACCAAG CCAATATATT TTGAATATT GATGCAGACA AATGAAATAA TAAAGAGATT 3240  
 50 TTCATGGTTT ATAAAAATCT TTTTGTATAT GATAATAATC ATGATCACA CTGAGATCAA 3300  
 AAAAAATAT GACAGATTAT TTTTGTAAA AATGCAGTTT TAATTATCTT AGCTATATGA 3360  
 AATGATCAT ATCTGGAGGC ATGTATAGGT ATGATCTGTG TAAATCTGA CATAAAAAACA 3420  
 GTGCTATTCT GAGTGAAAA TTTTGTGATG TGCTTACATA ACCATGGTGA TTAATATGAG 3480  
 TTTATATTTT TTCTCAAAA TTTTAGCAGT GTGTAAAGTA AGTAATCTTT AACTGAACTC 3540  
 55 TGACCACTTA AAAAAAATC TAAAAATTGA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600  
 ATTTTAAAG ACAAGCATT CTAAATGAAC TCAATATAAA AACATTCAAT TGGAAATGTAC 3660  
 ATACTGAAA ATACAGGTTT TTTTGACCAA AAGTTTTTAT ATCTTTTCTT TTTATTATT 3720  
 TTTTCTCTAA GTGCCAACAA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTTGGG 3780  
 GACTTTTCCC ATATATTCTA CACTGGAGTG AATGAAGTTG TACTTCAATT CTAGAGAAAA 3840  
 60 GTTATACCCA GGTCCCAAT TGAGAAATGTC TTGCTTGATT GAAAACGACA TCATCCCTTG 3900  
 GTATACTCCA GGGATTGGTT TCAGGACCCC TGCAATTACC AAAATTGTG CACACTCAAG 3960  
 TCTCGACGTC ACCCTGCCT AAAGATAGAA TGGCTTCTCT GTTTTCTTC TGAATACAA 4020  
 CCAGAACCAA TGTGTCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTTAAT 4080  
 CCTGAATCT GGTGTAAAT CTGGTTACAG CATACTAGG ATTATAATGC TGCCTCAATT 4140  
 65 TCACAGCACT ACTTGCTTAT ATTGACAACA AATCATCTCG CTAAAGAGTG AATGTAGGCC 4200  
 AGGCGCGGTG GCTCATGCCT GTAATCCAG CACTTTGGGA GCGCGAGCG GGTGGATCAC 4260  
 GAGGTCAGGA GATCGAGACC ATCTGGCTA ACATGGTAAA ACCCGTCTC TACTAAAAAT 4320  
 AGAAAAAAG AAATTAGCCT AGCGTGGTGG CTGCGGGCG CCGTGTAGTC CAGCTATTG 4380  
 GGAGGCTAAG GCAGGAGAA GCGGTGAACC CGGGAGGCG AGCTTGCACT GAGCGAGGT 4440  
 70 CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATA 4500  
 AAAAAAATA AGAGTGAATG TAATAGTCTT GCAGAAATG AATGAATACC TTTGTTCAAT 4560  
 AAGGAAATA TGCACTGCTC ACTTTTTGA AGGAAATGCC AAGTTACGT TTTACAACA 4620  
 GGCAGAGATT TGTAAATCT GGGTTCAATT GTGATGACAT AAGTCAGCAA ACTGCGGGAA 4680  
 TACTGTCTCT TGTGTGATT TTGTGAATAG TAAGCATAAT TTTAGTTTG TATTATCAAT 4740  
 75 GAAAAATTC CTGAAATTA AAGCTGCCCT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800  
 TCCAGTATTG TATATGAGT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAATA 4860  
 TTTGCACACA TTTAAAAATA AATGTAAAGT TTGCTTTTAA ACTACTCGGA TGTGCTCTT 4920  
 CTGAACAAAA

**A212 Protein sequence:**

Gene name: Solute carrier family 26, member 4  
 Unigene number: Hs.159275  
 Probeset Accession #: AF030880  
 Protein Accession #: O43511  
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,  
347-369, 386-408, 420-442, 448-470, 486-508  
Cellular Localization: plasma membrane

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1	11	21	31	41	51	
MAAPGGRSEP	PQLPEYSCSY	MVSRPVYSEL	AFQQQHERRL	QERKTLRESL	AKCCSCSRKR	60
AFGLVKTLPV	ILEWLPKYRV	KEWLLSDVIS	GVSTGLVATL	QGMAYALLAA	VPVGYGLYSA	120
FFPILTYTIF	GTSRHISVGP	FPVVSIMVGS	VVLSMAPDEH	FLVSSSNGTV	LNTMTIDTAA	180
RDTRVLIAS	ALTLVLVGIQ	LIFGGLQIGF	IVRYLADPLV	GGFTTAAAFQ	VLVSQKLKIVL	240
NVSTKNYNGV	LSIIYTLVEI	FQNIQDNLIA	DFTAGLLTIV	VCMAVKELND	RFRHKIPVPI	300
PIEVITVITA	TAISYGANLE	KNYNAGIVKS	IPRGFLPEPEL	PPVSLFSEML	AASPSIAVVA	360
YAIASVGVKV	YATKYDYTID	GNQEFIAFGI	SNIFSGFFSC	FVATTALSRT	AVQESTGGKT	420
QVAGIISAAI	VMAILALGK	LLEPLQKSVL	AAVVIANLKG	MFMLCDIPR	LWRQNKIDAV	480
IWFTTCIVSI	ILGLDLGLLA	GLIFGLLTVV	LRVQFPWNKG	LGSIPSTDYI	KSTKNYKNIE	540
EPQGVKILRF	SSPIFYGNVD	GPKKCIKSTV	GFDAIRVYNK	RLKALRKIQK	LIKSGQLRAT	600
KNGIISDAVS	TNNAPEPDED	IEDLEELDIP	TKIEIQVDW	NSELPVKVNV	PKVPIHSLVL	660
DCAISFLDV	VGVRSLRVIV	KEFQRIDVNV	YFASLQDYVI	EKLEQCGFFD	DNIRKDTFFL	720
TVHDAILYLQ	NQVKSQEGQG	SILETITLIQ	DCKDTLELIE	TELTEELDV	QDEAMRTLAS	780

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**A213 DNA SEQUENCE:**  
 Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
 Unigene number: Hs.98280  
 Probeset Accession #: AA418000  
 Nucleic Acid Accession #: NM\_021614  
 Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51	
CGGGGGCAGC	AGCCCATGCC	TCCGGTGCAA	CAGCTGCGCC	TCCTCCGGTG	CCCCGGCGGC	60
GGGGGGCGGA	GATAACCTGT	CCCTGCTGCT	CCGCACTCC	TCGCCCGCGC	GCGCCTTCOG	120
GACCCGCAAC	TCTCGCGCGC	TGTGCGGCTC	GTCTGCTGCT	TGCTGCTGCT	GCTCGCTCGC	180
CCGGGGCAGC	CAGCTCAATG	TGAGCGAGCT	GACGCGGTCC	AGCCATGCCA	GTGCGCTCCG	240
GCAGCAGTAC	GCGCAGCAGT	CCGCGCAGCA	GTCGCGGTCC	GCCTCCCACT	ACCACCACTG	300
CCACAGCCTG	CAGCCCGCGC	CCAGCCCCAC	GGGCAGCCTC	GGCAGTCTGG	GCTCCGCGCC	360
CCCGCTCTCG	CACCAACACC	ACCACCCGCA	CCCGGCGCAC	CACCAAGACC	ACCAGCCCCA	420
GCGCGCGCGC	GAGAGCAACG	CCTTCAACGA	AATAGCCATG	AGCAGCTGCA	GGTACAAACG	480
GGGCGTCAAT	CGGCGGCTCA	GCAACTTGAG	CGCGTCCCGC	CGGAACCTCC	ACGAGATGGA	540
CTCAGAGGCG	CAGCCCCCTG	AGCCCCCGCG	GTCTGTGCGA	GGAGGTGGCG	GCGGTCCTTC	600
CCCGTCTGCA	GACGCTGCGC	CCGCGCGCGC	TGTTTCGTCC	TCAGCCCCCG	AGATCGTGGT	660
GTCTAAGCCC	GAGCACAAAC	ACTCCAACAA	CCTGGGCGTC	TATGGAACCG	GCGGCGGAGG	720
GAGCACTGGA	GGAGCGGCGC	GCGGTGGAGG	GAGCGGGCAC	GGCAGCAGCA	GTGGCACCAC	780
GTCCAGCAAA	AAGAAAAACC	AGAACATCGG	CTACAAGCTG	GGCCACCGGC	GCGCCCTGTT	840
CGAAAAGCGC	AAGCGGCTCA	GCGACTACGC	GCTCATCTTC	GGCATGTTCC	GCATCGTGGT	900
CATGGTCAAT	GAGACCGAGC	TGTCGTGGGG	CGCCTACGAC	AAGGCGTCCG	TGTATTCCCT	960
AGCTCTGAAA	TGCCTTATCA	GTCTCTCCAC	GATCATCTCG	CTCGGTCTGA	TCATCGTGTA	1020
CCAAGCCAGG	GAAATACAGT	TGTTTATGTT	GGACAATGGA	GCAGATGACT	GGAGAATAGC	1080
CATGACTTAT	GAGCGTATTT	TCTTATCTCT	CTTGGAATA	CTGGTGTGTG	CTATTCTATC	1140
CATACCTGGG	AATTATACAT	TCACATGGAC	GGCCCGGCTT	GCCTTCTCCT	ATGCCCCATC	1200
CACAACCAAC	GCTGATGGGG	ATATTATTTT	ATCTATACCA	ATGTTCTTAA	GACTCTATCT	1260
GATTGCCAGA	GTCATGCTTT	TACATAGCAA	ACTTTTCACT	GATGCCTCCT	CTAGAAGCAT	1320
TGGAGCACTT	AATAGATATA	ACTTCAATAC	ACGTTTGTGT	ATGAAGACTT	TAATGACTAT	1380
ATGCCCAGGA	ACTGTACTCT	TGGTTTTTAG	TATCTCATTA	TGGATAATTG	CCGCATGGAC	1440
TGTCCGAGCT	TGTGAAAGGT	ACCATGATCA	ACAGGATGTT	ACTAGCAACT	TCCTTGGAGC	1500
GATGTGGTTG	ATATCAATAA	CTTTTCTCTC	CATTGGTTAT	GGTGACATGG	TACCTAACAC	1560
ATACTGTGGA	AAAGGAGTCT	GCTTACTTAC	TGGAATTATG	GGTGCTGGTT	GCACAGCCCT	1620
GGTGGTAGCT	GTAGTGGCAA	GGAAAGCTAGA	ACTTACCAAA	GCAGAAAAAC	ACGTGCACAA	1680
TTTCATGATG	GATACTCAGC	TGACTAAAAG	AGTAAAAAAT	GCAGCTGCCA	ATGTACTCAG	1740
GGAAACATGG	CTAATTTACA	AAATACAAA	GCTAGTGAAA	AAGATAGATC	ATGCAAAAGT	1800
AAGAAAAACAT	CAACGAAAAT	TCTTGCAAGC	TATTCATCAA	TTAAGAAAGT	TAAAAATGGA	1860
GCAGAGGAAA	CTGAATGACC	AAGCAACAC	TTTGGTGGAC	TTGGCAAAGA	CCCAGAACAT	1920
CATGTATGAT	ATGATTTCTG	ACTTAAACGA	AAGGAGTGAA	GACTTCGAGA	AGAGGATTGT	1980
TACCTTGGAA	ACAAAACCTAG	AGACTTTGAT	TGGTAGCATC	CACGCCCTCC	CTGGGCTCAT	2040
AAGCCAGACC	ATCAGGCAGC	AGCAGAGAGA	TTTCATTGAG	GCTCAGATGG	AGAGCTACGA	2100
CAAGCACGTC	ACTTACAATG	CTGAGCGGTC	COGTCCTCG	TCCAGGAGGC	GGCGGTCTCT	2160
TTCCACAGCA	CCACCAACTT	CATCAGAGAG	TAGCTAGAAG	AGAATAAGTT	AACCACAAAA	2220
TAAGACTTTT	TGCCATCATAT	TTTAGCTTTT	ATTGTAAGGC	CCCTATGGTT	2280	
CTAATCAGCG	TTATCCGGGT	TCTGATGTCA	GAATCCTGGG	AACCTGAACA	CTAAGTTTAA	2340
GGCCAAAATG	AGTGAAAAC	CTTTTTTTTT	CTTTCAGATG	CACAGGGAAT	GCACCTATTA	2400
TTGCTATATA	GATTGTTCTC	CCTGTAATTT	CACCTAATTT	TTATTCATGC	ACTTCAAAAC	2460
AACCTTTACTA	CTACATTATA	TGATATATAA	TAAAAAAGT	TAATTCGGA		

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**A214 Protein sequence:**  
 Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
 Unigene number: Hs.98280  
 Probeset Accession #: AA418000  
 Protein Accession #: NP\_067627  
 Signal sequence: none found  
 Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488  
Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGGASSPS ADAAAAAASV 60  
SSAPEIVVSK PEHNNNNLA LYGTGGGGST GGGGGGGSG HGSSSGTKSS KKKNNIGYK 120  
10 LGHRRALFEK RKRLLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180  
LLGLIIVYHA REIGLPMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIP GNYTFTWTAR 240  
LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRP 300  
VMKTLMTICP GTVLLVFSIS LWIIAAMTVR ACERYHDQOD VTSNPLGAMW LISITFLSIG 360  
YDGMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFMDTQLTKRVK 420  
15 NAAANVLRET WLIYKNTKLW KKIDHAKVRK HQRKFLQAIH QLRSVKMBQR KLNDAQNTLV 480  
DLAKTQNIIMY DMISDLNERS EDPEKRIIVTL ETKLETLLGS IHALPGLISQ TIRQQQRDFI 540  
EAQMESYDKH VTYNERSRS SSRRRRSSST APPTSSESS

A215 DNA SEQUENCE:

20 Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Nucleic Acid Accession #: NM\_016029  
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
CTGCGATCCC GCAGGCGCAG GACGCGACTC TGGTGCGGGC GGTCTTCTTC CCCCCGAGCT 60  
GGGCGTGCGC GCGCCGAATG AACTGGGAGC TGCTGCTGTG GCTGCTGTG CTGTGCGCGC 120  
30 TGCTCTCTCT CTGTGTGCGC CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180  
TATGGGCGGA GTGGCAGGGA CGACGCCAGC AATGGGAGCT GACTGATATG GTGGTGTGGG 240  
TGACTGGAGC CTGAGTGGGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACATAGGAG 300  
TTTCTCTGTG GCTGTGAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360  
TAGAGAATGG CAATTATAAA GAAAAAGATA TACTTGTITT GCCCCTTGAC CTGACCGACA 420  
35 CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480  
TGGTCAACAA TGGTGGAAAT TCCAGCGTGT CTCTGTGTCAT GGATACACAG TTGGATGTCT 540  
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGGTGC CTTGACAAAA TGTGTTCTGC 600  
CTCAGATGAT CGAGAGGAAG CAAGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660  
40 TATCTGTACC TCTTTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA 720  
ATGGCTCTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCGAG 780  
GACCTGTGCA ATCAAAATAT GTGGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840  
GCAATAATGG AGACCACTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900  
TCAGCATGGC CAATGATTGG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960  
45 CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020  
AAAGGATTGA GAACTTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080  
AGACAAACAA TGACTGAAAA GAGCACCTGT ACTTTTCAAG CCACCTGGAGG GAGAAATGGA 1140  
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200  
ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260  
50 AGATTGCCAT GAATCTTGCA AA

A216 Protein sequence:

55 Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Protein Accession #: NP\_057113  
Signal sequence: 1-26  
Transmembrane domains: 183-206, 221-243  
60 Cellular Localization: plasma membrane

65 1 11 21 31 41 51  
MNWELLWLL VLCAILLLLV QLLRFLRADG DLTLLEWAEQ GRRPEWELTD MVVVVTGASS 60  
GIGEELAYQL SKLGVSLVLS ARRVHELERV KRCLENGNL KEKDILVLPL DLTDTGSHEA 120  
ATKAVLQEPG RIDILVNNNG MSQSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMIER 180  
KQKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYPGIIVS NICPGPVQSN 240  
70 IVENSLAGEV TTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLLVTVLWQY 300  
MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

A217 DNA SEQUENCE:

75 Gene name: Homo sapiens mRNA; cDNA DKFPz56401763 (from clone DKFPz56401763)  
Unigene number: Hs.27373  
Probeset Accession #: F13036  
Nucleic Acid Accession #: AC012478  
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
ATGCGGCGCG TGCCGCTGCC GCGCCCGCTC CTGCCGCTGC TGCTGCTGCG GCTCCTGGCC 60  
GCTCCGCGCG CCGCGCGCCG CAGAGCGGAG TCCGTCTCCG CGCGGTGGCC CGAACCCGAG 120  
CGCGATCGCG GCCACCGCGC CGGCGCGGGG CCGCGGAACA CCACCCGTTT TGGGTCTGGG 180  
GCGGCGGGCG GCAGCGGCAG CTCACGCTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240

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ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCGTTGCGC 300  
 TTTTACCACC TCCTCATCGC CTGCCTGCTG CTGCGCGTCT TCAGGTCGGG AAAGAGGTTA 360  
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGA AATGGGCGCA 420  
 CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480  
 TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGAGCGTACT GACAGTTCCT 540  
 GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCGTGAT 600  
 GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660  
 TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGGT CGGAGGTGTT 720  
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGGTGTG AGGCATCTGC 780  
 TCAGACTGTG ACTGGCAAGC TOGTTTCCAC GTCACCAAA TGGAGTTGCT TCTGCCACCC 840  
 TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900  
 CTGAATCTCA TGAAGAACT GGAATCTCT GCCTTAAGCA GAAACACCG GGCCTCATCT 960  
 GCCAGGTGCT TGCACCTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020  
 CCTTGGTGGC ACTTCAGGCG CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAACCATG 1080  
 AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGCCAGC GGGGCACCTT TTGTGAAGAC 1140  
 AGAGCAGTAC CTAGCTGTG CCAGGGTAGC TCTTTCTCCA AACAGCTGGC CTGGAAGCCA 1200  
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260  
 ACCCATCTCT TCAAGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320  
 AGGGTGTTC GGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380  
 TGCCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440  
 ATCTGCTACC CTTGCTGTGC GTTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500  
 GTCCTTGGCT CATTGAGCA GAGCCACAA AAGGCAGCTG CTGCCACGG GAGCCTGTC 1560  
 AAACGAGGGC CCACTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620  
 GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCAGTGA GGATGTCACT 1680  
 CACCTGGAG GAGACTTGA TGGGTGGCA AATTCTTATT TGGAGGAAGA GGGTTTCCAG 1740  
 GATGGCAGAT GCCAGAAAGT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800  
 TGTGAGAGG TCACAGGTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860  
 TCCCCCGAC AGCCCTGTG TCTGTCCAG CCCTGA

# A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)  
 Unigene number: Hs.27373  
 Probeset Accession #: F13036  
 Protein Accession #: FGENESH predicted  
 Signal sequence: 1-27  
 Transmembrane domains: 94-115, 448-469  
 Cellular Localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MRVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRFRGSG 60  
 AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF A FTLLIACLL LRVFRSGKRL 120  
 KKTRYDIIT TPAERVEMAP LNEEDEDED STVPDIKYRV SLPAALRRQL PGQQTLLTVP 180  
 VPPFILDID LPARCSGRPD GGIRPGKTCF PAWHPVPSW SAATWGVKDW TWKPSCVGGV 240  
 ETKINVMYKT PAPSCVSGIC SDCHMQARFH VTTMELLPP FGHFPKVPPT STPHGFRQLQ 300  
 LNLMEKLDS ALRNRTRAPS ARCLPLVLAE MAAESDLPN PWHFSAATGS PIKTLTYOTM 360  
 STLGLDVFQ AGQRTGFCED RAVTKVLQGS SFSKQLRWK ALESQFPHL RLLRECPPLS 420  
 THEPVLARS ARQASALTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILL RHPHLDFYK 480  
 ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAAGGEPV KRGPSSQLTR HTCPGWIITH 540  
 ANLQITPDTQ QGEGPREVDY HFGGDLGVA NFYLEEBGQ DGRQCKMVLN SEEGPPSLTG 600  
 CERLTGSHHF SSSKSWSEFL SPRQPLFLSR P

# A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGA 60  
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATGT 120  
 CAGCAAGAGT ACACACACCT GGTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180  
 TCCATATTGA GCTATTACCC AAGTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240  
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300  
 GAACCCAAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAA 360  
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGCTGTGA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAA TGTGAAGTGT 540  
 ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGGTTTGCA GTCACCACT GGGAACTTC 600  
 AGCTACAAAT CTTCTGCTG TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCAAT GTATGTCTCT TGGAGAATGG AGTGTCTCTA TTCCAGCCTG CAATGTGGTT 720  
 GAGTGTGTA CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGA 780  
 AGCTTCCCAT GGAACACAA CTTGTACATT GACTGTGAAG AAGGATTGA ACTAATGGGA 840  
 GCGCAGAGCC TTCACTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 GCTGTGACAT GCAGGGCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
 CTTGCTGGAG AGTTCACTT CAAATCATCC TGCAACTTCA CTTGTGAGGA AGGCTTCATG 1020  
 TTGCAAGGAC CAGCCAGGT TGAATGCACC ACTCAAGGAC AGTGGACACA GCAAAATCCA 1080  
 GTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATGT 1140  
 CTTCTAGTGT CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200  
 GGTTTTGTGT TGAAGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGA GTGGGACAC 1260

5 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCC GAAGGGTTTG 1320  
 GTGAGGTGTG CTCATTCCTT TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCTTTCAGC 1380  
 TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440  
 TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGA 1500  
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTGGCA CTGTGTGCA GTTCGCTGT 1560  
 CCTGAAGGAT GGAGCTCAA TGGCTCTGCA GCTCGACAT GTGGAGCCAC AGGACACTGG 1620  
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCTT GGTAGCTGGA 1680  
 CTTTCTGCTG CTGACTCTC CCTCTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740  
 TGCTTACGGA AAGCAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAGCCT TGAATCAGAC 1800  
 10 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

#### A220 Protein sequence:

15 Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 20 Transmembrane domains: 555-573  
 C-lectin domain: 23-139  
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 MIAEQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYYTHLVAI QNKEEIEYLN 60  
 SILSYSPSY WIGIRKNNV WVVGTQKPL TEEAKNWAP EPNNRQKDED CVEIYIKREK 120  
 DVGMMNDERC SKKLALCYT AACTNTSCSG HGEVETINN YTCKCDPGFS GLKCEQIVNC 180  
 30 TALESPHEGS LVCSPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
 ECDAVTNPAN GFVECFQNPQ SPPWNITCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPAQVECT TQGWQIQIP 360  
 VCEAFQCTAL SNPERGYMNC LPSAAGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420  
 EKPTCEAVRC DAVHQPPKGL VRCASHPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480  
 35 WTEEVPSQOV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKAIKFVP ASSCQSLSD 600  
 GSYQKPSYIL

#### Taxol Prostate

40 A221 DNA SEQUENCE  
 Gene name: ESTs; Liprin A2  
 Unigene number: Hs.306480  
 Probeset Accession #: N51002  
 Nucleic Acid Accession #: N51002  
 45 Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGATGTGTG AAGTGATGCC CAGGATTAAT GAGGACACCC CAATGAGCCA AAGGGGTGCC 60  
 50 CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120  
 GAAAGGGATC GTCTTCTAGA CACCCTTCGG GAGACCCAGC AAAGCCTCTC ACTTGCCCTAG 180  
 CAAAGACTTC AGGATGTCAAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGACGC 240  
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300  
 CGGAATTTG CTGCACGTGAC AAAAGAATTA AATGCCTGCA GGGAACTACT TCTAGAAAAG 360  
 55 GAAGAAGAAA TCTCTGAATC TAAAGCTGAA AGAAACRACA CAAGACTATT ACTGGAGCAT 420  
 TTGGAGTGCC TTGTGTGACG ACATGAAAGA TCACCTAAGAA TGACGGTGGT AAAACGGCAA 480  
 GCGCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCAGT GAAATCTTTG 540  
 TTTGAGCACC ACAAGGCCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600  
 AGAGTCTCTG CACTGGGAAG AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCTTGGCT 660  
 60 GAACAAAATG TTCATATACA AAGAAAATG GCATCARGCG AGGGATCCAC AGAGTCAGAA 720  
 CATCTTGAGG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTC CAATGGTTCT 780  
 ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAACCTAC AAGAATTGCT TGAAGAAGCAA 840  
 AACTATGAAA TGGCCAGAT GAAAGAACGT TTAGCAGCCC TTTCTTCCC AGTGGGAGAG 900  
 GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATT AAACAGAAGA AATGAACACC 960  
 65 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAAGAAAT 1020  
 ACAACCCCTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080  
 AATGATAAAC TAGAAAATGA GTTAGCAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140  
 AAAAAAGAGC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200  
 AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAAGTGG CTCAGAGAA TGCAGCCCTA 1260  
 70 ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAAGCTA TGAGACATTT AGAGGGTCAA 1320  
 CTGAAAGAGA AGAATCAAGA ACTTCAAAGA GCTAGGCAAA GAGAGAAAAT GAATGAGGAG 1380  
 CATAACAAGA GATTATCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCCTA 1440  
 CAACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA 1500  
 TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAGG ATTAGCAGAA 1560  
 75 GAAATTGAAA AGCTGAGATC TGAACCTGAC CAATTGAAAA TGAGAAGTGG CTCITTAATT 1620  
 GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680  
 TCCCTAGTGG ACAGCCAGTG TGATTACAGA ACAACTAAAG TAATAAGAG ACCAAGGAGA 1740  
 GGGCGCATGG GTGTGCGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800  
 AATAGACTC AACAGATTGG AGTACTAAGC AGCCACCCCT TTGAAGTGA CACTGAAATG 1860  
 80 TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTATGCT CAATGGATCT TCTCTCTCCA 1920  
 AGTGGTCATT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAACT GGATGCCATC 1980  
 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040  
 ATTGAAAATA GAGTGGCTAG TGTGAGCCTC GAAGGCTCGA ATTTGGCAAG GGTCCACCCA 2100

5 GGTACCTCCA TTAATGCCTC TGTTACAGCT TCATCGCTGG CCAGTTTCATC TCCCCCAGT 2160  
 GGACACTCAA CTCCAAAGCT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220  
 GTCATGACAC TGCCAAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCAGT TGTGGAAGAA 2280  
 GATGGTCCGAG AGGACAAAGC AACAAATTAA TGTGAAACIT CTCCTCCTCC TACCCTTAGA 2340  
 GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400  
 TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTTGGTAGTG CCAACAGCAG CCAAGACTCT 2460  
 CTTACAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520  
 AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCCTTTATGG AGACTGAAGC TGCAGCTCAG 2580  
 GAGTCCCTGG GGTTAGGCAA ACTCGGAAC CAAGCTGAGA AGGATCGAAG ACTAAAGAAA 2640  
 10 AAGCATGAAC TTCTGAAGA AGCTCGGAGA AAGGATTAC CTTTGGCCCA GTGGGATGGG 2700  
 CCAACTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760  
 TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGCTCTGCTT TATCTGACAC TGAGATCCAG 2820  
 AGAGAAATGG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTGATTAGC AATCCAGGAG 2880  
 ATGGTTTCCC TAACAAGTCC TTCAGCTCCT CCAACATCTC GAACTCCTTC AGGCAACGTT 2940  
 15 TGGGTGACTC TCGAAGTAAAT GGAATACTCT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000  
 GAAGGAAGCT GGGCCAGTG TCCGGTTTTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060  
 CATGAGTGA TGGAAATGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120  
 TTTATGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCGGT 3180  
 20 GTCCATTAA AATAGGTGGA TAGTTTCCAT CGAACAAAGT TACAATATGG AATTATGTGC 3240  
 TTAAGAGGT TGAATTATGA CAGAAAGAA CTAGAAGAA GACGGGAAGC AAGCCAACAT 3300  
 GAAATAAAG ACGTGTGGT GTGGAGCAAT GACCGAATTA TTGCTGGAT ACAAGCAATT 3360  
 GGACTTCGAG AATATGCAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420  
 CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480  
 ACCCAGGCAA GGCAGATTCT TGAAGAGAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540  
 25 AGCGGACTGG ATGAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAGGCAG 3600  
 TTTCTCTCTC TGAAGTACA TGGAAATCAGC ATGATGCTGG GGTCTCAGA AACATTACCA 3660  
 GCTGGATTTA GGTAAACCAC AACCTCTGGG CAATCAAGAA AAATGACAA AGATGTTGCT 3720  
 TCATCAAGAC TGCAGAGGTT AGACAACCTC ACTGTTCCGA CATACTCATG TCTCGAGTAA 3780  
 30 GCGGCGCTT TAA

**A222 Protein sequence:**

Gene name: ESTs; Liprin A2  
 Unigene number: Hs.306480  
 35 Probeset Accession #: N51002  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: none found  
 40 AAA domain: 286-539  
 SAM domains: 895-964, 1017-1084, 1105-1177  
 Cellular Localization: not determined

1 11 21 31 41 51  
 45 MMCEVMPPTN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDLTL ETQESLSLAQ 60  
 QRLQDVIYDR DSLQRLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEK NACREQLLEK 120  
 EEEISELKAE RNNTLRLLLEH LECLVSRHER SLRMTVVVKRQ AQSPSGVSSE VEVLKALKSL 180  
 FEHHKALDEK VRERLRVSLR RVSALEBELA AANQEIVALR EQNVHIQRKM ASSBGSTESE 240  
 50 HLEGMEPGQK VHEKRLSNGS IDSTDTSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300  
 VEQEAETARK DLIKTEEMNT KYQDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360  
 NDKLENELAN KEAILRQME EKNRQLQERLE LAEQKLQOTM RKAETLPEVE AELAQRILAAL 420  
 TKAERHGNH EERMRHLEQ LEEKNQELQR ARQREKMEEB HNKRLSDTVD RLLTESNERL 480  
 QLHLKERMAA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKRLSELD QLMRTGSLI 540  
 55 EPTIPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRPRR GRMGVRRDEP KVKSLGDHWE 600  
 NRTQOIGVLS SHPFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTAL MMLQELDAI 660  
 NKEIRLIQEE KESTELRAEE IENRVASVSL EGLNLARVHP GTSITASVTA SSLASSPPPS 720  
 GHSTPKLTPR SPAREMDRMG VMTLPSDLRK HRRKIIVVEE DGREDKATIK CETSPPPTPR 780  
 ALRMTHTLPS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKKI KSSIGRLFGK 840  
 60 KEKARLQQLR CFMTEAATAQ ESLGLGLGT QAEKDRRLK KHELLEBAR KGLPFAQWDG 900  
 PTVVAMLEW LGMPAWYVAA CRANVKSAGI MSALSDTEIQ REIGISNPLH RLKRLAIQE 960  
 MVSILTSPSAP PSTRTPSGNV WTHEEMENL AAPAKTKESE EGSNAQCFV LQTLAYGDMN 1020  
 HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMVDSFH RTSLQYGIMC 1080  
 LKRLNYDRKE LERRREASQH EIKDVLVWSN DRIIRWQAI GLREYANNIL ESGVHGSILA 1140  
 65 LDENFDYSSL TLLLIQIPTN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200  
 FPPREVHGIS MMPGSSETLP AGFRLITTSQ QSRKMITDVA SSRLQLRLNS TVRTYSCLE

**A223 DNA SEQUENCE**

Gene name: CDA14  
 70 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51  
 ATGAGGCGAC TGAATCGGAA AAAAAGTTTA AGTTTGGTAA AAGAGTTGGA TGCTTTTCG 60  
 AAGGTTCTCT AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120  
 80 TTTACAACCTA TGGCTTTATT AACCATATAT GAATTCCTCAG TATATCAAGA TACATGGATG 180  
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240  
 ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTAGC AGAAACAATG 300  
 GTTGCACTCG CATAGTGGTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360  
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420  
 CAAGATGTGA TATTTAAAG TCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480

5 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATAAAA 540  
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600  
 CATTTGGCAG CACTTGTCAC CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTG 660  
 TCTTTGGAG AGCTTGTTCC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAATTGCT 720  
 10 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780  
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840  
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTCTCTT 900  
 ATGGTGACAG TTAAGTGGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960  
 15 ATTGTTGGAG GAATCTTTT AACAAACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020  
 GAAATAATTT GCTGTCGTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080  
 GAGGATGGCC ACACAGACAA CCACCTTACCT CTTTATAGAA ATAATACACA TGA

15 A224 Protein sequence:  
 Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Protein Accession #: NP\_057654  
 20 Signal sequence: none found  
 Transmembrane domains: none found  
 Cellular Localization: nuclear

25 1 11 21 31 41 51  
 MRLNRKKTLLVKELDAPPKVPESYVETSASGGTVSLIAFTTMALLTIM EFSVYQDTWM 60  
 KYEYEVNDKDFSSKLRLINIDITVAMKQYVGVADVLDLAETMVASADGLVYEPTVFDLSPQQ 120  
 KEMQRLQLIQSRQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPNACRIHGLYVNM 180  
 30 VAGNFHITVGRKAIHPRGHAHLAALVNHESYNFSHRIDHLSFGELVPAIINPLDGTAKIA 240  
 IDHNMFPQYFIVTVPTKLHTYKISADTHQFVSUTERERIINHAAGSHGVSGIFMKYDLSSL 300  
 MVTVEEHMPFQCFEVRLLCGIVGGIFSTTGMLHGIGKFIV EIIICCRFLRG SYKPVNSVFP 360  
 EDGHTDNHLP LLENNTH

35 Uterine  
A225 DNA SEQUENCE:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 40 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 CGGCACCAAGAGCACTGGCC AAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGATG 60  
 CTACACTCAGCTTTGGGTCTCTGCCTCTTA CTGCTCAGAGTTTCTTCCAA CCTTGCCATT 120  
 GCAATAAAAAAGGAAAAGAGGCCTCTCAGACACTCTCAA GAGGATGGGGAGATGACATC 180  
 ACTTGGGTACAAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAA GAAGCCATTA 240  
 50 ATGGTTATTCATCACCTGGA GGATTGTCAA TACTCTCAAGCACTAAAGAA AGTATTGTCC 300  
 CAAAATGAAGAAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAACCACTGATAAGAATTATCACCTGATGGGCAATATGTGCTAGAATCATGTTTGTA 420  
 GACCTTCTT TAACAGTTAGAGCTGACATA GCTGGAAGAT ACTCTACAGATTGTACACA 480  
 TATGAGCCTC GGGATTATCC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540  
 55 CAGTCAGAGC TATPAGAGATGATAGAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTAT 600  
 GAAGAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660  
 TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720  
 TCTGAAAAA AAAAAA AAAAAA

60 A226 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 65 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

70 1 11 21 31 41 51  
 MMLHSALGLCLLLVTSSNL AIAIKKEKRP POTLSRGWGD DITWVQYEE GLFYAQSKSK 60  
 PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120  
 75 FVDSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

80 A227 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Probeset Accession #: AA460530  
 Nucleic Acid Accession #: NM\_003667  
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)



```

1      11      21      31      41      51
|      |      |      |      |      |
GTGGCGGCAA CGGCACCTC AGTCCCCGCC GCGCTTCTCC TCGCCGCCCA CGCCGTGGGG 60
TCAGGAACGC GCGGTCTGGC GCTGCAGACG CCGCTGAGT TGCAGAAACC CACGAGCGG 120
CGCCCGCGCG GCCACGCGCC GTAGCAGTCC GGTGCTGCTC TCCGCCCGCG TCCGGCTCGT 180
GGCCCCCTAC TTCCGGCACC ATGGACACCT CCGGGCTCGG TGTGCTCTCG TCCTTGCGCTG 240
TGCTGTGTGA GCTGCGGACC GGGGGCAGCT CTCCAGGTC TGGTGTGTG CTGAGGGGCT 300
GCCCCACACA CTGTCTATGC GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG 360
ACCTGGGCTC CTGGAGCTG CCTTCCAACC TCAGCGTCTT CACCTCTTAC CTAGACCTCA 420
GTATGAACAA CATCAGTCAG CTGCTCCCGA ATCCCTGCC CAGTCTCCGC TTCTGGAGG 480
AGTTACGTCT TCGGGGAAC GCTCTGACAT ACATTCCCAA GGGAGCATT ACTGGCCTTT 540
ACAGTCTTAA AGTTCTTATG CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC 600
TGCAGAAATT GCGAAGCCTT CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC 660
CCCCAAGCTG TTTCAGTGGC CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT 720
TAACAGAAAT CCCCCTCCAG GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG 780
CCCTGAACAA AATACACCAC ATACCAGACT ATGCCCTTGG AAACCTCTCC AGCTTGGTAG 840
TTCTACATCT CCATAACAAT AGAATCCACT CCGTGGGAAA GAAATGCTTT GATGGGCTCC 900
ACAGCTTACA GACTTTAGAT TTAATTTACA ATAACCTTGA TGAATTCGCC ACTGCAATTA 960
CGACACTCTC CAACCTTAAA GAACCTAGAT TTATAGCAA CAATATCAGG TCGATACCTG 1020
AGAAAGCATT TGTAGGCAAC CCTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC 1080
AATTTGTTGG GAGATCTGCT TTTCAACATT TACCTGAAC AAGAACAACG ACTCTGAATG 1140
GTGCTCTACA AATAACTGAA TTTCCTGATT TAACCTGGAAC TGCAAAACCTG GAGAGCTCGA 1200
CTTTAACTGG AGCAGAGATC TCATCTCTTC CTCAAACCGT CTGCAATCAG TTACTTAATC 1260
TCCAAGTCTC AGATCTGTCT TACAACCTAT TAGAAGATT ACCCAGTTTT TCAGTCTGCC 1320
AAAAGCTTCA GAAATTTGAC CTAAGACATA ATGAATCTA CGAAATTTAA GTTGACACTT 1380
TCCAGCAGTT GCTTAGCCTC CGATCGCTGA ATTTGGCTTG GAACAAAATT GCTATTATTC 1440
ACCCCAATGC ATTTTCCACT TTGCCATCCC TAATAAGCT GGACCTATCG TCCAACCTCC 1500
TGTCGTCTTT TCCTATAACT GGGTTACATG GTTTAACTCA CTTAAATTA ACAGGAAATC 1560
ATGCCATTACA GAGCTTGATA TCATCTGAAA ACTTTCAGAA ACTCAAGGTT ATAGAAATGC 1620
CTTATGCTTA CCACTGCTGT GCATTGAGG TGTGTGAGAA TGCCTATAAG ATTTCTAATC 1680
AATGGAATAA AGGTGACAA AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT 1740
TTCAGGCTCA AGATGAACGT GACCTTGAAG ATTTCTGCT TGACTTTGAG GAAGACCTGA 1800
AAGCCCTTCA TTCAGTGAG TGTTCACCTT CCCCAGGCC CTTCAAACCC TGTGAACACC 1860
TGCTTGATGG CTGGCTGATC AGAATTGGAG TGTGGACCAT AGCAGTTCTG GCACTTACTT 1920
GTAATGCTTT GGTGACTTCA ACAGTTTTC GATCCCTCT GTACATTTC CCAATTAAC 1980
TGTTAATTGG GGTGATCGCA GCAGTGAACA TGCTCACGG AGTCTCCAGT GCGGTGCTGG 2040
CTGGTGTGGA TGCGTTCAC TTTGGCAGCT TTGCACGACA TGGTGCTCG TGGGAGAATG 2100
GGGTGTGTTG CCAATGCTAT GGTTTTTTGT CCAATTTTGC TTCAGAAATCA TCTGTTTTCC 2160
TGCTTACTGT CGAACCCCTG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA 2220
CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCAATTTGCT CTGTGCCCTG CTGGCCTTGA 2280
CCATGGCGCG AGTTCCCTCG CTGGGTGGCA GCAAGTATGG CCGCTCCCTC CTCTGCTGC 2340
CTTTGCCCTT TGCGGAGGCC AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT 2400
CCCTTGTGCT CCTCATGAT ACCATTGCTT ACACCAAGCT CTACTGCAAT TTGGACAAGG 2460
GAGACCTGGA GAATATTGAG GACTGCTCTA TGGTAAACCA CATTGCCCTG TTGCTCTTCA 2520
CCAAGTGCAT CCTAACTGC CCTGTGGCTT TCTTGTCTT CTTCTCTTCA ATAAACCTTA 2580
CATTATCAG TCCTGAAGTA ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTCTGCTCAT 2640
GTCTCAATCC CCTTCTCTAC ATCTTGTTC ATCCTCACTT TAAGGAGGAT CTGGTGAGCC 2700
TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAACACCC AAGCTTGATG TCAATTAATC 2760
CTGATGATGT CGAAAACAGC TCCTGTGACT CAACTCAAGC CTGGTGAACC TTTACCAGCT 2820
CCAGCATCAC TTATGACCTG CCTCCAGTT COGTGCCATC ACCAGCTTAT CCAAGTACTG 2880
AGAGTGCCA TCCTTCTCT GTGGCATTG TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940
AATGTTTTCA AAGGTTGAGA ACCTGAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000
ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

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**A228 Protein sequence**

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPHCHC EFDGRMLLRV DCSDLGLSEL 60
PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGF TGLYSLKVLN 120
LQNNQLRHVP TEALQNLRLS QSLRLDANI SYVPPSCPSG LHSRLRLWLD DNALTEIPVQ 180
AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240
LNYNNLDEFP TAIRTLNLK ELGFHSNNIR SIPEKAFVGN PSLLTIHFYD NPIQFVGRSA 300
FQHLPELRTL TIANGAQITE FPDLTGTANL ESLTLTGAQI SSLPQTVQNO LPNLQVLDLS 360
YNLLEDLPSP SVQQLKQKID LRHNEIYEIK VDTTQQLLSL RSLNLAWNKI AIHPNPFST 420
LPSLIKLDDL SNLLSFPFIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480
AFGVCEPAYK ISNQMNKGDN SSMDDLHKQD AGMFOAQDER DLEDFLDPE EDLKALHSVQ 540
CSPSPGPFKP CEHLLDGWL I RIGVWTIAVL ALTCLNVLTS TVFRSPLYIS PIKLLIGVIA 600
AVNMLTGVSS AVLAGVDAFT PGSFARHGAW WENGVGCHVI GFLSIFASES SVFLTLAAL 660
ERGFVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEF 720
STMGYMVALI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLPTNCILNC 780
PVAFLSFSLL INLTFFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKEO LVSLRKQTVV 840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
VAFVPCIL

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Table 75: See Table 1

Table 76A depicts Seq ID No; UnigeneID; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

5

10

Seq ID No:	Sequence ID No for sequences in table
Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
Pred Subcell Loc:	Predicted sub-cellular localization

	Seq ID No	Pkey	ExAccn	UnigeneID	Unigene Title	Pred Subcell Loc
15	Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolip	plasma membrane
	Seq ID 3 & 4	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	plasma membrane
	Seq ID 5 & 6	429423	AI016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	plasma membrane
	Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
20	Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
	Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
	Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
	Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
	Seq ID 17 & 18	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
25	Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
	Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
	Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
	Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
	Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	plasma membrane
	Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
30	Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
	Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
	Seq ID 35 & 36	423961	D13666	Hs.136348	perlestin (OSF-2os)	secreted
	Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
35	Seq ID 39 & 40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
	Seq ID 41 & 42	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
	Seq ID 43 & 44	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	secreted
	Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
	Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
40	Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
	Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
	Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
	Seq ID 57 & 58	411789	AF245505	Hs.72157	Adlican	secreted
	Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
45	Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
	Seq ID 63 & 64	421552	AF026892	Hs.105700	secreted frizzled-related protein 4	secreted
	Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
	Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
50	Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
	Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
	Seq ID 73 & 74	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	plasma membrane
	Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
	Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
	Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
55	Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
	Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
	Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
	Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
	Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
60	Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
	Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
	Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
	Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
65	Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
	Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
	Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
	Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
70	Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
	Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
	Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
	Seq ID 115 & 116	428179	AI127772	Hs.279695	serum/glucocorticoid regulated kinase-II	intracell
	Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
	Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
75	Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
	Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
	Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
	Seq ID 127 & 128	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	plasma membrane
	Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
80	Seq ID 131 & 132	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	secreted
	Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
	Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
	Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
5	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	A1572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
10	Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
15	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uroplakin 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uroplakin 2	plasma membrane
	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to DJ365012.1 [H.s.a	plasma membrane
20	Seq ID 176 & 177	402075			ENSP00000251056*:Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
25	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
	Seq ID 194 & 195	404875			NM_022819*:Homo sapiens phospholipase A2	intracell
30	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
35	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
40	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305:gi 3806122 gb AAC69198.1  (AF0	intracell
	Seq ID 221 & 222	405932			C15000305:gi 3806122 gb AAC69198.1  (AF0	intracell
45	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
	Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
50	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
55	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
	Seq ID 252	429466	M85835	Hs.12827	ESTs	
60	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
65	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
	Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrevin, alpha	secreted
	Seq ID 269 & 270	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
	Seq ID 271 & 272	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
70	Seq ID 273	458435	AJ418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 274	458435	AJ418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	plasma membrane
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	secreted
	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	plasma membrane
75	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	plasma membrane
	Seq ID 283 & 284	404049			NM_018937*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018938*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
80	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gbhd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
10	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
20	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progesterone-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
45	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
50	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
60	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188*gil12738842[refNP_073725.1] p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter)	plasma membrane
70	Seq ID 435 & 436	407242	M18728		gb:human nonspecific crossreacting antig	plasma membrane
	Seq ID 437 & 438	407242	M18728		gb:human nonspecific crossreacting antig	plasma membrane
	Seq ID 439 & 440	407242	M18728		gb:human nonspecific crossreacting antig	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
80	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

5	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT107???	plasma membrane
	Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT107???	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW369771	Hs.52620	integrin, beta 8	plasma membrane
10	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
15	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	secreted
	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neurosin/ovasin) (KLK8)	secreted
20	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	secreted
25	Seq ID 511 & 512	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	intracell
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
30	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (	secreted
35	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
40	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (lastisin)	secreted
	Seq ID 541 & 542	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	secreted
	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	plasma membrane
45	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
50	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418396	AF765805	Hs.26691	ESTs	plasma membrane
	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
55	Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
60	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	plasma membrane
	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656*Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656*Homo sapiens transmembrane pr	plasma membrane
65	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
70	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, liothyronine, type II	secreted
	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
75	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.295638	prostate differentiation factor	secreted
	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
80	Seq ID 621 & 622	428330	L22524	Hs.22556	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

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Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

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Table 76C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL\_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1876-2140,4252-4385,5922-6077

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Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

5	Seq ID No:	Sequence ID No for sequences in table		
	Pkey:	Unique Eos probeset identifier number		
	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung.	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
15	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
20	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
25	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
30	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
35	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
40	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
45	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
50	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
	Seq ID 69 & 70	416836	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 71 & 72	416836	breast, pancreas, uterine	Ab, sm, CTL, imaging
55	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 79 & 80	451398	breast, ovarian	CTL
60	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
65	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
70	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
75	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
80	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
75	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
80	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
80	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
80	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	sm
	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, diagnostic
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428296	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging



	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 429810	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
15	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	Ab,sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL, diagnostic
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	Ab, sm, imaging
	Seq ID 391 & 392 332180	lung	Ab,sm, CTL, imaging
	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
45	Seq ID 395 & 396 408790	lung	Ab, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, diagnostic
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, diagnostic
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
70	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
	Seq ID 447 & 448 428392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
75	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, CTL, diagnostic
	Seq ID 567 & 568 433466	prostate	Ab, sm, CTL, imaging
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, diagnostic
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, CTL, imaging
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, sm, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, CTL, diagnostic
	Seq ID 583 & 584 412628	prostate	Ab, sm, CTL, imaging
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
70	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, CTL, diagnostic
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, sm, imaging
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, CTL, diagnostic
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, imaging
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, CTL, diagnostic
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	Ab, sm, CTL, imaging
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	CTL
80	Seq ID 629 & 630 456662	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 631 & 632 418281	uterine, ovarian	CTL
	Seq ID 633 & 634 429903	lung	Ab, CTL, diagnostic

Table 78

Seq ID NO: 1 DNA sequence  
Nucleic Acid Accession #: NM\_001400  
Coding sequence: 251..1399

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50  
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AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	180
CTCGCCTCGC	CCTCTAGOGT	TCGTCTGGAG	TAGCGCCACC	COGGCTTCTT	GGGGACACAG	240
GGTTGGCACC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCCACCGCA	GCTCGGTCTC	300
TGACTACGTC	AACTATGATA	TCATCGTCCG	GCATTACAAC	TACAAGGGAA	AGCTGAATAT	360
CAGCGCGGAC	AAGGAGAACA	GCATTAAACT	GACCTCGGTG	GTGTTCAATC	TCATCTGCTG	420
CTTTATCATC	CTGGAGAACA	TCTTTGTCTT	GCTGACCAAT	TGGAAAACCA	AGAAATTCCA	480
CGACCCCATG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTGTG	CAGGAGTAGC	540
CTACACAGCT	AACCTGCTCT	TGCTGGGGGC	CACCACCTAC	AAGCTCACTC	CCGCCCAGTG	600
GTTTCTGCGG	GAAGGGAGTA	TGTTTGTGGC	CCTGTCAGCC	TCCGTGTTCA	GTCTCTCGC	660
CATCGCCATT	GAGCGCTATA	TCACAATGCT	GAAATGAAA	CTCCACAACG	GGAGCAATAA	720
CTTCGGCTCT	TTCTGTCTAA	TCAGCGCCTG	CTGGGTCTATC	TCCCTCATCC	TGGGTGGCCT	780
GCCTATCATG	GGCTGGAATC	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	840
CTACCACAAG	CACATATATC	TCTTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	900
CGTCACTCTG	TACTGAGAA	TCTACTCTCT	GGTCAGGACT	CGGAGCCGCG	CGCTGAAGTT	960
CCGCAAGAAC	ATTTCGAAGG	CCAGCGCGAG	CTCTGAGAAG	TGCTGGGCGC	TGCTCAAGAC	1020
CGTAATTATC	GTCTGAGGCG	TCTTCATCGC	CTGCTGGGCA	CGCTCTCTCA	TCTCTGCTCT	1080
GCTGGATGTG	GGCTGCAAGG	TGAAGACCTG	TGACATCTCT	TTCAAGAGCGG	AGTACTTCTT	1140
GGTGTAGCTG	GTGCTCAATC	CCGGCACCAA	CCCCATCAAT	TACACTCTGA	CCAACAAGGA	1200
GATGGGTGCG	GGCTCAATCC	GGATCATGTC	CTGCTGCAAG	TGCCCGAGCG	GAGACTCTCG	1260
TGGCAAAATC	AAGCGACCCA	TCATCGCCGG	CATGGAATTC	AGCCGACGCA	AATCGGACAA	1320
TTCTCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1380
CGTCAACTCT	TCTTCTTAGA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTTACTTGG	1440
TCGCTGGCCA	CCCCAGTGT	TGGAAGAAA	TCTCTGGGCT	TGCACTGTCT	CCAGGGAGGA	1500
GCTGCTGCAA	GCCAGAGGGA	GGAAGGGGGA	GAATACGAAC	AGCCTGGTGG	TGTCGGGTGT	1560
TGGTGGGTAG	AGTTAGTTCC	TGTGAACAT	GCACTGGGAA	GGGTGGAGAT	CAGGTCCCGG	1620
CCTGGAATAT	ATATTCTACC	CCCCTGAGC	TTTGATTTTG	CACAGAGCCA	AAGGTCTAGC	1680
ATTGTCAAGC	TCTTAAAGGG	TTCAATTTGG	CCCTCTCTCA	AGACTAATGT	CCCCATGTGA	1740
AAGCGTCTCT	TTGTCTGGAG	CTTTGAGGAG	ATGTTTTCCT	TCATTTTAGT	TTCAAAACCA	1800
AGTGAAGTGT	TGCATCTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCCAAC	CCCCACCTCT	1860
CCTTCCCTTC	ATACCCTCTC	TCAACGTTCT	TTTACTTTAT	ACTTTAACTA	CCTGAGAGTT	1920
ATCAGAGCTG	GGGTGTGGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTTGAGTACG	1980
TAGGCTGTGG	GAAGATGAAG	ATGTTTGGGA	GGTGTAAGAC	AATGTCTTTC	GCTGAGGCCA	2040
AAGTTTCCAT	GTAAGCGGGA	TCCGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTTCTT	2100
TAAAAAACAT	CTTTTCAATG	AAATGTGTTA	CCATTTCATA	TCCATTGAAG	CCGAAATCTG	2160
CATAAGGAAG	CCCACTTTAT	CTAAATGATA	TTAGCCAGGA	TCCTTGGTGT	CCTAGGAGAA	2220
ACAGACAAGC	AAAACAAAGT	GAAGACCGAA	TGGATTAACT	TTTGCAAAAC	AAGGGAGATT	2280
TCTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTCTTC	CCACTTTTGT	TGATGTTTAT	2340
TTCAAGATCT	TGTGTGATTC	ATTTCAAGCA	ACAACATGTT	GTATTTTGTG	GTGTTAAAGG	2400
TACTTTTCTT	GATTTTGTAA	TGTATTTGTT	TCAGGAAGAA	GTCATTTTAT	GGATTTTCTT	2460
AACCGGTGTT	AACTTTCTTA	GAATCCACCC	TCTTGTGCCC	TTAAGCATTG	CTTTAACTGG	2520
TAGGGAACGC	CAGAACTTTT	AAGTCCAGCT	ATTCATTAGA	TAGTAATTGA	AGATATGTAT	2580
AAATATTACA	AGAATAAATA	ATATATTACT	GTCTCTTTAG	TATGTTTTC	AGTGAATTA	2640
AACCGAGAGA	TGCTTGTGTT	TTTAAAAAAG	AATAGTATTT	AATAGGTTTC	TGACTTTTGT	2700
GGATCATTTT	GCACATAGCT	TTATCAACTT	TTAAACATTA	ATAAACTGAT	TTTTTTAAAG	

Seq ID NO: 2 Protein sequence  
Protein Accession #: NP\_001391

60  
65  
70

1	11	21	31	41	51	
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LENIFVLLTI	WTKKFKHRPM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
EGSMFVALSA	SVFSLLAIAI	ERYITMLQMK	LENGSNNPRL	FLILSACWVI	SLILGGLPIM	180
GNICISALSS	CSVLPLPYHK	HYILFCTTVF	TLILLSIVIL	YCRIYSLVRT	RSRRLTFRKN	240
ISKASRSSEK	SLALLKTVII	VLSVFIACWA	PLFILLLLDV	GCKVRTCDIL	FRAEYFLVLA	300
VLNSGTNPPI	YTLTNKEMRR	APIRIMSCKK	CPSGDSAGKF	KRPFIAGMEF	SRSKSDNSSH	360
PQKDEGDNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence  
Nucleic Acid Accession #: NM\_002205.1  
Coding sequence: 1..3149

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1	11	21	31	41	51	
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CGCGACCCCC	CGCTSSGTCC	GCTGCTGTGT	CTGCTSSGTG	CGCGCCACCC	CAGGGTCGGG	120
GGCTTCAACT	TAGACGCCGA	GGCCCCAGCA	GTAATCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
GGATTCTCAG	TGGAGTTTTA	CCGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
CCCAAGGCTA	ATACCAAGCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTT	300
TGGGGTGCCA	GCCCACACAC	GTGCACCCCC	ATTGAATTTG	ACAGCAAAAG	CTCTCGGCTC	360
CTGGAGTCCT	CAGTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
TGGTTGGGGG	CAACAGTTGG	AGCCCATGGC	TCTTCCATCT	TGGCATGCGC	TCCACTGTAC	480
AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
GATAACTTCA	CCCGAATTTT	GGAGTATGCA	CCCTGCCGCT	CAGATTTTTC	CTGGGACGCA	600

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GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT 660  
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CAGATGGCCT CTAATTCTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGACGGGCTG 1020  
GATGACTTGC TGGTGGGGGC ACCCTTGCTC ATGGATCGGA CCCCTGACGG GCGGCTCAG 1080  
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GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCTTTGG TGGGAGACC 1260  
CAGCAGGGAG TAGTGTTTGT ATTTCTGGG GCCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320  
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CTCTCGCCG TATCTCCAGT TCTCAACTTC TCCTTGGACC CCAAGCCCC AGTGGACAGC 1860  
CAGGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920  
ATCTTGTCTG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGT 1980  
GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCC TGAACCTCAC TTTCCATGCC 2040  
CAGAATGTGG GTAGGGTGG GGCCTATGAG GCTGAGCTTC GGTCACCGC CCCTCCAGAG 2100  
GCTGAGTACT CAGGACTCTG CAGACACCA GGAACCTTCT CCAGCCTGAG CTGTGACTAC 2160  
TTTGCGTGA ACCAGAGCCG CCTGCTGGT TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220  
GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280  
ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGAGCTGGTT 2340  
TCCTTTCGCG TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCACAGCT 2400  
GAGGCACTGC TATTTCCAGT AAGCGACTGG CATCCCGAG ACCAGCCTCA GAAGGAGGAG 2460  
GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520  
AGCCAGGGTG TGCTGGAATC CAGCTGTCCC CAGGCTCTGG AAGGTACGCA GCTCTATAT 2580  
GTGACCAAGG TTACGGGACT CAATGCACC ACCAATCACC CCATTAACCC AAAGGGCCTG 2640  
GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAAC GGAAGCTCC AAGCCGAGC 2700  
TCTGCTTCTT CGGGAACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760  
TGTGAGCTCG GGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAATTGCA TTTCCGAGTC 2820  
TGGGCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880  
TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCCA AAAAGAGCGT 2940  
CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAAGCA GCTATGGCGT CCCACTGTGG 3000  
ATCATCTCC TAGCCATCTT GTTGGCCTC CTGCTCTAG GTCTACTCAT CTACATCTCT 3060  
TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CGCCATGGA AAAAGCTCAG 3120  
CTCAAGCTC CAGCCACCTC TGATGCCTGA

Seq ID NO: 4 Protein sequence  
Protein Accession #: NP\_002196.1

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1 11 21 31 41 51  
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LESSLSSEGE EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVCTCYLST 180  
DNFRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTRGVV LGGPGSYFWQ QQLSATQEQ 240  
IAESYYPEYL INLVQQLQRT QRASSYYDDS YLGSYVAVGE FSGDDTDETV AGVPKGNLTY 300  
GVVTLNGSD IRLSYNFSGE QMASYFGYAV AATDVNGDGL DLLLVGAPLL MDRTPDGRPY 360  
EVGRVYVYLQ HPAGIEPTPT LTLTHGDEFG RFGSSLTPLG DLDQDGVNDV AIGAPFGGET 420  
QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTPDPFGSAL RGRDLDGNG YPDLVGSPG 480  
VDKAVVYRGR PIVSASASLT IFFAMPNPEE RSCSLBGNPV ACINLSFCLN ASGKHVADSI 540  
GPTVELQLDW QKQKGVRRRA LPLASRQATL QTLLLIQNGA REDCREMKIY LRNBSEFRDK 600  
LSPHIALNF SLDQPAFVDS HGLRPAHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660  
GEQNHVYLED KNALNLTFFA QNVGEGGAYE AELRVTAPE AEYSGLVHRP GNFSSLSQDY 720  
FAVNQSRLLV CDLGNPMKAG ASLWGGRLPT VPHLRDTKKT IQDFQILSK NLNNSQSDVV 780  
SFRLSVEAQA QVTINGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840  
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLLHR QKREAPSR 900  
SASSGQILK CPEAECFLR CELGPLHQE SSQLQLHFRV WAKTFLOREH QPFSLOCEAV 960  
YKALMPYRI LPRQLPKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020  
YKLGPFKRLS PYGTAMEKAQ LKPPATSDA

Seq ID NO: 5 DNA sequence  
Nucleic Acid Accession #: NM\_002211.1  
Coding sequence: 1..2397

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1 11 21 31 41 51  
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GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180  
TCTGCACGAT GTGATGATT AGAAGCCTTA AAAAGAAGG GTTGCCCTCC AGATGACATA 240  
GAAAATCCCA GAGGCTCCAA AGATATAAAG AAAATAAAA ATGTAACCAA CCGTAGCAAA 300  
GAAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA CGAGTTGGTT 360  
TTGCGATTAA GATCAGGGGA GCCACAGACA TTACATTAA AATTCAAGAG AGCTGAAGAC 420  
TATCCCATTT ACCTCTACTA CCTTATGAGC CTGTCTTACT CAATGAAAGA CGATTGTGAG 480  
AATGTAAAAA GTCTTGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGACTTC 540

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AGAATTGGAT TTGGCTCATT TGTGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600
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AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGG AAAACAGCGC 720
ATATCTGGAA ATTTGGATTG TCCAGAAGGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780
TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840
GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAA TGATGGACAA 900
TGTACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
CACCTTGTCC AGAACTGAG TGAATAATAT ATTACAGCAA TTTTGCAGT TACTGAAGAA 1020
TTTCAGCCTG TTTCAAGGA GCTGAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
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GAAGTCATT TTGAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCCATT 1260
GGAGATGAGG TTCAATTTGA AATTAGCATA ACTTCAATA AGTGTCCAAA AAAGGATTCT 1320
GACAGCTTTA CAAATAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
AATGGGACAT TTGATGTGG CGCTGCAGG TGCAATGAAG GCGTGTGTGG TAGACATTGT 1500
GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
AGTTCAGAAA TCTGCAGTAA CAATGGAGAG TGGCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
AGGGATAATA CAAATGAAAT TTATTCTGGC AAATCTGCG AGTGTGATAA TTTCAACTGT 1680
GATAGATCCA ATGGCTTAA TTGTGGAGGA AATGGTGTGT GCAAGTGTGT TGTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTT TGGATACTAG TACTTGTGAA 1800
GCCAGCAACG GACAGATCTG CAATGGCCCG GGCATCTGCG AGTGTGGTGT CTGTAAAGTGT 1860
ACAGATCCGA AGTTTCAAGG GCAAAAGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
GCTGAGCATA AAGATGTGTG TCAAGTGCAG GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
TGCAACAGG AATGTTCTTA TTTTAACATT ACCAAGTAG AAAGTCGGA CAAATTACCC 2040
CAGCCGCTCC AACCTGATCC TGTGTCCCAT TGTAAGGAGA AGGATGTGGA CGACTGTGG 2100
TTCTATTTTA CGTATTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAA 2160
CCAGAGTGTG CCATCGTCC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAAAT 2220
GTTCTTATG GCCTTGCATT ACTGCTGATA TGGAAAGCTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAATAAT 2340
CCTATTTATA AGAGTGCCGT AACACTGTG GTCATCCGA AGTATGAGG AAAATGA

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Seq ID NO: 6 Protein sequence  
Protein Accession #: NP\_002202.1

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LRLRSGEPT PTLKFKRAED YPIDLYLMD LYSYMKDDLE NVKSLGTDLM NEMRRITSDF 180
RIGGSPFVER TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTKNGE VFNELVKGQR 240
ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFTDA GFHPAGDGKL GSVLPNDQ 300
CHLENNMYT SHYDYPSIA HLVOQLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGT 360
SANSNNVIOL IIDAYNSLSS EVILENGKLS EGVITISYKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFISI TSNKCPKQDS DSKIRPLGF TEEVEVLIQY ICECEQSEB IPESPKCHEG 480
NGTFECACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVRK 540
RDNTNEIYSG KFCECDNFNC DRNGLICGG NGVCKRCVCE QNPNYTSAC DCSLDTSTCE 600
ASNGQICNGR GICECGVKC TDPKFGQTC EMCQTCLGVC AEHKECVQCR APNKGKKDT 660
CTQECDFNRI TKVESRDKLP QPVQDPFVSH CKEDVDDCW FYPTYSVNGN NEVMVHVVEN 720
PECPGTGPII PIVAGVVAGI VLIGLALLLI WKLLMIHHR REFAKFEREK MNAKWDGTEN 780
PIYKSAVTTV VNPKYEGK

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Seq ID NO: 7 DNA sequence  
Nucleic Acid Accession #: NM\_002425  
Coding sequence: 26..1453

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AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCCGACAA TACCTAGAAA AGTACTACAA CCTCGAAAG GATGTGAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTG TTAATAAAT CCAAGGAATG CAGAAGTCC TTGGGTGGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAAATGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTGTCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA AACTGGAAGC 720
TTTGATGTAC CCACTCTACA ACTCATTAC AGAGCTCGCC CAGTTCGCCC TTTGCAAGA 780
TGATGTGAAT GGCATTGATG CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
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GCTCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTTCTTAAAG ACAGATATT 960
TTGGGCTGAT TCCCACTGGA ACCCTGAACC TGAATTTTCT TGTATTTCTG CATTTTGGCC 1020
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CAAGGAAAAG AAGAAAACAT ACTTCTTGGC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
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GAAGAAGATG AGCCTTCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC 1620  
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 CTT

Seq ID NO: 8 Protein sequence  
 Protein Accession #: NP\_002416

1 11 21 31 41 51  
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 KIQQMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120  
 PDLPRDAVDS AIEKALKVNE EVIPLTFSRL YEGEADIMIS FAVKEHGDYF SFDGPGHSLA 180  
 HAYPPGGLY GDIHFDDDEK WTEDASGTLN FLVAHELGH SLGLFHSANT EALMYPLYS 240  
 FTSLAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDF ALSFDAISTL 300  
 RGEYLFKDR YFWRSHWNP EPEFHLISAF WPSLPSYLD AYEVSNRDTV FIFKGNEFWA 360  
 IRGNEVQAGY PRGIHTLGFP PTIRKIDAAV SDKEKKKCTYF PAADKYWRPD ENSQSMEQGF 420  
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Seq ID NO: 9 DNA sequence  
 Nucleic Acid Accession #: XM\_058189.2  
 Coding sequence: 169..774

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 TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTCTTAAGC AGGGCAAAAT GGGGTCTCGG 180  
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 AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC 300  
 AACTAGTGTG GTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360  
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAACTGTC 420  
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCTT 480  
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 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGAGCTT TCCTTACAGA TTCTAGCATA 600  
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 CTCATAACCC TCACTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720  
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 TGCAACATTA TTTAATATTC TGGAAAATTG GAAACACCCC AAAATTTCAA ACTCAGAGGA 1140  
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 ATAAAAATA AAGAGTACTA CATGTTTGA AAA

Seq ID NO: 10 Protein sequence  
 Protein Accession #: XP\_058189.1

1 11 21 31 41 51  
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 CRTLDGWEYA FBTAGRFLT DSSIWIQCLE PAHVVEWNII LPSILITLSG LQVIICLIRV 180  
 VMQLSKILCG SYSVIFQPI I

Seq ID NO: 11 DNA sequence  
 Nucleic Acid Accession #: NM\_002421.2  
 Coding sequence: 1..1409

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 GTTGAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT 240  
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCGTGATG GCCTCAGTTT 300  
 GTCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360  
 TACAGCCAG ATTTCGCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420  
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 CTGCTCATG CTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600  
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 ACCCTCAGT GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780  
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5 Seq ID NO: 12 Protein sequence  
Protein Accession #: NP\_002412.1

1 11 21 31 41 51  
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LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSLGLSHST DIGALMYPST 240  
15 TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
FYMRTNPFYP EVELNFISVF WPQLPNGLA AYEFADRDEV RFFKGNKYNA VQGNVLEHY 360  
PKDIYSSFGF PRIVKHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDPG YPKMIAHDFP 420  
GIGHKVDVAV MKDGFYFFFH GTRQYKDFPK TKRILTLQKA NSWFNCRKN

20 Seq ID NO: 13 DNA sequence  
Nucleic Acid Accession #: NM\_002421.2  
Coding sequence: 1..1409

1 11 21 31 41 51  
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GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCGAT 240  
30 GCTGAAACCC TGAAGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300  
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TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420  
TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480  
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540  
CTTGCTCATG CTTTCAAC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600  
35 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660  
GGCCATTCTC TTGGACTCTC CCACTCTACT GATATCGGGG CTTTGATGTA CCTAGCTAC 720  
ACCTTCAGTG GTGATGTTC GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780  
GGAGCTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAGAGC ATGTGACAGT 840  
40 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAGG TGATGTTCTT TAAAGACAGA 900  
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TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCGGACAG AGATGAAGTC 1020  
CGGTTTTTCA AAGGAATAA GTACTGGGCT GTTCAGGAC AGAATGTGCT ACACGGATAC 1080  
CCCCAAGACA TCTACAGCTC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140  
45 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200  
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTT 1260  
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AATAGCTGGT TCACTGCAG GAAAAATTAG

50 Seq ID NO: 14 Protein sequence  
Protein Accession #: NP\_002412.1

1 11 21 31 41 51  
55 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60  
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120  
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDHRD NSPFDGPGGN 180  
60 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSLGLSHST DIGALMYPST 240  
TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
FYMRTNPFYP EVELNFISVF WPQLPNGLA AYEFADRDEV RFFKGNKYNA VQGNVLEHY 360  
PKDIYSSFGF PRIVKHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDPG YPKMIAHDFP 420  
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65 Seq ID NO: 15 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 141..1580

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75 CTTACAGGC CTGTGTGCT ATGGGTTCCC CCGCGGCCCC GGAGGGAGCG CTGGGCTACG 180  
TCGCGAGATT CACTCGCCAC TCCTCCGACG TGCTGGGCAA CCTCAACGAG CTGCGCTGCG 240  
GCGGATCCT CACTGACGTC ACGCTGCTGG TTGGCGGGCA ACCCTCAGA GCACACAAGG 300  
CAGTTCTCAT CGCTCGAGT GGCTCTCTCT ATTCAATTTT CCGGGGCCGT GCGGGAGTGG 360  
GGGTGGACGT GCTCTCTCTG CCCGGGGGTC CCGAAGGAG AGGCTTGGCC CCTCTATTGG 420  
80 ACTTCATGTA CACTTCGCGC CTGCGCCTCT CTCAGGCCAC TGCAACGACA GTCTAGCGG 480  
CCGCCACCTA TTTCAGATG GAGCAGCTGG TCCAGGCATG CCACCGCTTC ATCCAGGCCA 540  
GCTATGAACC TCTGGGCATC TCCCTGCGCC CCTTGAAGC AGAACCCCA ACACCCCA 600  
CGGCCCTCC ACCAGGTAGT CCCAGGCGCT CCGAAGGACA CCGAGCCCA CTTACTGAAT 660  
CTCGAAGCTG CAGTCAAGG CCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTGCACT 720  
GGAAAAAGTA CAAGTACATC GTGCTAAACT CTCAGGCTC CCAAGCAGG AGCCTGGTGG 780

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GGGAGAGAAG TTCTGCTCAA CCTTGCCCCC AAGCCAGGCT CCCCAGTGGG GACGAGGCCT 840  
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 TCTTCCCTTA GTGGGTTTGG GACATCTTCT GGCAAGTGTC CAGATGCCAG AACCTTCTTT 2940  
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 TTCAAGTAGG ATTAAGAGGT TGGTTGAGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA 3240  
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 TCTCCCCATG GCSSGLDSL PVGDEKPYKC QLCRSSFRYK GNLAHRTVH TGEKPYHCIS 3540  
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Seq ID NO: 16 Protein sequence  
 Protein Accession #: FGENESH predicted

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1 11 21 31 41 51  
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 EHVVAQCHRF IQASYEPLGI SLRPLEARPP TPPTAPPPOS PRRSEGHDPD PTESRSCSQG 180  
 PPSASPDPK ACNWKYKYI VLNSQASQAG SLVGERSSGQ PCPQARLPSP DEASSSSSSS 240  
 SSSSEEGPIP GPQRLSFTA ATVQFKGAP ASTPYLLTSQ AQDTSGSPSE RARPLPGSEF 300  
 PSCQCEAVA GCSSGLDSL PVGDEKPYKC QLCRSSFRYK GNLAHRTVH TGEKPYHCIS 360  
 CGARFNRPAN LKTHSRHSG EKPYKCTCG SRFVQVAHLR AHVLIETGEK PYPCTCGTR 420  
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 Coding sequence: 1..2049

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 AATGGGAACC CCCGGAAGCG CCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG 180  
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 CGGAGTGACA GCGCGGGGCT AGGGCGCCCTG GAGAATAAGA TATTTTCTGT TACCAACAAC 300  
 ACAGAATGTG GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCAA 360  
 AGCCTGTTC ACTCACCTGA GAGAGAAGTC TTGGAAGAG ACCTAGTACT TCCTCTGCTC 420  
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 CAAACAACCT CGGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTCTGCTTT 540  
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 GAGGTTGTGA GTGGGCTGGC GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTCGCAA 720  
 CGTCTCTTCA TTTTGAAAAA AGAAGGTTAT GTGAAGATAC TTACCCCTGA AGGAGAAATT 780  
 TTCAAGGAGC CTATTATTGA CATTACAAA CTTGTTCAAA GTGGAATAAA GGGAGGAGAT 840



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GTCTTTCTTG AAGTTGCAGA ACTCCACAGA AAGCATCTGG GAGGACAACT GCTCTTTGGC 1080
CCTGACGGCT TTTTGTACAT CATTCTTGGT GATGGGATGA TTACACTGGA TGATATGGAA 1140
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25 Seq ID NO: 18 Protein sequence  
Protein Accession #: XP\_039209

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1 11 21 31 41 51
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SLFHSPPREV LERDLVLP LL CKDYCKEFFY TCRGHIPGFL QTTADEFCFY YARKDGGLCF 180
PDFPRKQVRG PASNYLDQME EYDKVEEISR KHKHNCFCIQ EVVSGLRQPV GALHSGDGSQ 240
RLFILKEGY VKILTPGEI FKEPYLDIHK LVQSGIKGGD ERLLSLAFH PNYKKNKLY 300
VSYTTNQERW AIGPHDHLR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
PDGFLYIILG DGMITLDDME EMDGLSDFTG SVLRDLVDVT MCNVPYSIPR SNPHFNSTNQ 420
PEVFVHGLH DGRCAVDRH PTDININLTI LCSDSNGKNR SSARILQIIK GKDYSESEPSL 480
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GSCRGYFSGH ILGFGEDELG EYVILSSSKS MTQTHNGKLY KIVDPKRFELM PEECRATVQP 600
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45 Seq ID NO: 19 DNA sequence  
Nucleic Acid Accession #: NM\_014331.2  
Coding sequence: 1..1506

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ACCATCTGGA CGGTGTGTGG GGTCTGTGTA CTATTGAGAG CTITGTCTTA TGCTGAATTG 300
GGAACAACCTA TAAAGAAATC TGGAGGTCTAT TACACATATA TTTTGAAGT CTTTGGTCCA 360
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5 TTATCTGTCA TTTTITTTTT TCACATCAGT TTGATCAGGA AAGTGATATA CACATCTTAG 2280  
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Seq ID NO: 20 Protein sequence  
 Protein Accession #: NP\_055146.1

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 25 LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEFFFIQCEI PELAIKLITA VGITVVMVLN 180  
 SMSVSWARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240  
 YGMYAYAGWF YLNFVTEVEE NPEKTIPLAI CISMATITGV YVLTNVAYFT TINAEELLS 300  
 NAVAVTFSER LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360  
 RKHTPLPASI VLHPLTMIML FSGDLDSLNL FLSPARWLF IGLAVAGLIYL RYKCPDMHRP 420  
 30 FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLGT VPAYYLFIIW DKKPRNFRIM 480  
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35 Seq ID NO: 21 DNA sequence  
 Nucleic Acid Accession #: NM\_002422.2  
 Coding sequence: 64..1497

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 AGCACTCTGA GGGGAGAAAT CCTGATCITT AAAGACAGGC ACTTTTGGCG CAAATCCCTC 1020  
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 GTGATGCCG CATATGAAGT TACTAGCAAG GACCTCGTTT TCATTTTAA AGGAAATCAA 1140  
 60 TTCTGGGCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACCCCTA 1200  
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 CCAGGCTTTC CCAAGCAAAT AGCTGAAGAC TTTCAGGGA TTGACTCAA GATTGATGCT 1380  
 GTTTTGAAG AATTGGGTT CTTTATTTT TTTACTGGAT CTTACAGTT GGAGTTTGAC 1440  
 65 CCAATGCAA AGAAAGTGAC ACACACTTTG AAGAGTAACA GCTGGCTTAA TTGTGAAAG 1500  
 AGATATGTAG AAGGCACAA ATGGGCACCT TAAATGAAGC TAATAATTCT TCACCTAAGT 1560  
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 GGAACCTGAG CGTGAATCTG TATCTGCGG GTCATTTTTA TGTATTACA GGGCAITCAA 1680  
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 70 AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTGCT TATTTAATAA 1800  
 AGACGATTG TCAGTTGTTT T

Seq ID NO: 22 Protein sequence  
 Protein Accession #: NP\_002413

75 1 11 21 31 41 51  
 MKSLPILLLL CVAVCASYPL DGAARGEDTS MNLVQKYLEN YYDLEKDVQ FVRRKDSGPV 60  
 VKKIREMQKF LGLEVTGKLD SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTIVRIN 120  
 YTFDLFKDAV DSAVEKALKV WEEVTPLTFS RLYEGRADIM ISFAVREHGD FYPFDGPGNV 180  
 80 LAHAYAPGPG INGDHAFDDQ EQWTKDTTGT NLPLVAABEI GHSLGLEHSA NTEALMYPLY 240  
 HSLTDLTRFR LSQDDINGIQ SLYGPPFDSP ETPLVPTFV PPEPGTPANC DPALSFDAVS 300  
 TLRGEILIFK DRHFWRKSLR KLEPELHLIS SFWPSLPSGV DAAYEVTSKD LVFIFKGNQF 360  
 WAIRGNEVRA GYPRGHTILG FPPTVRKIDA AISDKENKNT YFFVEDKYWR FDEKRNEMEP 420  
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Seq ID NO: 23 DNA sequence  
Nucleic Acid Accession #: NM\_006528  
Coding sequence: 57..764

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GCGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCTCG	CCCTAGACT	180
ACGACACCTG	CCGGGCCCTA	CTTCTCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
GCCAGTTCCT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCGGCTG	CAAGTGAGTG	360
TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTCTT	TAATCTAAGT	TCCATGACAT	420
GTGAAAAATT	CTTTCCGGT	GGGTGTCACC	GGAAACGGAT	TGAGAACAGG	TTTCCAGATG	480
AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAATTCC	ATCATTTTGC	TACAGTCCAA	540
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CCTGTGATGC	TTTCACTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660
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GCTTTGCCAG	TAGAATCCGG	AAAATTCGGA	AGAAACAATT	TTAAACATTC	TTAATATGTC	780
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GCGATGAGAA	ACAAATCATT	GGTGATTTAT	TCACCACTTT	TTATTAATAC	AAGTCACTTT	900
TTCAAAATAT	CCGATTTTAT	TATATATAAC	TAGCTGCTAT	TCAAATGTGA	GCTCACTATT	960
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AAATATGACT	CACTCATTTT	TTGGGTCGT	ATTCTGTATT	TCAGAAGAGG	ATCATAACTG	1080
AAACAACATA	AGACAATATA	ATCATGTGCT	TTTAACATAT	TTGAGAATAA	AAAGGACTAG	1140
CC						

Seq ID NO: 24 Protein sequence  
Protein Accession #: NP\_006519

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TCCKFFSGGC	HNRNFIENRFP	DEATCMGFCA	PKKIPSFQYS	PKDEGLCSAN	VTRYFFNPRT	180
RTCAFTYTG	CGNDNNFVS	REDCKRACAK	ALKKKKKMPK	LRFASRIRKI	RKKQF	

Seq ID NO: 25 DNA sequence  
Nucleic Acid Accession #: NM\_005458.1  
Coding sequence: 1..2825

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GGCTGGGGCG	GGGGCGCCCC	CCGGCGCGCG	CCAGCAGACC	CGCGCTCTCT	CATCATGGGG	180
CTCATGCGCG	TCACCAAGGA	GCTGGCCAAG	GGCAGCATCG	GGCGGGTGTG	GCTCCCCGCC	240
GTGGAAGTGG	CCATCGAGCA	GATCCGCAAC	GAGTCACTCC	TGCGCCCTTA	CTTCTCGAC	300
CTGCGGCTCT	ATGACACGGA	GTGCGACAAC	GCAAAAGGGT	TGAAAGCCTT	CTACGATGCA	360
ATAAAATACG	GGCCGGAACCA	CTTGATGGTG	TTTGGAGGCG	TCTGTCCATC	CGTCACATCC	420
ATCATGTGAG	AGTCCCTCCA	AGGCTGGAAAT	CTGGTGCGAGC	TTTCTTTTGC	TGCAACCAAG	480
CCTGTTCTAG	CCGATAAGAA	AAAATACCCCT	TATTTCTTTC	GGACCGTCCC	ATCAGACAAT	540
GCGGTGAATC	CAGCCATTCT	GAAATTGCTC	AAGCACTACC	AGTGAAGCG	CGTGGGCACG	600
CTGACGCAAG	ACGTTTCAGAG	GTTCCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
GGCGAGGAGA	TTGAGATTTC	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCAAGTTC	720
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CGCTGCCTCC	GGAAGAATCT	GCTTGCTGCC	ATGAGGGGCT	ACATTGGCGT	GGATTTCGAG	960
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GGCATCTGGG	TCATGCGCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
CGGCACCAAG	GGATCCAGGA	CTTCAACTAC	ACGGACCAAC	CGCTGGGCG	GATCATCTCT	1200
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GAGAGAAATG	GGACCATTA	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	1320
GAGTACAACG	CTGTGGCCGA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	1380
TCCGAACACC	CAAAAGACAA	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	1440
CTCTACAGCA	TCCTCTCTGC	CCTCACTATC	CTCGGATGTA	TCATGGCCAG	TGCTTTTCTC	1500
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ACCGTGGGCT	ACACGACCGC	TTTTGGGGCC	ATGTTTGCAA	AGACCTGGAG	AGTCCAAGCC	1740
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CTGCGAAGGA	CAGTGGAGAA	GTACAGCATG	GAGCGGAGCT	CAGCAGGACG	GGATATCTCC	1920
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TATGCTGGCT	ACAGCACTCT	CATGTTGTTT	GGTTGTTTCT	TAGCTTGGGA	GACCCGCAAC	2040
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ATCATGTGCA	TCATCGGGGC	CGCTGTCTCC	TTCTGACCCC	GGGACCAGCC	CAATGTGCAG	2160
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GTGCGGAAGC	TCATCACCTT	GAGAACAAC	CCAGATGCAG	CAACGCAGAA	CAGGCGATTTC	2280
CAGTTCACTC	AGAAATCGAA	GAAAGAAGAT	TCTAAAACGT	CCACCTCGGT	CACCATGTGT	2340
AACCAAGCCA	GCATATCCCG	CCTGGAGGGC	CTACAGTCAG	AAAACCATCG	CCTGCGAATG	2400

5 AAGATCACAG AGCTGGATAA AGACTTGGAA GAGGTCACCA TGCAGCTGCA GGACACACCA 2460  
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 CACGCTACC TCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTGAGCCC CTGCGTCAGC 2760  
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10 Seq ID NO: 26 Protein sequence  
 Protein Accession #: NP\_005449.1

15 1 11 21 31 41 51  
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 IKYGNHLMV FGVCPSPVTS IIAESLQGNV LVQLSFAATT FVLADKKKYP YFRTVPSPDN 180  
 AVNPAILKLL KHYQWKRVTG LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SPSNDPCTSV 240  
 KKLGNVDVRI ILGQFDQDMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS 300  
 20 RCLRKLLAA MEGYIGVDFE PLSSKQIKTI SGKTPOQYER EYNNKRSVG PSKFHGYAYD 360  
 GIWVIKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRILL NAMNETNFFG VTGQVVRNG 420  
 ERMGTIKFTQ PQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP 480  
 LYSILSALT I LGMIMASAPL FFIKRNQK LKIMSSPYMN NLIIILGGLMS YASIFLFGLD 540  
 GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IPKNVKKKK IIKDQKLLVI 600  
 25 VGGMLLIDL ILICQWAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660  
 YAYKGLMLF GCFLAWETR N VSIPALNSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ 720  
 FCIVALVII CSTITLCLVF VPKLITLRTN PDAATQNRFF QFTONQKRED SKTSTSVTSV 780  
 NQASTSRLEG LQSENHRLRM KITELDKDLE EVMQLQDTP EKTYYIKQNH YQELNDILNL 840  
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 30 HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L

Seq ID NO: 27 DNA sequence  
 Nucleic Acid Accession #: NM\_000450.1  
 Coding sequence: 117..1949

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 40 TTGCTTCACA GTTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAGAG AGTGGAGCCT 180  
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 AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAGAAGA GATTGAGTAC CTAAATCCA 300  
 TATTGAGTCA TTCAACAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG 360  
 TCTGGTAGG AACCAGAAA CCTCTGACAG AAGAAGCCAA GAATCTGGCT CCAGGTGAAC 420  
 45 CCAACATAG GCAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAGATG 480  
 TGGCATGTG GAATGATGAG AGGTGACGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG 540  
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 CCTGGAATC CCTGAGCAT GGAAGCCTGG TTTGCACTCA CCCACTGGGA AACTTCAGCT 720  
 50 ACAATCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGAGAGCCA 780  
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 60 CTAGTGCTTC TGGCAGTTT CATTATGGGT CCAGCTGTGA GTTCTCTGT GAGCAGGTT 1320  
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 75 TCTACTCTC AGGATCAAGA AAGTGTGGC TAATGAAGGG AAAGATATT TTCTTCCAG 2220  
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 GGTAAAGTT ACTTATTCTA GATTACCCCT TCATTGTTTA TTAACAAT ATGTTACATC 2760  
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20 Seq ID NO: 28 Protein sequence  
Protein Accession #: NP\_000441.1

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DVGMMNDERC SKKLLALCYT AACTNTSCSG HGECVETINN YTKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVINPAN GFVECFQNPQ SPFWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300
AVTCRAVRGP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPQVQECT TQGWTTQIIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWEN 420
EKPTCEAVRC DAVHQPQKGL VRCASHPIGE FTKSSCAFS CEEGFELYGS TOLECTSQGQ 480
WTEEVPSQV VKCSLAVPG KINMCSGSEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
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40 Seq ID NO: 29 DNA sequence  
Nucleic Acid Accession #: NM\_007036  
Coding sequence: 56..610

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CAGACCAAC ATTTTAGGAA CTCTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT 720
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AGTATTTACC TGATTTTAT TCTTGAAGTT GGCCAACAGA GTTGTGAATG TGTGTGGAAG 1920
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TTGTTCATA AAAAGAACA AGATAC

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80 Seq ID NO: 30 Protein sequence  
Protein Accession #: NP\_008967.1

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90

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1 11 21 31 41 51
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ICDRGTGRKL KPFPPQYSVT KSSNRFVSLT EHDMAAGDGN IVREEVVKEN AAGSPVMRKW 180

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LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM\_000963

Coding sequence: 135..1949

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ATACAGCAAA TCCTTGCTGT TCCCACCCAT GTCAAAACCG AGGTGTATGT ATGAGTGTGG 240
GATTGTACCA GTATAAGTGC GATTGTACCC GGACAGGATT CTATGGAGAA AACTGCTCAA 300
CACCGGAATT TTTGACAAGA ATAAATTTAT TTCTGAAACC CACTCCAAAC ACAGTGCAC 360
ACATACTTAC CCACCTTCAAG GGATTTTGA ACGTTGTGAA TAACATTCCC TTCTTCGAA 420
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GAGCCCTTCC TCCTGTGCTC GATGATTGCC CGACTCCCTT GGGTGTCAA GGTAAAAAGC 600
AGCTTCTCTG TTTAAATGAG ATTGTGGAAA AATTGCTTCT AAGAAGAAAG TTCATCCCTG 660
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Seq ID NO: 32 Protein sequence  
Protein Accession #: NP\_000954

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10 NMMFAFFAQH FTHQFFKTDH KRGPAFTNGL GHGVDLNHIY GETLARQRKL RLFKDGKMKY 240  
QIIDGEMYPF TVKDTQAEMI YPPQVPEHLR FAVGQEVFGL VPGLMMYATI WLREHNRVCD 300  
VLKQEHPEWG DEQLFQTSRL ILIGETIKIV IEDYVOHLSG YHFKLKFDPE LLFNKQFQYQ 360  
NRIAAEFNTL YHWHPLLPDT FQIHDQKYNV QQFIYNNISIL LEHGITQFVE SFTRQIAGRV 420  
AGGRNVPPAV QKVSQASIDQ SRQMKYQSFN EYRKRFMLKP YESPEELTGE KEMSAELEAL 480  
YGDIDAVELY PALIVEKPRP DAIFGETMVE VGAPPSLKLGL MGNVICSPAY WKPSTFGSEV 540  
15 GFQINTASI QSLICNNVKG CPFTSFSVPD PELIKTVIIN ASSSRSLDD INPTVLLKER 600  
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CGCTCTCTGT ACACGGTGTG CTGCGAGCAG TTTGCGCGGG TGTTCGTGCA GGTGCTGTGC 1080  
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ACCACGACA GCGCCGCTT TGTGACGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200  
TCTGCAAGGA GAACGTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260  
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Protein Accession #: NP\_001499.1

50 1 11 21 31 41 51  
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55 KGLYQKEVTD HMYSLACSDI LVPLIGMPME FYSLIWNPLT TSSYTLSCKL HTFLFEACSY 120  
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VNVPSHRGLT CNRSSTRHHE QPETSNMISC TNLSSRWTFV QSSIFGAFV YLVVLLSVAF 240  
MCNWMQVLM KSKQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRILVV TLAVCWMPNQ 300  
IRIRMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLTVSSSQ FRRVFVQVLC 360  
60 CRLSLQHANH EKRLRVHAHS TDSARFVQR PLLPASRRQS SARRTEKIFL STFQSEAEPP 420  
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Coding sequence: 28..2538

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75 ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420  
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80 CAAATTGGTA CCTCAATTC AAGATTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780  
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 KLREIEBGKG SPTYFAPSNE AWDNLDSDIR RGLSENVNVE LLNALHSHMI NKRMLTKDLK 180  
 NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVHVHIDRVL TQIGTSIQDF 240  
 IEAEDDLSSP RAAATSDIIL EALGRDGHFT LFAPTNEAPE KLPRGVLERF MGDKVASEAL 300  
 MKYHILNTLQ CSESIIMGAV FETLENTIE IGCODGSITV NGIKMVNKID IVTNNGVIHL 360  
 IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLSM 420  
 VORLLKLILQ NHILKVKVGL NELYNQIILE TIGGKQLRVF VYRTAVCIEN SCMEKSKQSG 480  
 RKGATHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTOPGD WTLFVPTNDA 540  
 FKMGTSSEKE ILIRDKNALQ NIILYHLTPG VPIGKGFEFG VTNILLKTQG SKIPLKEVND 600  
 TLLVNLKSK ESIDIMTTNGV IHVVDKLLYP ADTPVGNLQ LLEILNKLIKY IQIKFVRGST 660  
 FKEIPVTYIT TKIIFKVVEP KIKVIBGSLQ PIKTEGPTL TKVKIEGEPE FRLLIKEGETI 720  
 TEVIHGEPII KTKYKIIDGV PVEITEKETR EERIITGPBI KYTRISTGGG ETEETLKKLL 780  
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GGAGGTTTCAG TGAATTGTGT AGGAGAGGTT GTCGTGGGCC AGAATTTAAA CCTATACTCA 2160
CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGTCTG CCGGTGGAGA 2220
TCCACCCGGA ACCTGTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
AAAAATCTAA GTGTTTCTAA AATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
GTAGACAGTA TATACTAAC AACCAAGAC TACATATTGT CACTGACACA CACGTTATAA 2400
TCATTTATCA TATATATACA TACATGCATA CACTCTCAA GCAATAATT TTCACTTCA 2460
AAACAGTATT GACTTGATA CCTTGTAAAT TGAATATTT TCTTTGTAA AATAGAATGG 2520
TATCAATAAA TAGACCATTA ATCAG
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Seq ID NO: 38 Protein sequence  
Protein Accession #: NP\_002407

30

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1 11 21 31 41 51
MKKSGVLELL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
IEIIATLKNQ VQTCNLNPSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR 120
QKKT
```

Seq ID NO: 39 DNA sequence  
Nucleic Acid Accession #: NM\_006670  
Coding sequence: 85..1347

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1 11 21 31 41 51
CCGGCTCGGG CCTCCGGGCG CAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC 60
AGCTCCGGGG AAAAGCGAGC CGCGATGCTT GGGGGGTGCT CCGGGGGCCC CGCGCGGGG 120
GACGGGGCGTC TGGCGGTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCTCGTCT 180
TCTCCCACTT CCTCGGCATC CTCTTCTTCC TCTCGGCGCG CGTTCCTGGC TTCCGCCGTG 240
TCGCGCCAGC ACCTCGTCCC GGACCACTGC CCGCGCTGCT GCGAGTGTCT CGAGGCAGCG 300
CGCACAGTCA AGTGCCTTAA CGCAATCTG ACCGAGGTGC CCAAGGACCT GCCCGCTAC 360
GTGCGCAACC TCTTCTTAC CGCAACCCAG CTGGCGGTGC TCCTTCCGGG CGCCTTCCGC 420
CGCGGGCGCG CGCTGGCGGA GCTGGCGCGG CTCACCTCA GCGGCAGCGG CCGGACGAG 480
GTGCGCGCGG GCGCCTTGA GATCTGCGCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
CCACTGGCGG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCT CTGCGCCCC 600
AGTCCCTCTG TGAAGTGAAT CCTGAACCA ATCGTGCCCC CTGAAGATGA CCGGCAGAAC 660
CGGAGCTTCC AGGCGATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTACCTGCG CGCGGATGT GCTGGCCCAA 780
CTGCCAGGCC TCAGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTC 840
TCCTTCGCGA ACCTGACACA TCTAGAAAGC CTCCACCTGG AGGACATGCG CCTCAAGGTC 900
CTTCACAATG GCACCTCGGC TGAGTTGCAA GGTCTACCCC ACATTAGGCT TTTCTGGAC 960
AACATTCCTT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
GAGGTAGTGC AGGGCAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC GATTTCTTCC CCCATCCCTG 1140
CAAACTCTTT ATGTCTTCT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
GTTTTGTATT TGAACGCGAA GGGGATAAAA AAGTGGATGC ATAAATCATG AGATGCTGTC 1260
AGGGATCACA TGAAGGGTGA TCATTACAGA TATGAATCA ATGCGGACCC CAGATTAACA 1320
AACTCAGTT CTAACCTGGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
TAGATACAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCCCTG TTATGTAAAG 1500
TTTCTGGGTG TGTCTGTGTA ATGTAAGAGC ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
TTCTTTTCTT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
ACAGATAGCA TTCAACAAA GCTGCCTCAA CTTTTCGAG AAAAATACTT TATTCATAAA 1740
TATCAGTTTT ATTCTCATGT ACCTAAGTGG TGGAGAAAAT AATTGCATCC TATAAAGTGC 1800
CTGCAGAGCT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CTGTCATCCA 1860
AGAGCATGCT TACATTTTAC TGTCTGCAAT ATTACAAAAT ATAACCTTGA ACTTCATAAC 1920
TTCTTTGACA AAGTAAATTA CTTTCTTGAT TGCAGTTTAT ATGAAATGT ACTGATTTT 1980
TTTTAATAAA CTGATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
ATTCTTAAAA GAA
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Seq ID NO: 40 Protein sequence  
Protein Accession #: NP\_006661

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1 11 21 31 41 51
MPGGCSRGPA AGDGLRLRL LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPPLD 60
QCPALCESE AARTVKCVNR NLTEVFTDLP AYVRNLFITG NQLAVLPAGA FARRPPLAEL 120
AALNLGSRSL DEVRAFAFEH LPSLRQLDLS HNPLADLSFP APGSGNASVS APSPLVELIL 180
NHIVPPEDER QNRSPFGMVV AALLAGRALQ GLRLRLASLN HFLYLPDVL AQLPSLRHL 240
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LSNNSLVSLT YVSRNLTSL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDCD 300  
HMADMVTLWK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDCEPILPP SLQTSYVFLG 360  
IVLALIGAIF LVLVLYLNRKG IKWMHNRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

5 Seq ID NO: 41 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..927

10 1 11 21 31 41 51  
ATGCGCTGGG GGTGCTCCCG GGGCCCCGCC GCGGGGACG GCGCTCTGCG GCTGGCGCGA 60  
CTAGCGCTGG TACTCTCTGG CTGGGTCTCC TCGTCTCTC CCACCTCCTC GGCATCCTCC 120  
TTCTCTCTCT CGGCGCCGTT CTGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCCGGAC 180  
15 CAGTGCCCGC CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240  
AATCTGACCG AGGTGCCACG GGACCTGCCG GCCTACGTGC GCAACCTCTT CCTTACCGCG 300  
AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCG 360  
AGCCTCAGCG ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCTGACCTA CGTGTCTTTC 420  
CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTTTCAC 480  
AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACATTA GGGTTTTCCT GGACAACAAT 540  
20 CCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600  
GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGTCTCTC 660  
TTGGAACCTA ACAGTGTGTA CCTGGACTGT GACCCGATTC TTCCCCATC CCTGCAAAAC 720  
TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCTT CTGTGTTTGT 780  
TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840  
25 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900  
AGTCTAACT CGGATGTCTT CGAGTGA

30 Seq ID NO: 42 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
MPGGCSRGA AGDGRRLRLR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPLPD 60  
35 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFITG NQLASNHFLY LPRDVLALQLP 120  
SLRHLDSNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELOGL PHIRVFLDNN 180  
PWVCDCHMAD MVTLKETEY VQKDRLTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240  
SYVFLGIVLA LIGAIFLLVL YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300  
SSNSDVLE

40 Seq ID NO: 43 DNA sequence  
Nucleic Acid Accession #: NM\_058173  
Coding sequence: 68..340

45 1 11 21 31 41 51  
AGCGCCTTGC CTCTCTTAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT 60  
CACCACCATG AAGTCTTAG CAGTCTGGT ACTCTTGGGA GTTCCATCT TTCTGGTCTC 120  
TGCCAGAAAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGA 180  
50 TGATGAAGCC CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240  
TACCACTGCA ACCACCGCTG CTCTACCACT TGCTCGTAAA GACATTCAG TTTTACCCAA 300  
ATGGGTGGG GATCTCCCGA ATGGTAGAGT GTGCTCCCTG GATGGAATCA GCTTGAGTCT 360  
TCTGCAATTG GGTCACAACT ATTCATGCTT CCGTGATT CATCCAATA CTACCTTGC 420  
CTAGGATATC CCTTTTATCT CTAATCAGTT TATTTTCTTT CAAATAAAAA ATAACATGA 480  
GCGAGCTAAC AT

55 Seq ID NO: 44 Protein sequence  
Protein Accession #: NP\_477521

60 1 11 21 31 41 51  
MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETTAAT TTATTAAPT 60  
ATTAASTTAR KDIPVLPKWV GDLNPRVCP

65 Seq ID NO: 45 DNA sequence  
Nucleic Acid Accession #: NM\_000095.1  
Coding sequence: 26..2299

70 1 11 21 31 41 51  
CAGCACCCAG CTCCCGGCCA CGCCCATGGT CCGGACACC GCCTGCGTTC TTCTGCTCAC 60  
CTGGCTGCC CTGGGCGCT CCGGACAGGG CCAGAGCCCC TTGGGCTCAG ACCTGGGCC 120  
GCAGATGCTT CGGAACTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180  
GCGGCAGCAG GTCAGGGAGA TCACGTTCTT GAAAAACAG GTGATGGAGT GTGACGCGTG 240  
CGGGATGCAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CGGCCCCCTG TCCACTGCGC 300  
75 GCGGATGCAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CGGCCCCCTG TCCACTGCGC 360  
GCCCGGCTTC TGCTTCCCGG CGGTGGCGTG CATCCAGAGC GAGAGCGCGG GCCGCTGCGG 420  
CCCTGCCCC GCGGGCTTCA GGGGCAACGG CTGCACTGC ACCGACGTCA ACGAGTGCAA 480  
CGCCACCCC TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCGCTGCGA 540  
GGCTTGGCCG CCGGGGTACA CGGCCCCAC CCACAGGGG GTGGGGCTGG CTTTGGCCAA 600  
80 GGCCAAACAG CAGGTTTGCA CGGACATCAA CAGTGTGAG ACCGGGCAAC ATAACGTGCT 660  
CCCAACTCC GTGTGCATCA ACACCGGGG CTCCTTCCAG TGCGGCCCGT GCCAGCCCGG 720  
CTTGTGGGCG CCGAGGCGT CCGGCTGCCA GCGGCGCGCA CAGCGCTTCT GCCCGAGCG 780  
CTGCGCCAGC GAGTGCCAGC AGCATGCAGA CTGGTCTCTA GAGCGCGATG GCTCGCGGTC 840  
GTGCGGTGT CCGGTTGGCT GCGCGGCAA CGGATGCTC TGTGCTGCGC ACCTGACCT 900  
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCGGAGCGG CAGTCCCGTA AGGACAACCTG

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CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCTCG 960
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAG GACAACTGCC CGCTGGTGCG 1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCGG 1080
GTCCAGAGG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA 1140
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGTACCCCAA 1200
CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
GAAGAGCAAC CGGATCAGG CGGATGTGGA CCAAGACTTT GTGGGAGATG CTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC 1380
TAACAGTGCC CAGGAGGACT CAGACCAAGA TGCCAGGGT GATGCTGCG ACGACGACGA 1440
CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCCG CTGGTGCTTA ACCCGGGCCA 1500
GGAGGACCGG GACAGGGACG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGGTAGAC AAGATCGAGC TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGACCGC CAGATTGACC CCAACTGGGT 1680
GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGGACCCAG GCCTGGCTGT 1740
GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCAGC TTCCATGTGA ACACGGTCAC 1800
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAAG CAGATGAGGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
GGCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGGCGAA 1980
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCGCG 2040
AAACGTTGGT TGAAGGACA AGAAGTCTTA TCGTTGGTTC CTGCAGCACC GGGCCCAAGT 2100
GGGTACTATC AGGGTGGGAT TCTATGAGGG CCGTGAGCTG GTGGCCGACA GCAACGTGGT 2160
CTTGACACA ACCATGCGGG GTGGCGGCTT GGGGCTCTTC TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTCGCTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGTGGCGG CAAGCCTAGG GACCAGGGTG AGGACCGGCC GGATGACAGC CACCCTCACC 2340
GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAAGTGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGG

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Seq ID NO: 46 Protein sequence  
Protein Accession #: NP\_000086.1

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1 11 21 31 41 51
MVPDTACVLL LTLAALGASG GQGSPLGSDL GPQMLRELQE TNAALQDVVD WLRQVREIT 60
FLKNTYMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNAHPCFPVR RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INECETQQHN CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQRGAQRFPC DGSPSECEHE 240
ADCVLERDGS RSCVCRVWNA GNGILCGRDT DLDGFPDEKL RCPPEQCRKD NCVTVPNSSQ 300
EDVDRDGIQD ACDPDADGQD VPNEKDNCPV VRNPQDRNTD EDKWDGACDN CRSQRNDQK 360
DTDQDGRGDA CDDIDIGDRI RNQADNCPRV PNSDQKSDG DGIGDADQNC PQRSNPDQAD 420
VDHDFVGDAC DSDQDQDGGV HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480
RDNCRLVPNF QGEDADRDGV GDVQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD 540
PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
PGYQDSSSFY VVMWQKMEQT YWQANPFRAV ABEPQILKAV KSSTGPGEQL RNALNHTGDT 660
ESQVRLWKID PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
RLGVFCFSQE NIIWANLRYR CNDTIPEDEY THQLRQA

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Seq ID NO: 47 DNA sequence  
Nucleic Acid Accession #: NM\_001565.1  
Coding sequence: 67..363

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1 11 21 31 41 51
GAGACATCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC 120
ATTCAAGGAG TAAGTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CCTGTTAATC CAAAGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
CGTGTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
TGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
TAAACCCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCGTAGGAA 540
GGTTAATGTT CATCATCTTA AGCTATTGAG TAATACTCT ACCCTGGCAC TATAATGTAA 600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTCTGACC CTGCTTCAA TATTTCCCTC 660
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAAITC 720
TCAGAACTC AAATAACTAA AAGGTATGCA ATCAAACTCT CTTTATAAG AATGCTCTTT 780
ACTTCAATGA CTTCCACTGC CATCCTCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
CATACAATTC CAAACACATA CAGGAAGSTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
CTTATTATAT GAAAGACTGT ACAGAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG

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Seq ID NO: 48 Protein sequence  
Protein Accession #: NP\_001556.1

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1 11 21 31 41 51
MNQTALICC LIFLTLGSIQ GVPLSRTVRC TCISISNQPV NPSLEKLEI IPASQFCPRV 60
EIIATMKKKG EKRCNLNPEK AIKNLLKAVS KEMSKRSP

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Seq ID NO: 49 DNA sequence  
Nucleic Acid Accession #: XM\_057014  
Coding sequence: 143..874

1 11 21 31 41 51  
 5 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCTCGGAG 60  
 CGCGCGGAG CGAGACGCTG ACCACGTTCC TCTCTCGGT CTCCTCGCC TCCAGCTCCG 120  
 CGCTGCCCGG CAGCGCGGAG CCATGCGACC CCAGGGCCCC GCGGCTCCG CCGAGCGGCT 180  
 CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCGCGCG CCGTGGAGCG CCTCTGAGAT 240  
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG CGAGAGGGAG GTGGTGGACC TGTATAATGG 300  
 AATGTGCTTA CAGGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360  
 10 CATTCCGGGT ACACCTGGGA TCCCAGGTCC GGATGGATTG AAAGGAGAAA AGGGGGAATG 420  
 TCTGAGGGAA AGCTTTGAGG AGTCCCTGGAC ACCCAACTAC AAGCAGTGT CATGGAGTTC 480  
 ATTGAATTAT GGCATAGATC TTGGGAAAT TGCGGAGTGT ACATTACAA AGATGCGTTC 540  
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAATGCA GAAATGCATG 600  
 CTGTACAGCT TGGTATTCCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATGTA 660  
 15 AGCTATAATT TATTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTATCG 720  
 CACTTCTTCT GTGGAAGGAC TTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780  
 CTGGGTTGCT ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840  
 TTCTCGCATC ATTATTGAAG AACTACCAA ATAAATGCTT TAATTTTCAT TTGTACCTC 900  
 TTTTCTTATT ATGCTTGGGA ATGGTTCAT TAAATGACAT TTTAAATAAG TTTATGTATA 960  
 20 CATCTGAATG AAAGCAAGG CTAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020  
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTCTTAGT 1080  
 TGGTTAGATC ACTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTGT 1140  
 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200  
 TGTACAAATT GTAAATGTGA AGAATTTT TATATCTGT TAAATAAAAA TTATTTCCAA 1260  
 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 50 Protein sequence  
 Protein Accession #: XP\_057014

1 11 21 31 41 51  
 30 MRPGPAASP QRLRLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSFG ANGIPGTPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120  
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCORWYFT FNGAECSSPL PIEAIIYLDQ 180  
 35 GSPENNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240  
 LPK

Seq ID NO: 51 DNA sequence  
 Nucleic Acid Accession #: NM\_020974  
 Coding sequence: 81..3080

1 11 21 31 41 51  
 40 GGCGTCCGCG CACACCTCCC CGCGCGCGCG CGGCCACCGC CCGCACTCCG CGGCTCTGC 60  
 CGCAACCGC TGAGCCATCC ATGGGGGTCC CGGCGCGCAA CCGTCCCGGG GCGGCTGGG 120  
 45 CGGTGCTGCT GCTGTGCTG CTGTGCGCGC CACTGCTGCT GCTGGCGGG GCGGCTCCG 180  
 CGGTGCGGG CGGTGCGCG GGGCGCGAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240  
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATGAGC 360  
 50 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGT 420  
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGGCTGG 480  
 AGAACAAATG CGGCTGCCAG CATACTGTG TCAACGTCAT GGGGAGCTAT GAGTGTGCT 540  
 GCAAGGAGGG GTTTTCTCTG AGTGCAATC AGCACACCTG CATTCAACGC TCGGAAGAGG 600  
 GCCTGAGCTG CATGAATAAG GATCAGGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660  
 55 CGAGCGTCCG CTGTGAGTGC AGGCTGTGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 CGCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCGCTG 840  
 AGCGAGAGGA CACTGTCTGT GAGGTGACAG AGAGCAACAC CACATCAGT GTGGATGGG 900  
 ATAAACGGGT GAACCGGGG CTGCTCATGG AAACGTGTGC TGTCAACAT GGAGGCTGTG 960  
 60 ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCTGTT GGATTCACCT 1020  
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCG AATGGAGGTT 1080  
 GTGATCAATT CTGCAAAAC ATCGTGGGCA GTTTTGA CTG CCGCTGCAAG AAAGGATTTA 1140  
 AATTATTAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTG GATAGGACCT 1200  
 GTGACCACAG CTGCATCAAC CACCCTGGCA CATTGCTTGT TGCTTGCAAC CGAGGGTACA 1260  
 65 CCCTGTATGG CTTACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320  
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAAGTGCAC CTGGGTACA 1380  
 AGCTCCACTG GAATAAAAA GACTGTGTGG AAGTGAAGGG GCTCTGCCC ACAAGTGTGT 1440  
 CACCCCGTGT GTCCCTGCAC TGGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500  
 GTCACCTCG CATTACCTC TCTTCAGATG TCACCACCAT CAGGACAAAT GTAACCTTTA 1560  
 70 AGCTAAATGA AGGCAAGTGT AGTTTGA AAA ATGCTGAGCT GTTCCCGAG GGTCTGCGAC 1620  
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680  
 GCAGCTCTGG CAGCAAGCTC CCAGGAGCCC CTGGCCGACC AAGCAACCCCT AAGGAAATGT 1740  
 TTATCACTGT TGAGTTTGAG CTTGAAACTA ACCAAAGGA GGTGACAGCT TCTTGTGACC 1800  
 TGAGCTGCAT CGTAAAGGGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACCTCAGAA 1860  
 75 AGGCGGTCCA CAGGAGCAG TTTACCTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920  
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCCTG TGGAGTGGGC CAGGCTCATG 1980  
 CAGAAACACA ATGTGTCACT TGCAGGCTGT GGACCTATTA TGATGGAGCA CGAGAACGCT 2040  
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAATGACT TGTGAACCAT 2100  
 GCGCAAGACC AGGAAATCTT GGGGCCCTGA AGACCCAGA AGCTTGGAA ATGTCTGAAT 2160  
 80 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTCGAGATGG CTTTGCACCT TGCCAGCTCT 2220  
 GTGCCCTCCG CAGCTTCCAG CCTGAAGCTG GTCGAATTC CTGCTTCCC TGTGGAGGAG 2280  
 GCCTTGGCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340  
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 Protein Accession #: NP\_056234.1

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Seq ID NO: 59 DNA sequence

Nucleic Acid Accession #: Eos sequence

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 GGGACCCCCG TGGTGAATCC TGACGGCTCC CCACTCTTG GGCAGGGCG ACATGGCACA 3840  
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 80 TTGAGGTG TCAGAAAAC CACCATCCC CTAACCTA CCAATGCAGC CACCACTACT 3960  
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 ACCACTACTA CGACGCCCCT GCCTACCACT ACACCGAGGC CCACTACTGC CACCAACCGC 4080  
 CGCACGACCA CAGGCGCTCC AACAAACCA GTCCGAACCA CTACGCGGAC AACCAACACC 4140  
 ACCACCCCA AACCACCACT TCCATCCCC ACCTGTCCCC CTGGAGCTT GGAACGGCAC 4200  
 GAGATGATG CCAACCTGAT AATGAGCTCC AATGGGATCC CAGAGTACTA CGCTGAAGAA 4260

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GATGAGTTCT CAGGCTTGGG GACTGACACT GCAGTACCTA CGGAAGAGGC CTACGTTATA 4320
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ACTGCTACCA CACCGAGGGT GATCCAGAG GAAGGSCCA TCAGTTCCTT TCCTGAAGAA 4440
GAATTTGATC TGGCTGGAAG GAAACGATT GTTGCTCCTT ACCTGACGTA CCTAAATAAA 4500
GACCCATCAG CCCCCGTCTC TCTGACTGAT GCACTGGATC ACTTCCAAGT GGACAGCCTG 4560
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AATTCGAGT GCTCAGTATT TCCAGGAATA GCATATGCAC GCTGTTCTTG CTTCATGGA 5700
TGCTACATCT TTTCTGTTT TCTCATTTT GATTCTTCCA AAATAACTG AATTAAAGCT 5760
TCAGGTCCTT TTGTATGCG TAGAAAGGAA TTATTAATAA CACCACCAA GAAATAAAT 5820
ATATCCTACT TGAAATTAC TCTATGACT TACCCTATG TAGAATAAAT GTATCAAATC 5880
TTATTTGTAA ATTCTCAAT TTGATATATA TATGATATA TGCATATACA TATCCACACT 5940
TGCTGCAAG AATATTGATT AAAATTGCTA AATTGTACT TGTTCACAA AAAAAAAA 6000
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Seq ID NO: 60 Protein sequence  
Protein Accession #: Eos sequence

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1 11 21 31 41 51
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TPESAPTTAP ENLANVWPVNG KPTVVAASWD ALPETEGKVK VCLLDITGLFS VSPFPQSAKS 180
FQNTFFHTPR LSNHLEQSPS PILETLLLPW MWVCSLGNAI FSKSGPQTGE AWDLTPKPSL 240
SLCQCECST QHDFSCILAYL IDIQTKQVNK DPQLEGSVFG PCFLFYFLTF MLDIGGFSFI 300
MCYEDPVSSL TGNLSKSVAA SKADVQONTE DNGKPEKPEP SSPSPRAPAS SQHPSVPASP 360
QGRNAKDLIL DLKNIKILANG GAPRKPQLRA KKAELDLQS TEITGEEELG SREDSPMSPS 420
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SPLSKGKGKG EDAPATNSNA PSRSTMSSSV SSHLSRTQV SEGAEASDGE SHDGDREDG 660
GRQAEATAQT LRARPASGHF HLLRHKPFPA NGRSPSRFSI GRGPRLQPS SPOSTVPSRA 720
HPRVPSHDS HPKLSGSIHG DEEDEKPLPA TVVNDHVPSS SRQPSRGWE DLRRSPQRA 780
SLHRKEPIPE NPKSTGADTH PQGKYSSLAS KAQDVQQSTD ADTEGHSPKA QPGSTDRHAS 840
PARPPAARSQ QHFSVPRMT PGRAPEQQPP PPVATSQHHP GPQSRDAGRS PSQPRLSLTQ 900
AGRPRPTSQ RSHSSSDPYT ASSRGMLEPTA LQNDQEDAGQ SYDDSTEVE AQDVRAPAHA 960
ARAKEAAASL PKHQVESPT GAGAGGDHRS QRGHAASPAR PSRPGGPQSR ARVPSRAAPG 1020
KSEPPSKRFL SSKSQSVSA EDEEEDAGF PKGKEDLLS SSVKWPSSS TPRGGKDADG 1080
SLAKEEREP AIALAPRGSL APVKRPLPPP PGSSPRASHV PSRPPPSRAA TVSPVAGTHP 1140
WPRYTTTRAP GHFSTTPMLS LRQRMHARF KNPLSRQPAR PSYRQYNGR PNVEGKVLPG 1200
SNKPMGQRI INGPQGTQWV VDLDRGLVLN ABGRYLQDSH GNPLRIKLGG DGRITVDLEG 1260
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TPKPTTPIPT CPPGTLERHD DDGNLIMSSN GIPECYAED EFSGLETDTA VPTTEAYVIY 1440
DEDEFEFSR PPTTEPSTT ATTPRVIEE GAISFFEEE FDLAGRKRFP APYVTYLNKD 1500
PSAPCSLTD LDHPQVDSL DIIIPNDLKS DLPPHAPRN ITTVAVEGCH SFVIVDWDKA 1560
TPGDLVTGYL VYSASYEPI RNKFTQASS VTHLPIENLK PNTRYVFKVQ AQNPHGVGPI 1620
SPSVSVFTES DNPLLVVRPP GGELSGSHSL SNMIPATRTA MDGNM

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Seq ID NO: 61 DNA sequence  
Nucleic Acid Accession #: NM\_022743  
Coding sequence: 128..1237

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AAAGCTGATG CGATGCTCTC AGTGCCTCGT CGCCAAATAC TGTAGTGCTA AGTGTGAGAA 180
AAAAGCTTGG CCAGACACCA AGCGGGAATG CAAATGCCTT AAAAGCTGCA AACCAGATA 240
TCTCTCAGAC TCCGTTCGAC TTCTTGGCAG AGTTGTCTTC AAACCTATGG ATGGAGCACC 300
TTCAGATCA GAGAAGCTTT ACTCATTTTA TGATCTGGAG TCAATATTA ACAAACTGAC 360
TGAAGATAAG AAAGAGGGCC TCAGGCAACT CGTAATGACA TTTCAACATT TCATGAGAGA 420
AGAAATACAG GATGCTCTC AGCTGCCACC TGCCCTTGAC CTTTGTGAAG CCTTTGCAAA 480
AGTATCCTGC AACTCTTTC CCACTGTAA TGCGGAGATG CAGGAAGTTG GTGTTGGCCT 540
ATATCCAGCT ATCTCTTTC TCAATCACAG CTGTGACCCC AACTGTTOGA TTGTGTTCAA 600
TGGGCCCCAC CTCTTACTGC GAGCAGTCCG AGACATCGAG GTGGGAGAGG AGCTCACCAT 660
CTGCTACTCG GATATGCTGA TGACCAGTGA GGAGCGCCGG AAGCAGCTGA GGGACAGTA 720
CTGCTTTGAA TGTGACTGTT TCCGTTGCCA AACCAGGAGC AAGGATGCTG ATATGCTAAC 780

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TGGTGATGAG CAAGTATGGA AGGAAGTTCA AGAATCCCTG AAAAAAATTG AAGAACTGAA 840
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TGAAACGGCT CCCGATATCA ACATCTACCA GCTGAAGGTG CTCGACTGCG CCATGGATGC 960
CTGCATCAAC CTCGCCCTGT TGGAGGAAGC CTGTCTCTAT GGTACTCGGA CCATGGAGCC 1020
ATACAGGATT TTTTCCCGAG GAAGCCATCC CGTCAGAGGG GTTCAAGTGA TGAAGTTGG 1080
CAAACTGCAG CTACATCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140
TGATATTATG AGAGTGACAC ATGGCAGAGA ACACAGCCTG ATTGAAGATT TGATTCTACT 1200
TTTAGAAGAA TGGCAGCGCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAATA 1260
CGGCGTGTGT CTTTGTGAA TGCCCTATTG AGGTACACA CTCTATGCTT TGTTAGCTGT 1320
GTGAACCTCT CTTATTGAA ATTCTGTTCC GTGTTTGTGT AGGTAAATAA AGGCAGACAT 1380
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ATTTGGTTGA GGATGCCAAA AAAAAAATA AAAAAA

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Seq ID NO: 62 Protein sequence  
Protein Accession #: NP\_073580

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SEKLYSFYDL ESNINKLTED KKEGLRQLVM TFQHFMRREEI QDASQLPPAF DLFEAPAKVI 120
CNSFTICNAE MOEVGVGLYP SISLNLHSCD PNCISIVFNGP HLLLRVRDI EVGEELTICY 180
LDMLMTSEER RKQLRDQYCF ECDPCRCQTQ DKDADMLTGD EQVWKEVQES LKIEELKAH 240
WKWEQVLAMC QAIISNSER LPDINIYQLK VLDCCAMDACI NLGLLEALP YGRTMEFPYR 300
IFFPGSHFVR GVQVMKVGL QLHQGMFPQA MNLRLAFDI MRVTHGREHS LIEDLILLE 360
ECCANIRAS

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Seq ID NO: 63 DNA sequence  
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Coding sequence: 238..648

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1 11 21 31 41 51
| | | | |
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CGGAGCTCCG CGGCGCGACC CGCGGCCCC GCTTTGCTGC CGACTGGAGT TTGGGGGAAG 120
AAACTCTCCT CGCGCCGAGA AGATTCTTC CTGCGGGAAG GGACAGCGAA AGATGAGGGT 180
GGCAGGAAGA GAAAGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240
TTCCTCTCCA TCCTAGTGGC GCTGTGCTGC TGGCTGCACC TGGCGCTGGG CGTGCAGGGC 300
GCGCCCTGCG AGGCGGTGCG CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCACGCGG 360
ATGCCCAACC ACCTGCACCA CAGCACGCGA GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420
GAGGAGCTGG TGGAGCTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTCTG TGCCATGTAC 480
GCGCCCATTT GCACCTGGGA GTTCTGTGAC GACCTATCA AGCGGTGCAA GTCCGTGTGC 540
CAACGCGCGC GCGACGACTG CGAGCCCTTC ATGAAGATGT ACAACACAG CTGGCCCGAA 600
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CAGGAAAGGC CTCCTGATGT TGAAGTAAA CGCCTAAGCC CCGATCGGT CAAGTGTAAA 780
AAGGTGAAGC CACTTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTATGCC 840
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TTTTTGTGAT GAAAGGGGAT TTTTGAAGA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860
TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTATAGT AGAAACTTAA AAACAAAAAT 1920
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Seq ID NO: 64 Protein sequence  
Protein Accession #: NP\_003005.1

1 11 21 31 41 51

5 MFLSILVALC LMLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60  
YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPKCSV CQRARDDCEP LMKMYNHSWP 120  
ESLACDELFP YDRGVCSISPE AIUTDLPELV KWIDITPDMV VQERPLDVDC KRLSPDRCKC 180  
KKVKPTLATY LSNYSYVIH AKIKAVQSRG CNEVTTVVVD KEIFKSSSPI PRTQVPLITN 240  
SSQCPHILP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQNEER LQEQRRTVQD 300  
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10 Seq ID NO: 65 DNA sequence  
Nucleic Acid Accession #: BC010423  
Coding sequence: 248..1780

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ACATATTTTC TGTAAATATA CATGCGCCGG GAGCTTCTTG CAGGAATACT GCTCCGAATC 2520  
ACTTTTAAT TTTTCTTTT TTTTCTTCTG CCCTTTCAT TAGTGTATT TTTTATTAT 2580  
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60 CTGTAAAAAA ACCAAACACC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 66 Protein sequence  
Protein Accession #: AAH10423

65 1 11 21 31 41 51  
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QVGQVAVARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA 120  
DEGEYECRVV TFPAGSFQAR LRLRLVLPPL PSINPGPALE EQGLTLAAS CTAEGSPAPS 180  
70 VTWDEYVKT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL IQDQRITHIL 240  
HVSFLAEASV RGLEDQNLWH IGREGAMLC LSEGQPPPSY NWRLDGGPLP SGVRVDGDTL 300  
GFPLTTEHS GIYVCHVSNF PSSRDSQVTV DVLDPOEDSG KQVDLVASV VVVGVIAALL 360  
FCLLVVVVVL MSRYHRRKAQ QMTQRYEEL TLTRENSIRR LSHHTDPRS QPEESVGLRA 420  
EGHPDLSKDN SSCSVMSEEP EGRSYSTLT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ 480  
75 AMNHFVQENG TLRAKPTGNG IYINGRGLHV

80 Seq ID NO: 67 DNA sequence  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274..1782

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GTGAAGGAA AGGAAGATCA TTTTCATGCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180

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GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTGT GGTCACTTCT 480  
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CTAGTGCCCA GLPGLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 1620  
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ATGACAGAAAT GCTGGGCTCA CAATCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740  
ACACTTGCCA AAATGTCAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800  
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
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Seq ID NO: 68 Protein sequence

Protein Accession #: NP\_001194

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GEIHRALLI SVTVCSLLLV LLIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
EQSQSSSGSS GLPGLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 240  
WFRTEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNIV KKNGTCCIAV LGLAVKFISD 360  
TNEVDIPNT RVGTRKYMPP EVLDESILNRN HFQSYIMADM YSFLILNWEV ARRCVSGGIV 420  
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Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 166..1737

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CGCGTAGCTG TTTCAITTTT CTTCGTGAA GTCTTCACCT ACAGCATCAT CAAGACATTT 300  
GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360  
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CAGGACCGCG CTGCTTTTAT ATTATCTACG ATGGCCATTG CAGAAGTTTT CGGAAGGATC 1200  
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TAAATGATT TCTTTTTTCT TTTTCTTCT TCCTATGGTC TTGCTGTAAT AAACACTCT 2160
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Seq ID NO: 70 Protein sequence  
Protein Accession #: Eos sequence

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SRISWIIIS V FVLTFPSAPL ATVLNRFHG RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120
IGIISGLGY C FSFLPTVTIL SQYFGKRSI VTAVASTGEC PAVFAPAPAI MALKERIGWR 180
YSLLFVGLL Q LNVIFGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240
GVELTTSFN X VPTHNLELE PKADMQQVLV KTSRPPSEKK APLLDPSILK EKSFIYALF 300
GLFATLGFFA P SLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
IELICVILL T VSLFATTFAT EFWGLMSCSI PFGFMVGTIG GTHIPLAED DVVGIEKMSS 420
AAGVYIFIQ S IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
RHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

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Coding sequence: 166..1737

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GCGGTAGCTG TTTCAATTTT CTTCGTTGAA GTCTTCACCT ACGGCATCAT CAAGACATTT 300
GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
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Protein Accession #: NP\_004685

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YSLLFVGLL Q LNVIFGALL RPIIIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240
GVELTTSFN X VPTHNLELE PKADMQQVLV KTSRPPSEKK APLLDPSILK EKSFIYALF 300
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IELICVILL T VSLFATTFAT EFWGLMSCSI PFGFMVGTIG GLTFHLLKM MSWALQKMSS 420
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Seq ID NO: 74 Protein sequence  
Protein Accession #: NP\_002175.1

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65 SCTVDYSTVY FVNIEVWVEA ENALGKVTSD HINFDPVYKV KFNPPHNLVS INSEELSSIL 240  
KLITWNPSTK SVIILKYNQ YRTKDASTWS QIPPEDTAST RSSFTVQDLK PFTEYVFRIR 300  
OMKEDKGWY SDWSEEASGI TYEDRPSKAP SFWKIDPSH TGGYRTVQLV WKTLPPEAN 360  
GKILDYEVTL TRWKSHLQNY TVNATKLTVN LTNDRYLATL TVRNLVGKSD AAVLTIPACD 420  
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80 ESTQPLDSE ERPEDLQVLD HVDGGDLILP RQYYPKQNC QHESPDISH FERSKQVSSV 840  
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Seq ID NO: 76 Protein sequence  
 Protein Accession #: NP\_071414

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 VEAIDEDCSF QYSQICNYEI VTIDVPFAID RGNIRNTEK LSYDKHQHYE ILVTAYDCGQ 240  
 KPAAQDTLVQ VDVKPVCKPG WQDWTKRIEY QPGSGSMPLF PSIHLETCDG AVSSLIQIVTE 300

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 NEFNLEVISL HEDQVSDKEH VNHLIVQPPF LQSVHHPESR SSIQHSSVVP SIATVVIIS 840  
 VCMLVEVWAM GVYRVRIAEQ HFIQETAAK ESEMWDSDSA LTITVNPMEK HEGPGHGEDE 900  
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Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482..3007

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Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

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 LLEQENHSPIL TGSNMKYKTT NQSTFPLSFO DASSLYRNIL EKERELQQLG ITEYLKRNIA 780  
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Seq ID NO: 80 Protein sequence  
 Protein Accession #: NP\_057724.1

1 11 21 31 41 51  
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 IRISQLAEF VPLDYSVPIE IPTIKCKPDK LPLFKROYEN BIFVGSKTAD PCCYGHTQFH 300  
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 Coding sequence: 1..2070

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Seq ID NO: 82 Protein sequence  
Protein Accession #: FGENESH predicted

1 11 21 31 41 51

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GPEVIAGRVQ ATGCSPLDLP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH 240
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GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPKGKRGRLA GGSADTVRSP ADSLSMSSFQ 480
SVKISINSAN SQGKARPPQG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQSQARK 540
EKAEASNAGN SQGKARPPQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLQ 600
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Coding sequence: 557..1954

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	GAGCTAAAGG	CATGCCACAG	CAACCAAGAA	GGACAGGAAG	GCTTCTGAGG	AGAGACCTCT	4680
55	GAGGTGGGTC	TTGGAGAGGA	AGGACTTAGG	GAGGCAGAGT	GGAGGAAGTG	AGAGGACACC	4740
	CCAGCCAAAG	AGGGCGGCAG	GACCAAGGCG	TCAGAAAGCA	GGGCGCTGCA	GAGGGGCTGT	4800
	GTGCCACAGG	GTGAAGAGTT	TGTGTGGCAG	AAGGCGAGGG	GGCTTGCAATC	AGGGGTGACA	4860
	GCTGCTCTTT	TGTCCACAGCA	TAGCCCTCTG	ACATCCCTGG	AGAGCTGGGG	CGTCCACAA	4920
	TCTAAGTCA	AGCCCCATC	CTAACCTCTG	TGTTGCAAGT	AGGGTGAGCT	GTCTGTGGGC	4980
60	AGGAGGGAAG	ACTCTTGGAG	ATGAGCCTGG	TGAAGGGATA	ATGGCATCCC	GGGCCGAGGA	5040
	GCAGCACAGG	CAGAGGCTCT	GGGAGAGTTT	AAGGAGTGTA	GGGGAGGAAA	TGGCAGAGAA	5100
	TGAGCCAGAA	AAAGAAAGGT	TAGGGCAGGT	CCTGGAGGAC	ATGAGTGGCT	GTTTGGGCTT	5160
	TATCCAGCAG	TGGGGGAGCC	TTGGCAGGCT	TGTGGCTTAG	ATAGGTGCTT	TAGAAAGCCC	5220
	ACCAGCAGTT	GCTGGGCCAC	CCCGCTGGCT	GGGTCTCTGT	CTAAGGCAGG	AAATACAAGA	5280
65	ATGAGCAGGA	AAAGACCCCC	TCAAGGCTCA	CGTCTAGTGT	GGGAGACAAG	AAACACAGAT	5340
	GGGCAATATA	ACAGATGTC	TGGTTCCAGT	AAGTGCAGTG	AAGAACAGCG	GAGGCTGGAT	5400
	GCAGGGAGTG	ATGGAGGGGG	CTTTGTAAGG	GGAGGTGGGG	GGAAGCCTGT	CTCAGAGGAC	5460
	ACCAGATGG	AGCGCAGGAG	CAGCACGTGG	CAGTCAATG	GCAGGCCGTT	AGGGCAGAGG	5520
	GAGCTGGGCA	GGGCACAGCA	GGGCAGGAGT	GTGTTTGATG	TGTCCTGGGA	ACCSCCTTGA	5580
70	GGCGTCTGT	TGGCTGGAGT	GCTGCAGGTG	TCAAGGAAAT	TGTAGGAGAT	GTCTCTTGAG	5640
	TGTGATGGAA	TATAACCAGA	TTTCCAGAAG	GAAGTGCAT	GATCTGAGCT	AAAAAGGTCA	5700
	GTGTGGGAAA	TGGCTTGACG	GGGACAGGAG	TGGGAGCAGG	GAGATAGGAG	ACAATGTGTA	5760
	CCAGGACAGC	AGAAAGACAT	CCCGGTAGC	CTGGAACAGG	GAGACGGTGT	GGAGATGGTG	5820
	GCAGTCCGAT	AATGAGAGCC	GTAGGGCAAG	GCCAGCAGGA	TCCTAGAGTG	AGACGGGAGG	5880
75	TAAAGTCACC	GGGACTTGGT	GTCTCCACGT	CAGGGGCAAG	GGAAGGGGAG	AGGACAAGGG	5940
	TGACCCCGGA	GTTTAAAGAT	GGGACCGGGG	CCAGACGCAG	TGGCTCATGC	CTGTAATCCT	6000
	AGCACTTTGG	GAGGCTGAGG	CGGGCGGATG	GCTTGAAGTC	AGGAGTTTGA	AACCGGCTTG	6060
	GCCAAACATGG	TGAAACCCCG	TCTCTACTAA	AATATACAAA	AATTAGCCCTG	CGGTGGTGGT	6120
	GCATGCCCTGC	AGTCCCAAGT	ATTCAAGAGG	CTGAGGCGAC	AAGAAATCGCT	TGAACCTGGG	6180
80	AGGCGGAGGT	TGCAGTGAGC	CGAGATCCCG	CCATAGCACT	CCAGCCTTAG	CCTGGGCGAC	6240
	AGAGCGAGAC	CACATC					

1 11 21 31 41 51  
 5 VETPPQGSVH SGHLGSVVD PHTGTGNAGE RGRPRGKARV LALDSGGMDS SPSLPLIRT 60  
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 ILLAGNMMEK AQMLCQRHRR KSSVTDSESS LVNRPTLGQF TEEIHAIEVC YAECLLQRAA 180  
 LTFLQGSSHG GAVRPRALHD PSHACSCPPG PGRQHLFLQ DENMVSFIKG GIKVRNSYQT 240  
 YKELDSLVSQ SYQCKGENHP HFEGGVKLG VAFNLTLML PTRILRLLEF VGFSGNKDYG 300  
 10 LLQLEEGASG HSFRSVLCVM LLLCYHTFLT FVLGTGNVNI EAEKLLKPY LNRYPKGAIF 360  
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Seq ID NO: 89 DNA sequence  
 Nucleic Acid Accession #: AF007170  
 Coding sequence: 73..1725

1 11 21 31 41 51  
 20 AAGGAGGCGC CCTCCGGGAA AAGCGACGCG AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60  
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 25 TTGAGCAGCC TGGTGAACCG CCCACGCTG GGCCTATTCA CTGAAGAAGA AATCCACGCT 360  
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 AACATGTTGA GCTTCATCAA AGGCGGCATC AAAGTTGGA ACAGCTACCA GACCTACAAG 480  
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 30 AGGATCCTGA GGTGTGTGGA GTTGTGTTGG TTTTCAGAA ACAAGGACTA TGGGCTGCTG 660  
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 50 CCGCTGCCC TGCCCTGCTT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860  
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 Protein Accession #: AAC39582.1

1 11 21 31 41 51  
 70 KEAASGKSDR RTPESSLHEA LDQCMTALDL FLTNQFSEAL SYLKPRTKES MYHSLTYATI 60  
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 EVCYAECLLQ RAALTFLQDE NMVSFIKGI KVRNSYQTYK ELDSLVSQSS YCKGENHPHF 180  
 EGVKVLGVFA FNLTSLMLPT RILRLLEFVG FSGNKDYGLL QLEEGASGHS FRSVLCVMLL 240  
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 ECCEAQQHWK QFHMCYHEL MWCFTYKQW KMSYFYADLL SKENCWSKAT YIYMKAAYLS 360  
 MFGKEDHKPF GDDEVELFRA VPGLKLKIAG KSLPTEKFAI RKSRRYPSSN PISLPVPALE 420  
 MMYIWNQYAV IGKQPKLTDG ILEIITKAE MLEKGPENEY SVDDECLVLK LKGLCLKLYLG 480  
 80 RVQBAEENFR SIASANEKIK YDHYLIPNAL LELALLMEQ DRNEBAIKIL ESAKQNYKTY 540  
 SMESRTHFRI QAATLQAKSS LENSRRSMVS SVSL

Seq ID NO: 91 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 31..906



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5 GACTGCGTAC TGCAGTGGCA AGAGCAGAAC TGCTCTGGGG GCGCTCTGAA TCACTTCCGC 180  
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CATGGCAAGT GGCCCTTCTC CCGGTTCTCG TTCTTTCAAG AGCCGGCATC GGCCGTGGCC 360  
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10 GCCTCTCCCC CCATGTACCA CACCTGTGTG GCTTTCGCC TGGTGTCCCT CAATGCATGG 480  
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15 CTGGCTGGT GCTGTGGAA CCGCGGCGG CTGCCTCAG TGGCAAGTG CGTGGTGGTG 720  
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20 CCCTTCTCCC CTCAACCTT GAGATGATT TCTCTTTTCA ACTTCTTGA CTGGACATG 1020  
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CTCCTGGAGC TGAATCTGGG TGGAACTGAG TGTGCTCTTA GCTCTACCGG GAGGACAGCT 1200  
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25 GCCCTCTGTC TACCTGGGAG ACCAGGGACC ACAGGCCCTA GGGATACAGG GGGTCCCTT 1320  
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30 GTTGAGAGCC TGCCACCGTG TGTCCGGAGT GTGGCCAGG CTGAGTGAT AGGTGACAGG 1620  
GCCGTGAGCA TGGGCTGTGG TGTGTGTGAG CTCAGGCACCT AGGTGCGCAG TGTGGAGAGC 1680  
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35 TAATCACTTG TGGAGGCCCA CTGGGCCCAA GACGCCACCT GGGCGGACAG CAGGAGCTCT 1920  
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45 GAGGGGAGCT ATGCTAGGAC TCCAACTCA GGGACTCGGG TGGCCTGCGC TAGCTTCTTT 2520  
TGATACTGAA AACTTTTAAG GTGGGAGGGT GGCAGGGATG GTGCTTAATA AATCAATTC 2580  
AAGCCTCAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 92 Protein sequence

Protein Accession #: Eos sequence

50 1 11 21 31 41 51  
MAGLAARLVL LAGAAALASG SQGDREPVYR DCVLQCEBQN CSGGALNHFR SRQPIYMSLA 60  
55 GWTCDRDKCY ECMVTVGLY LQEGHKVPQF HGKNPFSRFL FQEPASAVA SFLNGLASLV 120  
MLCRYRFTVP ASSPMYHTCV AFAWVSLNAN FWSVTFHTRD TDLTERMDYF CASTVILHSI 180  
YLCCVRTVGL QHPVAVSAFR ALLLLMLTVH VSYLSLIRFD YGNLVANVA IGLNVVNWNL 240  
ANCLNNQRLR PHVRKCVVVV LLLQGLSLLE LLDFFPLFWV LDAHAHWHSI TIPVHVLFPS 300  
FLEDDSLYLL KESEDKPKLD

Seq ID NO: 93 DNA sequence

Nucleic Acid Accession #: NM\_033419.1

Coding sequence: 18..980

65 1 11 21 31 41 51  
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70 AGTGCAGAGA CAGAACTGTC TCTGGGGGCG CTCTGAATCA CTTCGCTCC CGCCAGCCAA 180  
TCTACATGAG TCTAGCAGGC TGGACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG 240  
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CCTTCTCCCG GTTCTCTGTC TTTCAAGAGC CGGCATCGGC CGTGGCCTCG TTTCTCAATG 360  
GCCGTGCCAG CCTGGTGTAT CTCTGCCGCT ACCGCACCTT CGTGCCAGCC TCCTCCCCCA 420  
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75 TTTTCCACAC CAGGGACACT GACCTCACAG AGAAAATGGA CTACTTCTGT GCCTCCACTG 540  
TCATCTTACA CTCAATCTAC CTGTGCTGCG TCAGGACCGT GGGGCTGCAG CACCCAGCTG 600  
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80 ACGTGGTGTG GTTGGTCTTC CTGCTGCAGG GGCTGTCCCT GCTCGAGCTG CTGACTTCC 840  
AGTGGTGGT GGTGGTCTTC CTGCTGCAGG GGCTGTCCCT GCTCGAGCTG CTGACTTCC 900  
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5 CCTCACCAGC CTTGGAGTCT GTTCTAGGGA AGGCCTCCCA GCATCTGGGA CTCGAGAGTG 1200  
 GGCAGCCCTC CTAGCTCCTG GAGCTGAAGT GGGGTGGAAC TGAGTGTGCT CTTAGCTCTA 1260  
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 CAGGGGGTCC CTTCTGTGTA CCACCCCCCA CCTCCTCCA GGACACCACT AGTGTTGCT 1440  
 GGATGCTTGT TCTTTGGCCA GCCAAGGTTT ACGGGATTC TCCCCTATGG ATCTTGAGGG 1500  
 ACCAAGCTGC TGGGATTGGG AAGGAGTTTC ACCCTGACCA TTGCCCTAGC CAGGTTCCCA 1560  
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 10 GCATAGGTGA CAGGGCCGTG AGCATGGGCC TGGGTGTGTG TGAGCTCAGG CTTAGGTGCG 1740  
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 GGTGGGTGTG TTAGCGTGGG TTAGGGGAAC GTGTGTGCGC GTGCTGTGGG GCATGTGAGA 1860  
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 15 GTCACCATCA ATAATCACTT GTGGAGCGCC AGCTCTGCCC AAGCGCCAC CTGGGCGGAC 1980  
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 25 CCAAGAGCA GTCTCGATG TTGAAGCAGA CTGGATTTT GCTCTGCCCC TGACCCCTTG 2520  
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Seq ID NO: 94 Protein sequence  
 Protein Accession #: NP\_219487.1

30 1 11 21 31 41 51  
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 35 LWPAKVHGDG PHGILRDQAA GIGKEFHPDH CPSQVPRRP HTPFQGGSS KPRARILCCC 180  
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Seq ID NO: 95 DNA sequence  
 Nucleic Acid Accession #: XM\_090469  
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40 1 11 21 31 41 51  
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 50 ATGTCTCTTC CTGAGTGTCT CAGTGTCTGAT GCTGGCCAGG TGGAGCAGAG AAGACAATG 360  
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 55 AGGGCACCTT GCGGCCACAC AAGGCGAGAG GCCCGCTTG CCTCAGCAG GCCCTGGGG 600  
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 60 CTGATCAGG AATCACCAGG TTCATTCCA ATAGGTTTAT GTACAGAAC AGCTGAACCA 900  
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Seq ID NO: 96 Protein sequence  
 Protein Accession #: XP\_090469

65 1 11 21 31 41 51  
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 70 NSADTDWTE EGPSGLDAFV AAHQEDTFPL KDIKHTSTFR QSVQONCIY SPREKPCGNV 180  
 RAPCAPPRRE APLALSRPWR LSRSPAPSPR TMAPFFTS DRELDPGPPP GLRSSAAAPH 240  
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Seq ID NO: 97 DNA sequence  
 Nucleic Acid Accession #: NM\_003474.2  
 Coding sequence: 37..3036

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 CTTTITTAATA AATGAAAGGC TAGAAGAGCT CAGCGCGCGC GCGGGCCGTG CGCGAGGGCT 180  
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	GCCGGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
	GCTGATGAAG	TTGTCACTGC	CTCTGTTGG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
	TTCCGATCCA	AGAAATCATCC	AGAAGTGCTG	AATATTGCGA	TACAAACGGG	AAGCAAAGAA	540
5	CTGATCATAA	ATCTGGAAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCACGTGT	720
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	CAGACATGGG	CAAGAAGGCA	TAAAGAGAG	ACCCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
	GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGCGATTAA	TAGAGATTGC	TAATCACGTT	GACAAGTTT	ACAGACCACT	GAACATTGG	1080
	ATCGTGTGG	TAGGCGTGG	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
15	CCATTACCCA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	1200
	TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTCC	AAGGGACCAC	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCAT	GGACCATTC	1320
	GACAAATCCC	TGGTGCAGC	CGTGACCCCTG	GCACATGAGC	TGGCCACAA	TTTCGGGATG	1380
	AATCATGACA	CATGGAACAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
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	GACTTGGAGA	ATGCGCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACTT	GCCGGAAGTC	1560
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	AAGCCGGAAG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
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	GGCTACTGCT	ACAAATGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTGAC	ACTCTGGGGA	1920
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30	AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2100
	GTTCCTATAG	AAACAAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
	CACGTGTACT	TGGGCGATGA	CATGCCGGAC	CCAGGGCTTG	TGCTTGACAG	CACAAAGTGT	2220
	GCAGATGGAA	AAATCTGCGT	GAATCGTCAA	TGTCAAAATA	TTAGTGTCTT	TGGGGTTTAC	2280
	GAGTGTGCAA	TGCACTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
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	GGCCCCATCC	GCAAGCAGCA	TAACCAAGGT	TTAACCATAG	GAATTCGTGT	GACCATCTCT	2460
	TGTTCTTTTG	CTGCGGATTT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGTCT	2520
	TTTACAAATA	AGAAGACCA	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
	CGTGGCTTCC	AACCTGTGCA	GGCTCACCTC	GGCCACCTTG	GAAGAAGSCT	GATGAGGAAG	2640
40	CCGCCAGATT	CCTACCCACC	GAAGGACAAT	CCCAGGAGAT	TGCTGCACTG	TCAGAATGTT	2700
	GACATCGACA	GACCCCTCAA	CGGCCCTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
	CTTCCTCCCC	TCCACCGGGC	CCCACTGTGA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
	AAGCCTGGAC	TTAGGCGAGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880
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	TGAAGACATA	AGTTTGCACT	ATCTTTTCAG	TCCAGTTGGA	GTTTTGTGTA	CCAACTTTTA	3120
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	CCAACTACCC	CCAGCTGTGC	TTATGGTACC	AGATGCAGCT	CAAGAGATCC	CAAGTAGAAT	3480
	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
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	TGAACCATTA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAA	4080
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	CTCTTCACTC	TTCAATGGCC	TGACTAGGGA	GCCATGTTTC	ACAAGTCTT	TAAAGTACT	4440
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Protein Accession #: NP\_003465

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5 YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAP KLSVRGSCG 180  
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LIEIANHVDK FYRPLNIRIV LVGVEVWMDM DKCSVSQDPF TSLHEFLDNR FMKLLPRKSH 300  
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10 DTLDRGKSCQ MAVEGGCGIM NASTGYPPFM VFSSCSRKDL ETSLEKGMV CLFNLPEVRE 420  
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ACRDSNSDC LPEFCTGASP HCPANVYLHD GHSCQDVGY CYNGICQTHE QQCVTLMGPG 540  
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15 IETNIPLQQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRQCC NISVFGVHEC 660  
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LAAGFVVYLK RKTILRLFT NKKTIEKLR CVRPSRPPRG PQPCQHLGH LGKGLMRKPP 780  
DSYPPKDNFR RLLQCCQNDI SRPLNGLNVP QPQSTQRLV PLHRAPRAPS VPARPLPAKP 840  
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20 Seq ID NO: 99 DNA sequence  
Nucleic Acid Accession #: NM\_003714  
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Protein Accession #: NP\_003705

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75 ISRKCPAIRE MVSQQLRECY LKHDLCAAA ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180  
CGEEVKBAIT HSVQVQCEQN WGSLSILSF CTSAIQKPFT APPERQFQVD RTKLRSRAHGG 240  
EAGHHLPEPS SRETGRGAKG ERGSKSHFNA HARGRVGGLG AQGPSGSSEW EDEQSEYSDI 300  
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80 Seq ID NO: 101 DNA sequence  
Nucleic Acid Accession #: NM\_005940  
Coding sequence: 23..1489

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Protein Accession #: NP\_005931

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YPLSLSPDDC RGQVHLQGP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300  
VSTIRBELFF FKAGFVRLRL GGQLQPGYPA LASRHWQGLP SPVDAAPEDA QGHIMFPQGA 360  
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Coding sequence: 351..4499

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Seq ID NO: 104 Protein sequence  
 Protein Accession #: NP\_149163.2

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Seq ID NO: 106 Protein sequence  
Protein Accession #: Eos sequence

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	PILIIPKILE	YSEEQLGNVV	HGVLCLFALF	LSECVKSLSF	SSSWIINQRT	AIRFRAVSS	240
	FAFEKLIQFK	SVIHITSGEA	ISFPTGDNVY	LPEGVICYGL	VLITCASLVI	CSISSYFIIG	300
	YTAFAIILCY	LLVFPPLAVF	TRMAVKAQHH	TSEVSDQRI	VTSEVLTCIK	LIKMYTWEKP	360
10	FAKIEGMEF	LTPCSKPGDG	MAFSMLASLN	LLRLSVFFVP	IAVKGLTNSK	SAVMRFKKFP	420
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	VGVCSSGIFT	KVTRKASTAL	HNKLPNKVFR	CPMSFFDTIP	IGRLNCFAG	DLEQLDQLP	900
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	RTGSGKSSLG	MAFLRVLEPM	AGRILIDGVD	ICSIGLEDLR	SKLSVIPQDP	VLLSGTIRFN	1200
	LDPEFRHTDQ	QINDALERTF	LTKAISKFPK	KLHTDVVENG	GNFSVGERQL	LCIARAVLRN	1260
25	SKILIDEAT	ASIDMETDTL	IQRTIREAFQ	GCTVLVIAHR	VTTVLNCDHI	LVMNGKQVVE	1320
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Seq ID NO: 107 DNA sequence

Nucleic Acid Accession #: NM\_024022

Coding sequence: 202..1563

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	GATGCTGTGT	CTGCACAGAT	CCTGTCACTG	CTGCCAATGA	AGTTTTTTCC	AATCATCGTC	360
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Seq ID NO: 108 Protein sequence

Protein Accession #: NP\_076927

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	VTALHHSYVY	REGCASGHVV	TLQCTACGHR	RGYSSRIVGG	NMSLLSQWV	QASLQFGYH	240



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 20 GTTGGACAGC CTGGCTTACC AGGACCCCGG GGGCCACAGG GACCACCTGG AATCCCTGGA 540  
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 25 GGACAGCCAG GCATCAAAGG TGATAGAGGT TTCCGGGAG AAATGGGACC AATTGGCCCA 840  
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 30 GGTCTTCTCG GGAAGCCAGG TCTGACTGGA CCCCTGGGGA ATATGGGACC CCAAGGACCA 1140  
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 65 TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTTACGAC ACAATAAAT 3180  
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Seq ID NO: 110 Protein sequence  
 Protein Accession #: NP\_000484.2

70 1 11 21 31 41 51  
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 80 KGETGPAGPA GYPGAKGERG SPGSDGKPGV PGKPLDGP KGNPLPGPKG DPGVGGPPGL 420  
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 ATKGLNGPTG PPGPPGPRGH SCEPGLPGPP GPPGPPGQAV MPEGPIKAGQ RPSLSGTPLV 540  
 SANQVGTGMP VSAFTVILSK AYPATGPIF FDKILYNRQ HYDPRTGIFT CQIPGIYFYS 600  
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Seq ID NO: 111 DNA sequence  
Nucleic Acid Accession #: NM\_000949  
Coding sequence: 285..2153

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1 11 21 31 41 51  
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AACTGCATAA CCTTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAT ATAACCATTT 2640  
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Seq ID NO: 112 Protein sequence  
Protein Accession #: NP\_000940

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SLTYHREGET LMHECPDYIT GGFNSCHFGK QYTSMWRTYI MMVNATNQMG SSFSELYVD 120  
VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW 180  
EIHFAQQOTE FKILSLHPQG KYLVQVRCKP DHGYNSAWSP ATFIQIPSDF TMNDITVWIS 240  
VAVLSAVICL IYVWAVALKG YSMVTCIFPP VPGPKIKGPD AHLLEKKGSE ELLSALGQDD 300  
FPPTSDEYDL LVEYLEVDDG EDQHLMSVHS KEHPSQGMKP TYLDPDTSRG RGSCDSPSLL 360  
SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPOCISME GKIPYFHAGG SKCSTWPLPQ 420  
PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQREVE 480  
SPHSETDQDT PWLLPQEKTP FGSAPKLDYV EIHVKNKDGA LSLLPKQREN SGKPKKPGTP 540  
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Seq ID NO: 113 DNA sequence  
Nucleic Acid Accession #: XM\_062811  
Coding sequence: 1..888

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GGCGACGCCA CCATCTGCTG CCGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCGGAG 240  
GCGCGCTCG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CAGCGCTGGC 300  
CGGGCGGACA AAGACGGGCC CGACGGCTCG GCAATGCCCA TCTACGTGCC GTTCTCTATT 360  
GTTGCTCCCG TGTGTGTCGC CTTTATCATC TTGGGGTCCC TGGTGGCAGC CTGTGTCTGC 420

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 CCCACGAATT TCTCTGTGCT GAACTGTGAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720  
 CAGTATCTGC ATCCCCCATA CGTGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780  
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 CCTCACACA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 114 Protein sequence  
 Protein Accession #: XP\_062811

1 11 21 31 41 51  
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 VGSVFVAFII LGSILVAACC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180  
 SSTAASSSSS ANSGARAPPT RSQTNCLPE PTMNNVYVNM PTNFSVLNQC QATQIVPHQG 240  
 QYLHPYVGY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 115 DNA sequence  
 Nucleic Acid Accession #: NM\_013257  
 Coding sequence: 223..1512

1 11 21 31 41 51  
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 TTTGATAAAG TTTATAACAC TTTAAAAAAA CAGTTTCTCT CTATGGCCCT GAAGATTCTT 240  
 GCCAGAGAGAA TATTTGGTGA TAAITTTGAT CCAGATTTTA TTAACAAAG ACGAGCAGGA 300  
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Seq ID NO: 116 Protein sequence  
 Protein Accession #: NP\_037389

1 11 21 31 41 51  
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 LPFHLQRRS FPEHRARFYA AEIASALGYL HSIKIVYRDL KPENILLDSV GHVVLDFGL 240  
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Seq ID NO: 117 DNA sequence  
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Coding sequence: 1..681

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  AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACCA TCCGGCTATG GGCCTGTCAG 240
  CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
  GAGAAGAAGA GGAAGTTTCA CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG 360
  ATCAAAACCC AGAAGGTCGG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
  TTCTTCCGGG TCATCTTCGA AGCCGCTTTC ATGTACGTCT TCTATGTCT GTACGACGGC 480
  TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
  TTTGTGTCCC GCGCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
  ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTTCG TAATTAGATA TTGTTCTGGG 660
  AAGTCAAAAA AGCCAGTTTA A
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Seq ID NO: 118 Protein sequence

Protein Accession #: NP\_003995.1

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  KNYCYDHYFP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEFKDIEE 120
  IKTKVRIEG SLWWTYTSI FFRVIFEAAF MVFVVMYDG FSMQLRVKCN AWPCPNTVDC 180
  FVSRPTEKT VTFVFMIAVSG ICILLNVTEL CYLLIRYCSG KSKKPV
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Seq ID NO: 119 DNA sequence

Nucleic Acid Accession #: XM\_061091.1

Coding sequence: 1..2481

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  CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGT TTCTTTGCTA TGAATTTTAA 240
  GTTGGGAAGC CTCTTTTGA GGCAAACGAA GTCCATGTAA GCAAAAGAAC CATCGGGAAG 300
  ATTTCACTCG CACGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCGTGTA 360
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  GTCTGTGACG GTCTGSACAT CAGCCCGGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
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  CTCTGACACA CAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
  GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACCTGCCA CCAAGCAGCT GAAGGAAAGG 720
  GGTGTCACTG TGTTCGTGT GGGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCACTG 780
  GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
  GGCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
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  CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCTC 1020
  TGCCCGCTGG CCTTTGGAGG GAGAGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
  GTGACCTCC TCCTCTGCTT GGACAGCTCT GCGGGCACCA CTCTGGACCG CTCTCTGCGG 1140
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Seq ID NO: 120 Protein sequence

Protein Accession #: XP\_061091.1

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Protein Accession #: Eos sequence

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15	TATCTGGAAG	ATTGTCTGCC	TGCCTTCTAC	TTCTCAAATC	TTTCTTGTA	AAGTTTCCAA	1320
	TTTTTTCAC	GAAACCTGAG	TTAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440
	TACACTCTTC	CCTCCTGCAG	TTTCTTCTCT	GCTCCCAACC	CCCATCTCAT	AGCATCCCCC	1500
	TCTATTTC	ATGCTCCTCT	CCAACGCTT	AGTTTCTGAA	TTTCTTTTAA	ATTACAGTTT	1560
20	TATGAAAGCA	TATTTTATTT	ACTTGGTGT	GAAATAGCCC	TCATAAAACC	TAAGCACTTG	1620
	GAAACACAAT	AATAGTATTA	ACTAAGTAGA	TCTATTGAAT	TTCAGAGAAG	AGCCTTCTAA	1680
	CTTGTTTACA	CAAAAACGAG	TATGATTTAG	CACTCATACT	AGTTGAAATT	TTTAATAGAA	1740
	TCAAGGCACA	AAAGCTCTTA	AACCATGTGG	AAAAATTAGG	TAATTATTGC	AGATTGATGT	1800
	CTCTCAATCC	CATGATTTGC	GCTTATGTTA	CAAGTTGTGT	TCACAGTTGA	GACTTAATTT	1860
25	CTCCTAATTT	CTTCTGCCCG	AAGGTAAGT	GGTGCCTCCA	GCTTACACGA	TCATAATTCA	1920
	AAGGTTGGTG	GGCAATGTAA	TACTTAATTA	AAATAATGAT	GGAAGAGCTA	TCTGGAGATT	1980
	ATGAGTAGC	TGATTTGAAT	TTTCAGTATA	AAACTTTAGT	ATAATTGTAG	TTTGCAAGT	2040
	TATTTTCAGT	TCACATGTAA	GGTATTGCAA	ATAAATTCIT	GGACAATTTT	GTATGGAAAC	2100
	TTGATATTAA	AAACTAGTCT	TGTTTCTTT	GCAGTTTCTT	GTAATTTTAT	AAACCAGGCA	2160
30	CAAGGTTCAA	GTTTAGATTT	TAAGCACTTT	TATAACAATG	ATAAGTGCTT	TTTGGAGAT	2220
	GTAACCTTTA	GCAGTTTGT	AACCTGACAT	CTCTGCCAGT	CTAGTTTCTG	GGCAGGTTTC	2280
	CTGTGTCAGT	ATTCCCGCTC	CTCTTTGCAT	TAATCAAGGT	ATTTGGTAGA	GGTGAATCT	2340
	AAGTGTTTGT	ATGTCCAATT	TACTTGATA	TGTAACCAT	TGCTGTGCCA	TTCATGTTT	2400
	GATGCATAAT	TGGACCTTGA	ATCGATAAGT	GTAAATACAG	CTTTTGATCT	GTAATGCTTT	2460
35	TATACAAAG	TTTATTTTAA	TAATAAAATG	TTTGTCTTAA	AAAAA		

Seq ID NO: 126 Protein sequence  
Protein Accession #: NP\_114148.1

40	1	11	21	31	41	51	
	MDARRVPQKD	LRVKQNLKPF	RYVKLISMET	SSSSDDSCDS	FASDNFANTR	LQSVREGCRT	60
	RSQCRHSGPL	RVAMKFPARS	TRGAINKKAE	SRQPSNSVT	DSNSDSEDES	GMNFLEKRAL	120
	NKQNKAMLA	KLMSLESEFP	GSFRGREPL	GSDSQSRPR	RRTFPGVASR	RNPERRARPL	180
45	TRSRRIILGS	LDALPMEEEE	EEDKYMLVRK	RKTVDGYMNE	DDLPRSRRSR	SSVTLPHIIR	240
	FVEEITEEEL	ENVCSNSREK	IYNRSLSGTC	HQCRQKTI	IDT KTNCRNPDCW	GVRGQPCGPC	300
	LRNRYGEEVR	DALLDPNWHC	PPCRGICNCS	FCRQRDRGCA	TGVLVYLAKY	HGFNGVHAYL	360
	KSLKQEFEMQ	A					

Seq ID NO: 127 DNA sequence  
Nucleic Acid Accession #: AF305616.1  
Coding sequence: 1..863

55	1	11	21	31	41	51	
	ATGCACCGCT	TGATGGGGGT	CAACAGCACC	GCCGCGCGCG	CCGCGCGGCA	GCCCAATGTC	60
	TCCTGCACGT	GCAACTGCAA	ACGCTCTTTG	TTCCAGAGCA	TGGAGATCAC	GGAGCTGGAG	120
	TTTGTTCAGA	TCATCATCAT	CGTGGTGGTG	ATGATGGTGA	TGGTGGTGGT	GATCAOGTGC	180
	CTGTGAGGCC	ACTACAAGCT	GTCTGCAOAG	TGCTTCATCA	GCCGGCACAG	CCAGGGGGGG	240
60	AGGAGAGAAG	ATGCCCTGTC	CTCAGAAGGA	TGCCCTGTGC	CCTCGGAGAG	CACAGTGTCA	300
	GGCAACGGAA	TCCAGAGGCC	GCAGGCTTAC	GCCCGGCTTC	GGCCCAACGA	CCGCTGGGCC	360
	GTGCCGCGCT	TGCCCGAGCG	GGAGCGCTTC	CACGCTTCC	AGCCCACTTA	TCCGTAACCTG	420
	CAGCAOGAGA	TCGACCTGCC	ACCCACCATC	TGGCTGTGAG	ACGGGGAGGA	GCCCCACCC	480
	TACCAAGGCC	CCTGCACCTT	CCAGCTTGGG	GACCCGAGAG	AGCAGCTGGA	ACTGAACCGG	540
65	GAGTCGGTGC	GCGCACCCCT	AAACAGAAC	ATCTTGAGCA	GTGACCTGAT	GGATAGTGCC	600
	AGGCTGGGCG	GCCCTGCCCC	CCCCAGCAGT	AACTCGGGCA	TCAGCGCCAC	GTGCTACGGC	660
	AGCGCGGGCG	GCATGGAGGG	GCCGCGCCCC	ACCTACAGCG	AGGTGATCGG	CCACTACCCG	720
	GGGTCTCTCT	TCCAGCACCA	GCAGAGCAGT	GGCGCGCCCT	CCTTGCTGGA	GGGGACCCGG	780
70	TCCACCAACA	CACACATCGC	GCCCTAGAG	AGGCAGGCCA	TCTGGAGCAA	AGAGAAGGAT	840
	AAACAGAAAG	GACACCTCT	CTAG				

Seq ID NO: 128 Protein sequence  
Protein Accession #: AAL09357.1

75	1	11	21	31	41	51	
	MHRLMGVNST	AAAAAGQPNV	SCTCNCKRSL	FQSMETILE	FVQIIIVV	MMVMVVITC	60
	LLSHYKLSAR	SFISRHSGQR	RREDALSSSE	CLWPESTVS	GNGIPEPQVY	APPRPTDRLA	120
	VPPFAQRERF	HRFPQTPYPL	QHEIDLPTTI	SLSDGEEPPP	YQGPCTQLRL	DPEQQLRLNR	180
80	ESVRAPPNRT	IPDSLDLMSA	RLGGPCPPSS	NSGISATCYG	SGGRMBGPPP	TYSEVIGHYP	240
	GSSFQHQSS	GPPSLLEGTR	LHRTIAPLE	SAAIWSKEKD	KQKGHPL		

Seq ID NO: 129 DNA sequence  
Nucleic Acid Accession #: NM\_004952.1

Coding sequence: 1..718

```
1      11      21      31      41      51
|      |      |      |      |      |
5  ATGGCGGCGG CTCCGCTGCT GCTGCTGCTG CTGCTGCTGC CCGTGCCGCT GCTGCCGCTG 60
   CTGGCCCAAG GGCCGCGAGG GGCCTGCGGA AACCGGCATG CCGTGTACTG GAACAGCTCC 120
   AACCAGCACC TGCAGCGAGA GGGCTACACC GTGCAGGTGA ACGTGAACGA CTATCTGGAT 180
   ATTTACTGCC CGCACTACAA CAGCTCGGGG GTGGGCCCCG GGGCGGGACC GGGCCCCGGA 240
   GGCGGGGGCAG AGCAGTACGT GCTGTACATG GTGAGCCGCA ACGGCTACCG CACCTGCAAC 300
10  GCCAGCCAGG GCTTCAAGCG CTGGGAGTGC AACCGGCCGC ACGCCCCGCA CAGCCCCATC 360
   AAGTTCCTGG AGAAGTTCCA GCGCTACAGC GCCTTCTCTC TGGGTACAGA GTTCCACGCC 420
   GGCCACGAGT ACTACTACAT CTCCACGCCC ACTCACAACC TGCACTGGAA GTGTCTGAGG 480
   ATGAAGGTGT TCGTCTGCTG CGCTCCACA TCGCACTCCG GGGAGAAGCC GGTCCCCACT 540
   CTCCCCCAGT TCACCATGGG CCCCATTGTG AAGATCAACG TGCTGGAAGA CTTTGAGGGA 600
15  GAGAACCCTC AGGTGCCCAA GCTTGAGAAG AGCATCAGCG GGACCAGCCC CAAACGGGAA 660
   CACCTGCCCC TGGCCGTGGG CATCGCCTTC TTCTCATGA CGTCTTGGC CTCCTAG
```

Seq ID NO: 130 Protein sequence  
Protein Accession #: NP\_004943.1

```
1      11      21      31      41      51
|      |      |      |      |      |
20  MAAAPLLLLL LLVPVPLPL LAQGPGGALG NRHAVYWNSS NOHLRREGYT VQNVNDYLD 60
   IYCPHYNSSG VGPGAGPGPG GGAEQYVLYM VSRNGYRTCN ASQGFKRWEC NRPHAPHSPI 120
25  KFSEKFORYS AFSLGYEFHA GHEYIYISTP THNLHWKCLR MKVFVCCAST SHSGEKFVPT 180
   LPQFTMGPNV KINVLEDFEG ENFQVPKLEK SISGTSPPKRE HLPLAVGIAF FLMTFLAS
```

Seq ID NO: 131 DNA sequence  
Nucleic Acid Accession #: NM\_012445.1  
Coding sequence: 276..1271

```
1      11      21      31      41      51
|      |      |      |      |      |
35  GCACGAGGGA AGAGGGTGAT CGGACCCGGG GAAGGTGCTG GGGCAGGGCG AGTTGGGAAA 60
   GCGGCAGCCC CGCCGCCCCC CGCAGCCCCC TCTCTCTCTT TCTCCACAGT CCTATTGCGC 120
   TCTCGCTGGA GGCCAGGCCG TGCAGCATCG AAGACAGGAG GAAGTGGAGC CTCAATTGGC 180
   GGCCGGGGCG GCGCGCTCGG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCCGACC 240
   GGTGCCGGCC GCGCTCCCGC TGCTCTCTGC GGTGTATGGA AAACCCACAG CCGCGCCGCG 300
   CCTCGGGCAA GGCCTCTCTG GCTCTCTCTC TGGCCACTCT CGGCGCCGCC GGCCAGCCTC 360
40  TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCCCAGCCAA ATACAGCATC ACCTTCACGG 420
   GCAAGTGGAG CCAGACGGCC TTCCCCAAGC AGTACCCCTT GTTCCGCCCC CCTTCGCGAGT 480
   GGCTTCTGCT GCTTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCACT 540
   ACGTCAGTAA CCGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCTTGGGCG CTGATGAAGG 600
   AGATCGAGGC GCGCGGGGAG GCGCTGCAGA GCGTGCAAGC GGTGTTTTCG GCGCCGCGCG 660
45  TCCCCAGCGG CACCGGGCAG ACGTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720
   TCTCGTTTGT GGTGCGCATC GTGCCAGGCC CGGACTGGTT CGTGGGCGTG GACAGCCTGG 780
   ACGTGTGCGA AGGGGACCGT TGGCGGGAAC AGGCGGCGCT GGACCTGTAC CCCTACGAGC 840
   CCGGAGCGGA CAGCGGCTTC ACCTTCTCTT CCCCCAATT CGCCACCATC CCGCAGGACA 900
   CCGTGACCGA GATAACGTCC TCTCTCTCCA GCCACCGGCG CAACTCTCTC TACTACCCGC 960
50  GGCTGAAGGC CTGCTCTCCC ATGCCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
   GGGCCTTCAT CCTTCCCGCC CAGTCTCTCG CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080
   CCTCAGTTCC AGAAAGCGCG CTGGACTGCG AGGTCTCCCT GTGGTCTGTC TGGGGACTGT 1140
   GCGGAGGCCA CTGTGGGAGG CTGGGACCA AGAGCAGGAC TCGCTACGTC CGGTCCAGC 1200
   CGCCCAACAA CCGGAGCCCC TGCCCCGAGC TCGAAGAAGA GGCTGAGTGC GTCCCTGATA 1260
55  ACTGCGTCTA AGACCAAGAG CCGCAGCCCC CTGGGGCCCC CGGAGCCATG GGGTGTGCGG 1320
   GGCTCTGTG CAGGCTCATG CTGCAGGCGG CCGAGGCACA GGGGGTTTGG CGCTGTCTCT 1380
   GACCGCGGTG AGCGCGCGCC GACCATCTCT GCCTGAAGG GCCCTCTGCT GGCCGCGCAG 1440
   GGCAATGGGA AACAGCCTCC TCCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG 1500
   TCTGCTCTCA GCCTCTCTCT CCGCAGGAT AAAGTCATCC CCAAGGCTCC AGCTACTCTA 1560
60  AATTATGTGC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCTTCTAT CGTCCAGGGG 1620
   CCGTGGCTCC ACCTGGTGGC AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680
   CTCTCCCGAG GCGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740
   GGAAGCGTCA GTGTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800
   TGCTCAC
```

Seq ID NO: 132 Protein sequence  
Protein Accession #: NP\_036577.1

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1      11      21      31      41      51
|      |      |      |      |      |
70  MENFSPAAL KALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60
   PLFRPAPQWS SLLGAHSSD YSMWRKNQYV SNGLRDPFAR GEAWALMKEI EAAGALQSV 120
   HAVFAPAPVP SGTGQTSDEL EVQRRLSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180
75  ALDLVPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPIARVT 240
   LVRLRQSPRA FIPPAVLPS RDNEIVDSAS VFETPLDCEV SLWSSWGLCG GHGRLGTRKS 300
   RTRYVRVQPA MNGSPCELE EEAECVPDNC V
```

Seq ID NO: 133 DNA sequence  
Nucleic Acid Accession #: NM\_019894  
Coding sequence: 1..1314

```
1      11      21      31      41      51
|      |      |      |      |      |
80  ATGTTACAGG ATCTCGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
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5  
 10  
 15  
 20

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AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTT GCGGCGAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGACTGTCT CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCCACTGTC AGGTGCTGGA CTGGGCCACA 360
GGGAAGTGGT TCTCTGCTGT TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAC AGCCAGGAGC TTGCTATGCG GAACTCAAGT 540
GGGCCCTGTG TCTCAGGCTC CTGGTCTGCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGTCTGT GAGGGAGGCA TCCTGGACCC CCACTGGGTC 720
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCGCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTACG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGATCAT TGGATGGGCG TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACATG TGCAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GGTACACAGG GGAAGTCAAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TGGGCTGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
AAGGTCTCAG CTAATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
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Seq ID NO: 134 Protein sequence

Protein Accession #: NP\_063947.1

25  
 30  
 35

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1 11 21 31 41 51
| | | | |
MLQDPDSQPL LNSLDVKPLR KPRIPMETFR KVGPIPIIAL LSLASIIIVV VLIKVILDKY 60
YFLCGQPLHF IPKRLQCDGE LDCPLGEDEE HCVKSPFPEG AVAVRLSKDR STLQVILDSAT 120
GNWFSAFDFN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELRMNRNS 180
GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWPWQV SIQYDQHVHC GGSILDPHV 240
LTAHCFRKH TDVFNWVRA GSKLGSFPP LAVAKIIIE FNPMPKND JALMKLQFPL 300
TFSGTVRPIC LPFFDEELTP ATPLWIIWGW FTQKNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAGIPEGGV DTCQGDSSGP LMYQSDQMHV VGIVSWGYGC GGPSTPGVYT 420
  
```

Seq ID NO: 135 DNA sequence

Nucleic Acid Accession #: NM\_003045

Coding sequence: 148..2037

40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

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1 11 21 31 41 51
| | | | |
CGATCCTGCC GGAGCCCCGC CGCCGCCGGC TTGGATTCTG AAACCTTCTT TGTATCCCTC 60
CTGAGACATC TTTGTGCAA GATCGAGGCT GTCCCTCTGG GAGAAGGTGG TGAGGCTTCC 120
CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAGG TCCTGCTCAA CATTGGGCG 180
CAGATGCTGC GGGCGAAGGT GGTGAGCTGT AGCCGGGAGG AGAOCGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC 300
GTCCCTGGCTG GAGCTGTGGC CGGTGAGAAT GCAGGCCCTG CCATTGTCTAT CTCCTTCTC 360
ATGCTGCGCG TGGCCCTCAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420
CCCAAGACGG GCTCAGCTTA CTTCTACAGC TATGTCAACG TTGGAGAGCT CTGGGCCCTC 480
ATCACCGGCT GGAACCTAAT CCTCTCTAC ATCATCGGTA CTTCAAGCGT AGCGAGGGCC 540
TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCATCG GGGAGTTCTC ACGGACACAC 600
ATGACTCTGA ACGCCCCCGG CGTCTGGCT GAAAACCCCG ACATATTCCG AGTGATCATA 660
ATTCTCATCT TGACAGGACT TTTAACTCTT GGTGTGAAAG AGTGGGCCAT GGTCAACAAA 720
ATATTCACTT GTATTAAAGT CTTGTCTCTG GGCCTCATAA TGGTGTGAGG ATTTGTGAAA 780
GGATCGGTTA AAAACTGGCA GCTCACGGAG GAGGATTTTG GGAACACATC AGGCCGTCTC 840
TGTTTGAACA ATGACACAAA AGAAGGGAAG CCGGGTGTG GTGGATTCAAT GCCCTTCGGG 900
TTCTCTGGTG TCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTCGTGGG CTTTGACTGC 960
ATGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCCGT GGGGATOGTG 1020
GCGTCCCTCT TGATCTGCTT CATGCCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG 1080
ATGCCCTACT TCTGCCTEGA CAATAACAGC CCCCTGCCCG ACGCCTTTAA GCACGTGGGC 1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT CGGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCAT TGTTTCCCAT GCCTCGGTTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
TTTAAATCT TAGCCACGCT CAATGATAGG ACCAAAACAC CAATAATGCG CACATTAGCC 1320
TCGGGTGCGG TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380
ATGTCATTG GCACTCTCTT GGCTTACTCG TTGGTGGCTG CCTGTGTGTT GGTCTTACGG 1440
TACCAGCCAG AGCAGCCTAA CTTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CCAGCAGAC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560
GCAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAAA ACATGGAGCC TTCCAAAATC 1620
TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACTTCTGCG 1680
ATTGTGACCG TGCTTGAAGT GGAGGCTCTC ACCAAAGGGG CGCTGTGGGC AGTCTTCTG 1740
CTGCGAGGCT CTGCCCTCTT CTGTGCGGTG GTACGCGGCG TCATCTGGAG CGAGCCGAG 1800
AGCAAGACCA AGCTCTCAT TAAGGTTCCC TTCTGTCAG TGCTCCCAT CCTGAGCATC 1860
TTGTTGAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTTGCTGTG 1920
TGGATGCTGA TAGGCTTCAT CATCTACTTT GGTATGGGCC TGTGACACAG CGAGGAGGCG 1980
TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCATG CAAGTGACGC 2040
ACAGCCCGCG CCCCCGAGG TGGCAGCAGC CCGGAGGGAC GCCCCAGAG GACCGGAGG 2100
CACCCACCC TCCCACCAG TGCAACAGAA ACCACCTGCG TCCACACCT CACTGCA
  
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Seq ID NO: 136 Protein sequence

Protein Accession #: NM\_003045

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1 11 21 31 41 51
| | | | |
  
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5 MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60  
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNLLLS 120  
 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPVL AENPDIFAVI IILILTGLLT 180  
 LGVKESAMVN KIFTICINVLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKBG 240  
 KPGVGGFMPF GFSGVLSGAA TCFYAFVGF D CIATTGEEVK NPQKAIPVGI VASLLICFIA 300  
 YFGVSAALTL MPPYFCLDNN SPLPDAFKHV GWEGAKYAVA VGSICALSAS LLSGMPFMPR 360  
 VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAMVA FLFDLKDLDV LMSIGTLLAY 420  
 SLVAACVLVL RYQPEQPNLV YQMASTSDLE DPADQNELAS TNSQLGLFLP EAEMFSLKTI 480  
 LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540  
 VVTGVINRQP ESKTKLSFKV PFLPVLPILS IFVNVYLMQ LDQGTWVRFA VWMLIGFIIT 600  
 FGyGLWHSBE ASLDADQART PDGNLDQCK

Seq ID NO: 137 DNA sequence

Nucleic Acid Accession #: NM\_032044.1

Coding sequence: 182..658

1 11 21 31 41 51  
 20 AAGATATAAA AGCTCCAGAA AGCTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60  
 GCCCTTAGAG TCTTGGTTCG CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA 120  
 AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCACCTAGCTA CATCCTCAGG GTAGGAGGAA 180  
 GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCTGGCCA AAACAGGAGT 240  
 CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTATAC ACAAGTCCAA 300  
 25 TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCGAGCTCG AGTGTCTAGT 360  
 TTACGGAAC GGAGCCAC TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC 420  
 AGAGTACATA AGTGGCTATC AGAGAAGCCA GCGATATGG ATTGGCCTGC ACGACCCACA 480  
 GAAGAGGAGC CAGTGGCAGT GGATTGATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG 540  
 CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTAAAC 600  
 30 TTGGAGCAGC AACGAATGCA ACAAGGCCA ACACCTCTCTG TGCAAGTACC GACCATAGAG 660  
 CAAGAATCAA GATTCTGCTA ACTCTGTCAC AGCCCGTCC TCTTCTCTTC TGCTAGCCTG 720  
 GCTAAATCTG CTCATTATTT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780  
 ACTACACTGG CTTTCTTAGG CTTAGAGACA GAAACTTTAG CATTGGCCCA GTAGTGGCTT 840  
 CTAGCTCTAA ATGTTTGCCC CGCCATCCTT TTCCACAGTA TCCTTCTTCC CTCTCTCCCT 900  
 35 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960  
 CTTTGGCCAT AAGAAGTAAA GATTGGAAGA CAGAAGGAAG AAACCTAGGA GTAAGCTTCT 1020  
 AGACCCCTTC AGCTTCTACA CCCTTCTGCC CTCTCTCCAT TGCCCTGACC CCACCCAGC 1080  
 CACTCAACTC CTGCTTGTGT TTCCCTTGGC CATAGGAAGG TTTACAGTA GAATCCTTGC 1140  
 TAGGTTGATG TGGGCCATAC ATTCCTTTAA TAAACCAITG TGACATAAG AAAAAAAAAA

Seq ID NO: 138 Protein sequence

Protein Accession #: NP\_114433.1

1 11 21 31 41 51  
 45 MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWYFHKSN CYGYFRKLRLN WSDAELEQCS 60  
 YGNAGHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLYRSWSG 120  
 KSMGNKHC AEMSNNNFLT WSSNECNKRO HFLCKYRP

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM\_051860.2

Coding sequence: 52..3042

1 11 21 31 41 51  
 55 GCTCACCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60  
 GTTAACTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC 120  
 GACCGGGGCA GAGCCTGCGG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180  
 CCCAACTCA CAGTCAACAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTGGAGGAT 240  
 60 AATGTACAGT CATGGAACCC TGGAGATACC CTGGTCAATG CCAGTACTGA TTACTCCATG 300  
 TACCAGGAGC AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAA 360  
 GTGCGAGGGA AACCAATGTA CTGCAATC GGGGAGGAGA TAGACGGCGT GCACATGCGG 420  
 GCGGAGGTTG GGCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480  
 TACCCCTACA GAAACCATC CTGCAATTC TTTGACTTCG ATACCTTTGG GGGCCATC 540  
 65 AAGTTTGCTC TGGGATTTAA GGCAGCACAC TTGGAGGGCA CGAGCTGAA GCATATGGGA 600  
 CAGCAGCTGG TGGTCACTA CCCGATTAC TTCCACCTGG CCGGTGATGT AGACGAAAGG 660  
 GGAGGTTATG ACCCACCAC ATACATCAGG GACCTCTCCA TCATCATAC ATTCTCTGCG 720  
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15

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20 Seq ID NO: 144 NP Protein sequence  
Protein Accession #: NP\_006008.1

1 11 21 31 41 51  
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HQVTRTKGRS RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFTDL NSINSVLGGG 240  
ILDRLRPNII PVLDEIKSMA TAIKETKEAL ENMNSTLKS L HQSQTLSSS LTSVKTSLRS 300  
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HRNLPTLEEY DSYWVLGLV ICSLLTLIVI FYILGLLQGV CGYDRHATPT TRGCVSNTGG 480  
VFLMWVGLS FLEFCHILMII VVLTFFVFGAN VEKLICEPYT SKELPRVLDL PYLLNEDWEY 540  
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40 Seq ID NO: 145 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 38..2605

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 GGAGTTTCAT GTTGGATCTG TCATTATCAA AAGTGATCAG CAATGAAGAA CTGGTCGGAC 3660  
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Seq ID NO: 146 Protein sequence

Protein Accession #:

1 11 21 31 41 51  
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 RKLADSNFKD LRTLNETPE QIKYILAQYN TTKDKAFTDL NSINSVLGGG ILDRLRPNII 240  
 PVLDEIKSMA TAIKETKEAL ENMNSTLKSL HQSTQLSSS LTSVKTSLSR SLNDPLCLVH 300  
 PSSETCNSIR LSLSQLNSNP ELRLPPVDA ELDNVNVLRL TDLDGLVQQG YQSLNDIPDR 360  
 VQRQTITVVA GIKRVLSNSIG SDIDNVQRL PIQDILSAFS VYVNTESYI HRNLPTLEEY 420  
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 LFLCNILMII VVLTFFVGAN VEKLICEPYT SKELFRVLDY PYLLNEDWEY YLSGKLPNKS 540  
 KMKLTFEQVY SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES LKVNLIIFLL 600  
 GAAGRNLQD FAACGIDRMN YDSYLAQTGK SPAGVNLISF AYDLEAKANS LPPGNLRNSL 660  
 KRDAQTIKTI HQQRVLPIEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL DFAQNFITNN 720  
 TSSVILEETK KYGRTIIGYF EHYLQWIEFS ISEKVASCCK VATALDTAVD VFLCSYIIDP 780  
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 VYGIHNPVMT SPSQH

Seq ID NO: 147 DNA sequence

Nucleic Acid Accession #: BC012089.1

Coding sequence: 236..2806

1 11 21 31 41 51  
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Seq ID NO: 148 Protein sequence  
 Protein Accession #: AAH12089.1

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 45 FCMCRCCNKC GGMHQQRQKE NGPFLRKCFA ISLVICII SIGIFYGFVA NHQVTRIKR 180  
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 IPVLDEIKSM ATAIRETKEA LENMNSTLKS LHQSTQLSS SLTSVKTSRLR SSLNDPLCLV 300  
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 RVQRQTITVV AGIKRVLNSI GSDIDNVTR LPIQDILSAF SVYVNMNTEY IHRNLPTLEE 420  
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Seq ID NO: 149 DNA sequence  
 Nucleic Acid Accession #: NM\_033049.1  
 Coding sequence: 28..1566

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 65 GAAACTGCGA CTAGTGGTCC TACAGTAGCT GCAGCTGATA CCACTGAAAC TAATTTCCCT 180  
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 70 ACACATAGTT CTTCCACAAT TCCTATACCT ACTGCTGCAG ACAGTGAGTC AACCCAAAT 360  
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Seq ID NO: 150 Protein sequence  
Protein Accession #: NP\_149038.1

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VASSLKCPDA CNAQHKQLI KSGGGAPECA CVPGYQEDAN GNCQKCAFY SGLDCKDKFQ 420  
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Seq ID NO: 151 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
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 Protein Accession #: Eos sequence

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 SGLMWTLALF CNISDRAFCE LLSSFPNYPYL HCMWHILICL AAYLGVCVFA YFDAASEIPE 240  
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50 Seq ID NO: 153 DNA sequence  
 Nucleic Acid Accession #: NM\_001432.1  
 Coding sequence: 167..676

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AGCAACGACG GAGCGTACTC CCTAGTCTTG GCGGGGGGCT ATGAGGATGA CGTGGACCAT 1500
GGGAATTTT TCACATACAC GGGTAGTGGT GGTCGAGATC TTTCCGGCAA CAAGAGGACC 1560
GCGGAACAGT CTTGTGATCA GAAACTCACC AACACCAACA GGGCGCTGGC TCTCAACTGC 1620
TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAGG ACTGGCGGTC GGGGAAGCCG 1680
GTCAGGGTGG TCAGCAATGT CAAGGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC 1740
AACCGCTACG ATGGCATCTA CAAGGTGTGT AAATACTGGC CGAGAAAGGG GAAGTCCGGG 1800
TTTCTCGTGT GCGCTACCTT TCTGCGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG 1860
GAGGGGAAGG ACCGATCAAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG 1920
GAAGCCCTGG CCAACCGAGA GCGAGAGAAG GAGAACAGCA AGAGGAGGGA GGAGGAGCAG 1980
CAGGAGGGGG TCTCGCGTGC CCCCAGGACG GGCAAGGGCA AGTGAAGCG GAACTCGGCA 2040
GGAGGTGGCC CGAGCAGGGC CGGGTCCCG CGCCGGACAT CCAAGAAAC CAAGTGGAG 2100
CCCTACAGTC TCACGGCCCA GCAGAGCAGC CTCATCAGAG AGGACAAGAG CAACGCCAAG 2160
CTGTGGAATG AGGTCTCTGC GTCACTCAAG GACCGGCCGG CGAGCGGCGAG CCGTGTCCAG 2220
TTGTTCCTGA GTAAAGTGGG GGAGACGTTT CAGTGTATCT GCTGTACAGA GCTGGTGTTC 2280
CGGCCCATCA CGCGCTGTG CCAGCACAAC GTGTGCAAGG ACTGCCTGCA CAGATCCTTT 2340
CGGCGACAGG TGTTCAGCTG CCTGCTGTC CGCTACGACC TGGGCGCAG CATATGCCATG 2400
CAGGTGAACC AGCCTCTGCA GACCGTCTCT AACCAGTCTT TCCCGGCTA CGGCAATGGC 2460
CGGTGATCTC CAAGCAGTTC TCGACAGGCG TTTTGTGAA AACGTGTGCG AGGGCTCGTT 2520
CATCGGCACT GATTTTGTTC TTATGGGGCT TAACCTAAAC AGGTAGTGT TTCTCCGTTT 2580
CCTAAAGAGG TTTGCTCTTC TTTTCTTTT TTTTATTTT TCAAATCTAT ACATTTTCAG 2640
GAATTTATGT ATTCTGGCTA AAAGTTGGAC TTCTCAGTAT TGTGTTTAGT TCTTTGAAAA 2700
CATAAAGCC TGCATTTCT CGACAAAAA ACACAAGATT TTTTAAAGAT GGAATCAGAA 2760
ACTACGTGGT GTGGAGGCTG TTGATGTTT TGGTGTCAAG TTCTCAGAAG TTGCTGCCAC 2820
CAACTCTTTA AGAAGCGCAG AGGATCAGTC CTCTCTAGG GTTCTGGGCC CCAAGGTGCA 2880
AGCAAGCATC TTCTGACAG CATTTTGTCA TCTAAAGTCC AGTGACATGG TTCCCGGTGG 2940
TGGCCCGTGG CAGCCCGTGG CATGGCGTGG CTCAGCTGTC TGTGTAAGTT GTTGCAAGGA 3000
AAAGAGGAAA ATCTCGGGC CTAGTTCAA CTTTGCCTC AAAGCCATCC CCCACGAGC 3060
TGCTTAGCGT CTGAGATCCG CGTGAAAAGT CCTCTGCCCA CGAGAGCAGG GAGTTGGGGC 3120
CAGCGAGAAA TGCCCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGACTGACGC 3180
TGTCCGACGA AGCGCGCCAC GGACGACGCG CAGCACACGA AGTCACGTGC AAGTGCCTTT 3240
GATTGTTTCC TTCTTCTTAA AGACGACAGT CTTTGTGTT AGCACTGAAT TATTGAAAA 3300
GTCAACGAGA TTCTAGAAAC TGCGGTATC CAGTCTCTCC TGACACGCGA TGGGTGCTGT 3360
GGAACCGTTT GAGCCTTATA GATCATTAC ATTCAATTTT TTTAACTCAG CAAGTGAGAA 3420
CTTACAAGAG GGTTTTTTTT TAATTTTTT TTCTCTTAAT GAACACATT TCTAAATGAA 3480
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TTGACGCCTA TACCTCAATA AAACAGGAT ATTTTAAATC ACATACCTGC AGACAAACTG 3660
GAGCAATGTT ATTTTAAAG GGTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT 3720
AGGGAAGATT GAGACAATTT TGTGTAGGCT TTTTCTAAG TCCAGTACTT TGTCCAGATT 3780
TTAGATTCTC AGAATAAATG TTTTACAG ATTGAAAAA AAAAAAAA
  
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Seq ID NO: 156 Protein sequence  
 Protein Accession #: NP\_037414.2

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1 11 21 31 41 51
MWIQVRTMDG RQHTVDLSL RLTKVELRR KIQLPHVEP GLQLPYRGK QMEDGHTLFD 60
YEVRLNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSESDKSSSTH GEAAAEYDSR 120
PADEDMDDET ELGLYKNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE 180
DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMNLNPNP NPKERGFWDY 240
AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPEGSPMV DNPMMRKS GP 300
SKXKICDDVN RLCRVCAHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSDEMYC 360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTEK TIVPSNHYGP 420
IPGIPVGTW RFRVQVSESG VHRPHVAGH GRSNDGAYSL VLAGGYEDDV DHGNFPTYTG 480
SGGRDLSGNK RTAEQSCDQK LTNINRALAL NCFAPINDQE GAEAKDWRSG KPVVRVNRVK 540
GGKNSKYAPA EGNRYDGIYK VVKYWPEKKG SGFLVWRYLL RRDDDEPGPW TKEGDKRIKK 600
LGLTMQYPEG YLEALANRER EKENSKREEE EQQEGGFASP RTGKGKWKRK SAGGGPSRAG 660
SPRRTSKTK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE 720
TFQCICQBEL VFRPITTVQ HNVCQCLDR SFRAQVFSQP ACRYDLGRSY AMQVNPQLQT 780
  
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Seq ID NO: 157 DNA sequence  
 Nucleic Acid Accession #: NM\_000756.1  
 Coding sequence: 186..776

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TCTCTGCGAG GAGGCGCGAG CACCGGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGCCC 180
CTAACATGCG GCTGCGGCTG CTTGTGTCCG CGGGAGTCCCT GCTGGTGGCT CTCCTGCCCT 240
CGCCGCGCAT GAGGCGGCTC CTGAGCCGCG GGCCGGTCCC GGGAGCTCGG CAGGCGCCGC 300
AGCACCTCA GCCCTTGGAT TTCTTCCAGC CGCGCGCGCA GTCCAGCAGC CCCAGCAGC 360
CGCAGGCTCG GCGGTCTCTG CTCCGCTATG GAGAGGAGTA CTCTCTCGCG CTGGGGAACC 420
TCAACAGAG CCCGCGGCTC CCCCTTTGCG CGGCTCTCTC GCTCTCTGCC GGAGGCGAGC 480
CGAGCCGCCC TCGCGCGGAA CAGGCGACCG CCAACTTTTT CGCGTGTGTT CTGACGACG 540
TGCTGCTGCC TCGGCGCTCG CTCGACAGCC CGCGGCTCT CGCGGAGCGC GCGCTAGGA 600
ATGCGCTCGG CGGCGACGAG GAGGACCGG AGAGAGAAAG GGGTCCGAG GAGCCTCCCA 660
TCTCCCTGGA TCTCACCTTC CACCTCTCTC GGAAGTCTT GGAATGCGC AGGCGCGAGC 720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAAGC 780
  
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GTGCGTTTGG CCAAAAAGAA TCTGCATTGA GCACAAAAAA AATTTAAAAA AATACAGTAT 840
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GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTAGCATGCG ACAAGTGTGA TTCACGTGCA 960
GCAGCAACAC AATGTTATTC GTTTTGTCTA OGTTTAGITT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAACGTTT TGTTTGAAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAGAGA ATGCCATTCT CTTGGGTGGG 1140
TAAGACTAAA TCTGTAAAGCT CTTTGAAACA ACTTCTCTT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTCC AGTCTCTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAGT TGCAAAGGT

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Seq ID NO: 158 Protein sequence  
Protein Accession #: NP\_000747.1

1 11 21 31 41 51  
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ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLAGGSGS RPSPEQATAN FFRVLLQQLL 120  
LPRRLDSPA ALAERGARNA LGGHQBAFER ERRSEPPIS LDLTFHLLRE VLEMARAEQL 180  
AQQAHNRKL MEIIGK

Seq ID NO: 159 DNA sequence  
Nucleic Acid Accession #: NM\_001200.1  
Coding sequence: 325..1514

1 11 21 31 41 51  
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TGCCCCAGCG GAGCCTGCTT CGCCATCTCC GAGCCCCACC GCCCCCTCAC TCCTCGGCCT 120  
TGCCCGACAC TGAGACGCTG TCCCGAGCGT GAAAAGAGAG ACTGCGCGGC CGGCACCCCG 180  
GAGAAGGAGG AGGCAAGAA AAGGAACGGA CATTGGTCTT TTGCGCCAGG TCCTTTGACC 240  
AGAGTTTTTC CATGTGGACG CTCTTTCAAT GGACGTGTCC CCGCGTGCTT CTAGACGCGA 300  
CTGCGGTCTC TTAAGGTTCG ACCATGGTGG CCGGACCCCG CTGTCTTCTA GCGTTGCTCG 360  
TTCCCGAGGT CTTCTGGGCG GCGCGGCGTG GCTCTGTTCG GGAGCTGGGC CGCAGGAAGT 420  
TCGCGGCGGC GTGCTGGGCG CGCCCTCAT CCGACCCCTC TGACGAGGTC CTGAGCGAGT 480  
TCGAGTTGCG GCTGCTCAGC ATGTTCCGCC TGAACAGAG ACCCACCCCC AGCAGGAGCG 540  
CCGTGGTGCC CCCCTACATG CTAGACCTGT ATCGCAGGCA CTCAGGTGAG CCGGGCTCAC 600  
CGCCCCGAGA CCACCGGTG GAGAGGCGAG CCAGCCGAGC CAACACTGTG CGCAGCTTCC 660  
ACCATGAAGA ATCTTTGAA GAACTACAG AAACAGTGG GAAACAACCC CGGAGATTCT 720  
TCTTAATTT AAGTTCTATC CCCACGGAGG AGTTTATCAC CTCAGCAGAG CTTAGGTTT 780  
TCCGAGAACA GATGCAAGAT GCTTTAGGAA ACAATAGCAG TTTCCTCAC CGAATTAATA 840  
TTTATGAAAT CATAAACCT GCAACAGCCA ACTCGAAATT CCCCCTGACC AGACTTTTGG 900  
ACACCGGTT GSTGAATCAG AATGCAAGCA GGTGGGAAAG TTTTGTATGTC ACCCCGCTG 960  
TGATGCGGTG GACTGCACAG GGACACGCCA ACCATGGATT CGTGGTGGAA GTGGCCCACT 1020  
TGGAGGAGAA ACAAGGTGTC TCCAAGAGAC ATGTTAGGAT AAGCAGGTCT TTGCACCAAG 1080  
ATGAACACAG CTGGTCACAG ATAAGGCCAT TGCTAGTAAC TTTTGGCCAT GATGGAAAG 1140  
GGCATCTCTT CCACAAAGA GAAAACGTC AAGCCAAACA CAAACAGCGG AAACGCTTCA 1200  
AGTCCAGCTG TAAGAGACAC CCTTTGTACG TGGACTTCAG TGACGTGGGG TGGAAATGACT 1260  
GGATTGTGGC TCCCGCGGGG TATCACGCTT TTTACTGCCA CGGAGAAATG CTTTTCCTC 1320  
TGGCTGATCA TCTGAATCTC ACTAATCATG CCATGTTTCA GACGTTGGTC AACTCTGTTA 1380  
ACTCTAAGAT TCCTAAGGCA TGCTGTGTCC CGACAGAACT CAGTGTCTATC TCGATGCTGT 1440  
ACCTTGACGA GAATGAAAG GTTGATTAAT AGAACTATCA GGACATGGTT GTGGAGGGTT 1500  
GTGGGTGTCG TAGTACAGC AAAATTAAAT ACATAAATAT ATATATA

Seq ID NO: 160 Protein sequence  
Protein Accession #: NP\_001191.1

1 11 21 31 41 51  
MVAGTRCLLA LLLPQVLLGG AAGLVPELGR RKFAAASSGR PSSQPSDEVL SEFELRLLSM 60  
FGLKQRPPTS RDAVVPFVYL DLYRRHSGQP GSPAPDHRLE RAASRANTVR SFFHEESLEE 120  
LEETSGKTR RFFFNLSIP TEEFITSDEL QVFEQMQDA LGNNSSFHRR INIYEIIPKA 180  
TANSKFPVTR LLD

Seq ID NO: 161 DNA sequence  
Nucleic Acid Accession #: NM\_001999.2  
Coding sequence: 1..8736

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CAGCCGCGCG CGCAACAGGT TCGGTCCGCT ACAGCAGGCT CTGAAGGCGG GTTCTTAGCG 180  
CCCGAGTATC CGGAGGAGGG TGCCGCGAGT GCCAGCCGCG TCCCGCGGGG AGGACAGCAG 240  
GACGTGCTCC GAGGGCCCAA CGTGTGCGGC TCCAGATTCC ACTCTACTG CTGCCCTGGA 300  
TGGAGACGCG TCCCTGGAGG AAACCACTGC ATGTCCCGA TTTGTAGAAA TAGTTGTGGA 360  
GATGGATTTT GTTCCCGTCC TAACATGTGT ACTTGTTCGA GTGGGCAAT ATCATCAACC 420  
TGTGGATCAA AATCAATICA GCAGTGCAGT GTGAGATGCA TGAATGGTGG GACCTGTGCA 480  
GATGACCACT GCCAGTGCCA GAAAGGATAT ATTGGAACCT ATTGTGGACA ACCTGTCTGT 540  
GAAATGGAT GTCAAGATGG TGGACGTTGC ATCGCCCAAC CGTGTGCTTG TGTATTATGG 600  
TTCACTGGTC CACAGTGTGA AAGAGATTAC AGGACAGGCC CGTGTTCAC TCAGGTCAAC 660  
AACCAGATGT GCCAAGGCA GCTGACAGGC ATTGTCTGCA CGAAGACTCT GTGCTGTGCC 720  
ACCACTGGAC GGGCGTGGGG CCATCCCTGT GAGATGTGTC CAGCCAGGCC TCAGCCCTGC 780  
CGAGGGGGTT TCATCCCAAA CATCCGCACT GGAGCTTGCC AAGATGTTGA TGAATGCCAG 840  
GCTATCCAG GGATATGCCA AGGAGGAAAC TGTATCAATA CAGTGGGCTC TTTTGAATGC 900

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	TGCAGCATCA	TTCTCTGGGAT	ATGTGAAACT	GGTGAATGTT	CCAACACCGT	GGGAAGCTAT	1020
	TTTTGTGTTT	GTCCACGTGG	ATATGTAACC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080
5	AGAACAGGCA	TGTGTTTCTC	GGGCCTGGTG	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG	1140
	AGAAATGACGA	AAATGTCAGTG	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCATT	1200
	CCTGAAGCCT	GTCCTGTGAG	AGGTTCTGAG	GAATATCGCA	GACTTTGCAT	GGATGGACTT	1260
	CCAATGGGAG	GAATTCACAG	GAGTGTCTGG	TCCAGACCTG	GAGGCACTGG	GGGAAATGGC	1320
	TTTGCCCCAA	GTGGCAATGG	CAATGGCTAT	GGCCACGGAG	GGACAGGCTT	CATCCCCATC	1380
	CCTGGAGGCA	ATGGCTTTTC	TCCTGGCGTT	GGGGAGGCGG	GTGTGGGGGC	CGGGGGACAG	1440
10	GGACCTATCA	TCACCTGGACT	AACAATTCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT	1500
	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACCTGCT	CAAGCTACCG	ATGTGAATGC	1560
	AACATGGGTT	ATAAGCAGGA	TGCAAAATGA	GATTGTATAG	ATGTTGATGA	ATGCACATCA	1620
	AATCCCTGCA	CTAATGGAGA	TTGTGTTAAC	ACACCTGGTT	CCTATTATTG	TAAATGTCAT	1680
	GCTGGATTCC	AGAGGACTCC	TACCAAGCAA	GCATGCATTG	ATATTGATGA	GTGCATCCAG	1740
15	AATGGGTTTC	TTTGTAAAAA	CGGTGATGTC	GTGAACTCAG	ATGGAAGTTT	CCAGTGCAAT	1800
	TGCAATGCCG	GCTTTGAATT	AACATACAGT	GGAAAAAACT	GTGTTGATCA	TGATGAATGT	1860
	ACAACTACCA	ACATGTGTTT	GAATGGAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTGCAAA	CAGGATTGTT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA	1980
20	TGCGAGACCC	CAGGAATCTG	CATGAATGGG	CACCTGCATCA	ACAGTGAAGG	GTCCCTCCGC	2040
	TGTACTGTC	CCCAGGCGCT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCGGGT	2160
	GCAGTGACCA	AGTCCGAATG	CTGCTGTGCC	AATCCAGACT	ATGTTTGTGG	AGAACCCTGC	2220
	CAGCCATGCC	CTGCAAAAAA	TTCACTGAA	TTCCACGGCC	TTTGTAGTAG	TGGAGTAGGT	2280
25	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
	GGGATTGTG	AAACTTACG	TGGTAGTTAC	CGTTGTAATT	GCAACAGTGG	CTATGAACCA	2400
	GATGCTCTG	GAAGAACTG	TATTGACATT	GATGAATGTT	TAGTAAACAG	ACTGCTTTGT	2460
	GATAACGGAT	TGTGCCGAAA	CACGCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGSTAT	2520
	GTGTTTCAGGA	CTGAGACAGA	GACCTGTGAA	GATATAAATG	AATGTGAAGG	CAACCCATGT	2580
30	GTCAATGGGG	CCTGCAGAAA	CAACCTTGGA	TCTTTCAATT	GTGAATGTTT	GCCCGGCAGC	2640
	AAACTCAGCT	CCACAGGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
	ATCCAGGACA	GGCGCTGTGA	GGTGAATATT	AATGGAGCCA	CTCTGAAATC	TGAATGCTGT	2760
	GCCACCCCTG	GAGCGCGCTG	GGGGAGCCCC	TGTGAGCGGT	GTGAATGAGA	TACAGCTTGC	2820
	CCAAGAGGGC	TTGCCAGGAT	TAAAGTGTGT	ACGTGTGAAG	ATGTTAATGA	GTGTGAGGTG	2880
35	TTCCCTGGCG	TTTGTCACAA	TGGACGCTGT	GTCAACAGTA	AGGGATCTTT	TCATTGCGAG	2940
	TGCCCTGAAG	GCCTTACGTT	GGATGGGACT	GGCCGTGTAT	GTTTGGATAT	TGCGATGGAG	3000
	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTTCTCTG	AAAGTTCCGC	3060
	ATGGATGCTT	GCTGCTGTGC	TGTGCGGGCG	GCTTGGGGCA	CCGAGTGTGA	GGAGTGGCCC	3120
	AAACCTGGCA	CAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	TGCTAACCGA	3180
40	GGGGATGTTT	TTACTGGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
	GGGATGCTG	CTTATGGGAA	GTGCAGAAAT	ACAATCGGAA	GCTTCAAATG	CCGTTGCAAT	3300
	AGTGGCTTTG	CTCTAGACAT	GGAGGAAGA	AACCTGCACG	ACATCGACGA	GTGCAGGATT	3360
	TCTCTGACC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGCAG	3420
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45	TGTGAACGTA	ACCTCTCTCT	TTGTAGGGGT	GGCACCTGTG	TGAACACTGA	GGGCAGCTTT	3540
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	ACCTATCAGT	GCTCTTGCAA	TCCTGGATAT	CAGGCTACGC	CAGACCGCCA	GGGCTGTACA	3720
	GATATTGATG	AATGTATGAT	AATGAACGGA	GGCTGTGACA	CCCAGTGCAC	AAATTTCAGAG	3780
50	GGAGGCTACG	AATGCAGCTG	CAGTGAGGGT	TATGCCCTGA	TGCCAGATGG	GAGATCGTGT	3840
	CGAGATCTG	CTGATGTGAA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC	3900
	ATTCTGGAG	AGTATGCTGT	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA	3960
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	GAGAACACAA	AGGGATCCTT	CATTTGCCAC	TGTCAGCTGG	GTTACTCAGT	GAAGAAGGGG	4080
55	ACCACAGATG	GTACAGATGT	GGATGAGTGT	GAAATTGGTG	CTCAATACTG	CGACATGCAT	4140
	GCCTCATGTC	TGAATATCCC	AGGAAGCTTC	AAGTGTAGCT	GCAGAGAAGG	CTGGAATTGGA	4200
	AACGGCATCA	AGTGTATTGA	TCTGGAGCAA	TGTTCTAATG	GAACCCACCA	GTGTAGCATC	4260
	AATGCTCAGT	GTGTAATATC	CCCCGGCTCA	TACCGCTGTG	CCTGCTCCGA	AGGTTTCACT	4320
	GGTGATGGCT	TTACCTGCTG	AGATGTTGAT	GAGTGTGCAG	AAAACATAAA	CCTCTGTGAG	4380
60	AAOCSGACGT	GCCTTAATGT	CCCCGGTGCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCACT	4440
	CCAGCTCAG	ACAGCAGATC	CTGCCAAGAT	ATTGATGAAT	GCTCCTTCCA	AAACATTGT	4500
	GTCTCTGGAA	CATGTAATAA	CCTGCTGGA	ATGTTTCATT	GCATCTGCGA	TGATGGTTAT	4560
	GAATTGGACA	GAACAGGAGG	GAACGTGACA	GATATTGATG	AGTGTGCAGA	TCCTATAAAC	4620
	TGTGTCAATG	GCCTATGTGT	CAACACGCTT	GGTGTCTATG	AGTGTAACTG	CCCACCCGAT	4680
65	TTTCAGTTGA	ACCCAACTGG	TGTGGGTTGT	GTGTGACAA	GTGTGGGCAA	CTGCTACCTG	4740
	AAGTTTGGAC	CTGAGGAGGA	TGGGAGTCTG	TCTTGCAACA	CCGAGATCCG	GGTGGGCGTC	4800
	AGTGCCTCTT	CATGCTGCTG	CTCTCTGGGA	AAGGCTGGG	GAACCCCTG	TGAGACATGC	4860
	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCGCG	GAGGTGAAGG	CTTCAGACCT	4920
	AACCCCATCA	CAATCATTTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
70	CAGGTTGGAA	ACTGCATCAA	CACCTTTGGG	AGCTTCCAGT	GTGAGTGGCC	ACAAGGCTAC	5040
	TACCTCAGCG	AGGATAACCG	CATCTGTGAG	GATATTGATG	AGTGTTTTGC	ACATCCTGGT	5100
	GTGTGTGGGC	CTGGGACCTG	CTATAACACC	CTGGGAAATT	ACACCTGCAT	TTGCCCACT	5160
	GAGTACATGC	AGGTCAATGG	AGGCCACAAC	TGCATGGACA	TGAGAAAAAG	CTTTTGCTAC	5220
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75	TGCTGTGCGA	CATATAATGT	GGGCAAGCT	GGGAACAAAC	CTTGTGAACC	ATGCCCACT	5340
	CCAGGAACAG	CTGACTTTAA	AACCATATGT	GGAAATATT	CTGGAATTCA	CTTTGACATT	5400
	CACACAGGAA	AAGCTGTTGA	CATTGATGAA	TGTAAGAGA	TTCCAGGCAT	TTGTGCAAT	5460
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80	CAGCGGAATG	CAGACTGCAT	CAATAGTCTT	GGTAGTTACC	GCTGTGAATG	TGCCGCGGGT	5640
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	GTGTGACGTC	ATGGCTGTGT	TGTTGATCTG	CAAGGAAGTT	ACCAGTGCAT	CTGCCACAAT	5760
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	CCATGTGGAA	ATGGAACTTG	TAAAAACACC	GTTGGATCCT	ATAACTGTCT	GTGCTACCCA	5880
	GGGTTTGAAC	TCACCTATAA	TAAATGATGC	CTGGACATAG	ATGAGTGCAG	TTCTTTT	5940

5 GGTCAAGTGT GCAGAAATGG ACGTTGTTTT AATGAAATGG GTTCTTTCAA GTGTCATGT 6000  
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 GAAGATCCCA ACATTGTCT TTTGGTTCC TGTACTAATA CTCCAGGGGG CTTCCAGTGC 6240  
 CTCTGCCCCC CTGGCTTTGT ACTATCTGAT AATGGAOSGA GATGCTTTGA TACTGCCAG 6300  
 AGCTTCTGCT TCACAAATTT TGAAAATGGA AAGTGTCTCG TACCCAAAGC TTTCAACACC 6360  
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Seq ID NO: 162 Protein sequence  
 Protein Accession #: NP\_001990.1

75

80

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	NPCTNGDCVN	TPGSYYCKKH	AGFORTPTKQ	ACIDIDECIQ	NGVLCKNGRC	VNSDGSFQCI	600
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	AVTKSECCCA	NPYGFGEPC	QPCPAKNSAE	FHGLCSSGVG	ITVDGRDINE	CALDPDICAN	780
	GICENLRGSY	RCNCSNGYEP	DASGRNCIDI	DECLVNRLLC	DNGLCRNTPG	SYSTCTPPGY	840
	VFRTEETCE	DINECESNPC	VNGACRNNLG	SFNCCECPGS	KLSTGLICIC	DSLKGTCLWN	900
10	IQDSRCEVNI	NGATLKSECC	ATLGAANGSP	CERCELDTAC	PRGLARIKGV	TCEDVNECEV	960
	FPGVCPNGRC	VNSKPSFHC	CPEGLTLDGT	GRVCLDIRME	QCYLKWDEDE	CIHPVPKFR	1020
	MDACCCAVGA	AWGTCECECP	KPGTKEYETL	CPRGAGFANR	GDVLTGRPFY	KDINECKAFP	1080
	GMCTYKCRN	TIGSFKCRN	SGFALDMEER	NCTDIDECRI	SPDLGSGGIC	VNTPGSPECE	1140
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	GSYECSCSEG	GSYRCSCAAG	ADIDECENNP	DICDGGQCTN	IPGEYRCLCY	DGFMASMDMK	1320
	TCIDVNECDL	NSNICMFGEC	ENTKGSFICH	QQLGSYVKKG	TTGCTDVDEC	EIGAHCMDMH	1380
	ASCLNIPGSF	KCSRCBGWIG	NGIKCIDLDE	CSNGTHQCSI	NAQCVENTPGS	YRCACSEGFT	1440
	GDGPTCSDVD	ECANENINLC	NGQCLNVPGA	YRCECEMGFT	PASDSRSCQD	IDECSPQNIC	1500
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	PPVNSTEYIT	LCPPGGGFRP	NPITILEDI	DECQELPLGL	QGGNCINTFG	SPQCECPQGY	1680
	YLSIEDTRICE	DIDECFAHPT	VCGPGTCYNT	LGNYTCICPP	EYMQVNGGHN	CMDMRKSEFY	1740
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	VPSLHDTRED	VNECLESPGI	CSNGQCINTD	GSFRCECPMG	YNLDYTGVR	VDTDECSIGN	2220
	PCNGTCTNV	IGSFECNCE	GFEPGPMNMC	EDINECAQNP	LLCALRCMNT	FGSYECTCPI	2280
	GYALREDQKM	KDIDECASEG	LHDCESRGM	CQNLTGTFMC	ICPPGMARRP	DGEGCVDENE	2340
35	CRTPKGCEN	GRCVNIIGSY	RCECNEGFQS	SSSGTECLDN	RQGLCPAEVL	QITCQMASSS	2400
	RNLVTKECC	CDGGRGWGHQ	CELCLPLGTA	QYKICPHGP	GYTTDGRDID	ECKVMENLCT	2460
	NGQCINTMGS	FRFCCKVGYT	TDISGTSID	LDECSQSPKP	CNYICKNTEG	SYQCSCPRGY	2520
	VLQEDGKTCK	DLDEBCTKH	NQQLCVNLT	GGFTCKCPFG	FTQHTACID	NNECGSQPLL	2580
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40	GYIQHYQWQ	CVDNECESNP	NACGSASCYN	TLGSYKACAP	SGFSFDQFSS	ACHDVNECSS	2700
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	CYCKINGYP	KDLSRQKRSI	HEPDPTAVEQ	ISLESVDMDS	PVNMKFNLSH	LGSKEHILEL	2820
	RPAIQPLNNH	IRYVISQOND	DSVFRIHQRN	GLSYLHTAKK	KLMPGTYYLE	ITSIPLYKKK	2880
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Nucleic Acid Accession #: NM\_013372.1  
Coding sequence: 63..617

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55	GGGGCAAGG	CGGGGCACT	GCCATGCCCG	GGGAGGAGGT	GCTGGAGTCC	AGCCAAGAGG	300
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	AGGATCTGAG	GGGACCTGT	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCACTCTG	2040
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35 Seq ID NO: 164 Protein sequence  
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45 Seq ID NO: 165 DNA sequence  
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Seq ID NO: 167 Protein sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 MPPLPSRMSR GPSLVTRML PITDRLLHLL GLEKTAFRYI AVSTLLLFLL FFLFRLLLRP 60  
 LRLCRSFYIT CRRRCFPQPP PRRNWLLGHL GMYLPNEAGL QDEKKVLDNM HHVLLVMMGP 120  
 VLPLLVLEVP DYIKPLLGAS AAIAPKDDLF YGFLKPWLGD GLLLSKGDKW SRHRRLLTPA 180  
 PHFDILKPYM KIFNQSDIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240  
 QEKMSDYISA IIELSALSVR RQYRLHLYLD FIYRSADGR RFRQACDMVE HFTTEVIQER 300  
 RRALRQQGAE AWLKAQKQKT LDFIDVLLLA RDEGKELSD EDIRAEADTF MFEGHDTTSS 360  
 GISWMLFNLA KYPEYQEKCR EEIQEVMKGR ELELEWDDL TQLPFTTMC I KESLRQYPPV 420  
 TLVSRQCTED IKLPDGR IIP KGIICLVSIY GTHHNPTVWF DSKVYNPYRF DPDNPQQRSP 480  
 LAYVPFSAGP RNCIQGSFAM AELRVVVALT LLRFRLSVDR TRKVRKRPEL ILRTENGLML 540  
 KVEPLPFRA

Seq ID NO: 168 DNA sequence  
 Nucleic Acid Accession #: AK058088.1  
 Coding sequence: 252..1772

1 11 21 31 41 51  
 AGGAAACCAA GGCAAGCTCC CCCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60  
 GCGCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCCC AGCTCTCTG 120  
 TAACTCAGAG GCCAGTGTGA TGGGAGTTC TCCACTCAGC ACACCTCCCC TGTAACACAG 180  
 CCTGTGGTGG GCAAAGGGC TTTGGAACGG TTGCTTGTCT TTTCTCTCCT GCGTAATTTT 240  
 CACTTTTATT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAAACG CCGGCTCACTG 300  
 GCTCAACCAA CCGGTGGGCT TTGCCCAAAC AGCCTTTCTC TGGGGACCTG CTCTCACTTT 360  
 CCGAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420  
 TATGCATTTC ACAATCCAG AAGTTTTTCT TTGAGAATT CAAGAACAAG GACATCCAAA 480  
 GTGGGAAGC AGATGTGATT CTCGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540  
 GGTCTTTTCA GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA 600  
 CACACCCCTT GAGGGAGCTG GAGGAGCTTC TGCGAGCTCA ATCCTTAAG AAGACCAAG 660  
 AAAAAATCCC TGCAAAGAGG ATCATCATT CCTTGAAGAT CAATGACCCA CTGCTCACTA 720  
 AAGTCGCTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTTG 780  
 AAGACCTACT GGGAGTGCTG GCTTCCGCCC ACATCTCTCA GTTCAGTGGC CTGTTTCAAA 840  
 GGTGCGTGA TGGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900  
 CCGGCTGCAA GTACAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATGA 960  
 ACTTGTCTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACCTGTCC 1020  
 ACAAGTGTCT GAAGTCCCCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080  
 TGCTTTTGTG GGTCTCTCTG CAACTGAAT ACAAGATTCA GGCAATTCG ACTTATGAAA 1140  
 CCGTGATGAC ATTTTTAAAG AGCTTTCCTG AGAACTGTTG CTTTCTGGAC CGGGACATAG 1200  
 GACGGAGCTT GAGGCGCTC TTCCTCTGCT TGCGTCTGCA CGGCATCACC AAGGCAAGG 1260  
 ATCTGGAGGT GCTGCGGCAC CTTAACTTCT TCCCAGATC ATGGCTCGAC CAGGTTACAG 1320  
 TCAACCATTA CCACGCACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380  
 CCCAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAACCTAT TCGAAAACGA 1440  
 TTGCTCTATA TGGATTCTTC TTTAAGATAA AGGGACTCAA ACATGATACT ACCTCTTATA 1500  
 GTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGAGC 1560  
 ACAACCACTG CAGCCTGCGA CGGGCAAGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620  
 TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACCATG CAAGCAGAAG TTTGGGTGA 1680  
 CCACGTCATC CTCGAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG 1740  
 TAAGTTTGGC ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800  
 CCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC

Seq ID NO: 169 Protein sequence  
 Protein Accession #: BAB71658.1

1 11 21 31 41 51  
 MIMSNTKAR LERVRTGSTN RWRLPKQPPS GDLLSLQMC KALSIDPEEA LRNPDRLCIS 60  
 QIQKFFPFEN KNKDIOGSEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQSTTHPL 120  
 RELEELLRAQ SPKRTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180  
 GVLASAHILQ FSGLFQRCVD VMIA RLKPST IKQFYAGCK YKEBQLTTGC EKWLEMNLPV 240  
 LGGTQIHLHK IPQDLHLKVL KSPRLFTFSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300  
 FPKSPENCCE FLDRDIGRSL RPLFLCLRHL GITKGDLEV LRHLNFFPES WLDQVTVNHY 360  
 HALENGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFPKIKGLK HDTTSYSFYM 420  
 QRIKHTDLES PSVAYEHNHV SLRAARLVKY EIRAEALVDG KMQEFRTNQI RQKFGLTTSS 480  
 CKSHTLKIQT VGPIPIVVSFA PIPPAS

Seq ID NO: 170 DNA sequence  
 Nucleic Acid Accession #: NM\_007000.1  
 Coding sequence: 1...777

1 11 21 31 41 51  
 ATGGCGTCTG CGGCAGCAGC GGAGGCCGAG AAGGGATCTC CAGTTGTGGT GGGCCTGCTA 60  
 GTTGTGGGCA ATATCATTTAT TCTGCTGTCA GGCTGTCTCC TGTGTGCTGA GACCATATGG 120  
 GTGACAGCGC ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180  
 TTGCTGTGTG CCGGATTGCG CATCTTCTGC GGCCTCTCCT TCTCATGGT AGCCAGTTTT 240

5  
10  
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GGTGTGGGTG CCGCACTCTG CCGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300
CTCATCGTCT ACATCTTCGA GTGCGCCTCC TGATCACAGT CCTACACCCA CCGTGACTAC 360
ATGGTGTCCA ACCATTCCTT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC 420
GACCAGGCCC AGGAGCTGAC CCGCCTCTGG GACCGGCTCA TGATTGAGCA AGAATGCTGT 480
GGCACAATCTG GTCCCATGGA CTGGGTGAAC TTCACGTCAG CCTTCCGGGC GGCCACTCCG 540
GAGGTGGTGT TCCCTTGCCC CCCACTGTGC TGTGCGCGGA OGGGAAACTT CATCCCCCTC 600
AAGAGGAGGG GCTGCCGCCT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660
CACATCGGCC ACGCCATCGA CAGCTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC 720
CTGATGTGGA CGTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA

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Seq ID NO: 171 Protein sequence  
Protein Accession #: NP\_008931.1

15  
20

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1      11      21      31      41      51
|      |      |      |      |      |
MASAAAAEAE KGSFVVVGLL VVGNIIILLS GLSLFAETIN VTADQYRVYP LMGVSGKDDV 60
PAGAMIAIFC GPSFFMVASF GVGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY 120
MVSNPSTLTK QMLTFYSADT DQGELTRLW DRVMIEQECG GTSGPMDWVN FTSAFRAATP 180
EVVFPWPLC CRRTGMFIPL NEEGCRLGHM DYLFRTKGCPE HIGHAIDSYT WGISWFGFAI 240
LMWTLFVMLI AMYFYTML

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Seq ID NO: 172 DNA sequence  
Nucleic Acid Accession #: NM\_006760.1  
Coding sequence: 39..593

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30  
35  
40  
45

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1      11      21      31      41      51
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GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCAGCAT GGCACCCCTG CTGCCCATCC 60
GGACCTTGCC CTGTATCTGT ATTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA 120
ACATCTCAAG CCTCTCTGGT CTGTGTGTCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCCT 180
TGCCCCCTG TCACCTTACA GGAGGCAATG CCACACTGAT GGTCCGGAGA GCCAATGACA 240
GCAAAAGTGT GACGTCCAGC TTTGTGGTGC CTCCGTGCCG TGGGCGCAGG GAACTGGTGA 300
GTGTGGTGGG CAGTGGTGTCT GGCTTCACAG TCACTCGGCT CAGTGATATC CAGGTGACAA 360
ACCTCGTGCC AGGAACCAAA TTCTACATT CTACCTAGT GAAGAAGGGG ACAGCCACTG 420
AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC 480
TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTGCCCATGT 540
TCTGTCTGCT GCTGGGCTTC ATCATTGCCC TGGCACTGGG CTCCCGCAAG TAAGGAGGTC 600
TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACA TCCAGTCTCC CAGCCACCT 660
GCTCCAGGCG CCCAGGCTGT TGGCTCCCTT GGTCGCCCTG CCTCCTCTCT CTGCCCTCCT 720
CTCCCTAGA GCCCTCTCCT CCCTCTGTCC CTCTCCTTGC CCCAGTGCC TCACCTTCCA 780
ACACTCCATT ATTCTCTCTA CCCCACTCCT GTCAGAGTGT ACTTCTCTCC CATTTTACCA 840
CTTTAAACAC CCCCAACACA ATTCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900
GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

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Seq ID NO: 173 Protein sequence  
Protein Accession #: NP\_006751.1

50  
55

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1      11      21      31      41      51
|      |      |      |      |      |
MAPLLPIRTL FLILLILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL 60
MVRRANDSKV VTSSFVPPC RGRRELVSIV DSGAGFTVTR LSAYQVTLNV PGTKFYISYL 120
VKKGATRESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLL VLGFIIALAL 180
GSRK

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Seq ID NO: 174 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2733

60  
65  
70  
75  
80

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1      11      21      31      41      51
|      |      |      |      |      |
ATGAAAGTTG GAGTGCTGTG GCTCATTCTT TTCTTCACTT TCACTGACGG CCACGGTGGC 60
TTCTGGGGA AAAATGATGG CATCAAAACA AAAAAAGAAC TCATTGTGAA TAAGAAAAAA 120
CATCTAGGCC CAGTCGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTCCAAG 180
GAGAAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTTGAAGC CTCCATTATT ATGGTCACAT 240
GGGCTAATTA GAATTATCAG AGCAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC 300
CTGCAGTGTG CTTGTGAAGA CAGCTACACC TGGTTTCCTC CCTCATGCTT TGATCCCCAG 360
AACTGCTACC TTCACACGGC TGGAGCACTC CCAAGCTGTG AATGTCACTT CAACAACCTC 420
AGCCAGAGTG TCAATTTCTG TGAGAGAACA AAGATTGGG GCACTTTCAA AATTAATGAA 480
AGGTTTACAA ATGACCTTTT GAATTCATCT TCTGCTATAT ACTCCAAATA TGCAAAATGA 540
ATTGAAATTC AACTTAAAAA AGCATATGAA AGAATTCAG GTTTTGAGTC GGTTCAGGTC 600
AGCCAATTTC GAAATGGAAG CATCGTGTCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA 660
TCGAACTGTC TGTCAGCCAT TGAACATGTT CCGGAGAAGG CTAAGACAGC CCTTCACAAG 720
CTGTTTCCAT TAGAGAGCGG CTCTTTCAGA GTGTTGGGAA AAGCCAGTG TAATGACATT 780
GTCTTTGGAT TGGGTCCAA GGATGATGAA TATACCTGCG CCGCAGCAG TGGCTACAGG 840
GGAAACATCA CAGCCAAGTG TGAGTCTCTT GGGTGGCAGG TCATCAGGGA GACTTGTGTG 900
CTCTCTCTGC TTGAAGAACT GAACAGAAT TTCAATATGA TTGTAGGCAA TGCCACTGAG 960
GCAGCTGTGT CATCTCTTGT GCAAAATCTT TCTGTATCA TCGGCAAAA CCCATCAACC 1020
ACAGTGGGGA ATCTGGCTTC GGTGGTGTCT ATTCTGAGCA ATATTTTCAT TCTGTCACTG 1080
GCCAGCCATT TCAGGGGTTC CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT 1140
ATCCTTAATT CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGCGGGAAGA AAGTATATGC 1200
AGCTCAGGCT TACTAGAGAC ATTGAAAAAC ATCAGCACTC TGGTGCCTCC GACAGCTCTT 1260
CCTCTGAATT TTCTCGGAAA ATTCATTGAC TGGAAAGGGA TTCAGTGAA AAAAGGCCAA 1320
CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTCCCATC 1380
AGAGGCCGTG TGTAAATTGG GTCAGACCAA TTCAGAGAT CCCTTCAGA AACTATTATC 1440

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5	AGCATGGCCT	CGTTGACTCT	GGGGAACATT	CTACCCGTTT	CCAAAAATGG	AAATGCTCAG	1500
	GTCAATGGAC	CTGTGATATC	CACGGTTATT	CAAAACTATT	CCATAAATGA	AGTTTTCTTA	1560
	TTTTTTTCCA	AGATAGAGTC	AAACCTGAGC	CAGCCTCATT	GTGTGTTTGT	GGATTTCAGT	1620
	CATTTGCACT	GGAAAGATGC	AGGCTGCCAC	CTAGTGAATG	AAACTCAAGA	CATCGTGACG	1680
	TGCCAATGTA	CTCACTTGAC	CTCCTTCTCC	ATATTGATGT	CACCTTTTGT	CCCTCTTACA	1740
	ATCTTCCCGG	TTGTAAAATG	GATCACCTAT	GTGGGACTGG	GTATCTCCAT	TGGAAGTCTC	1800
	ATTTTATGCC	TGATCATCGA	GGCTTTGTTT	TGGAAGCAGA	TTAAAAAAG	CCAAACCTCT	1860
	CACACAGTGC	GTATTGTCAT	GGTGAACATA	GCCCTGTCCC	TCTTGATTGC	TGATGTCTGG	1920
10	TTTATTGTGT	GTGCCACAGT	GGACACCAAG	GTGAACCCCT	CTGGAGTCTG	CACAGCTGCT	1980
	GTGTTCTTTA	CACACTTCTT	CTACCTCTCT	TTGTTCTTCT	GGATGCTCAT	GCTTGGCATC	2040
	CTGCTGGCTT	ACCGGATCAT	CCTCGTGTTC	CATCAGATGG	CCGACGATT	GATGATGGCT	2100
	GTGGGATTTT	GCTGGGTTA	TGGGTGCCCT	CTCATTATAT	CTGTCAATAC	CATTGCTGTC	2160
	ACGCAACCTA	GCAATACCTA	CAAAAGGAAA	GATGTGTGTT	GGCTTAACCT	GTCCAATGGA	2220
15	AGCAAAACCAC	TCCTGGCTTT	TGTTGTCCCT	GCACTGGCTA	TTGTGGCTGT	GAACCTCGTT	2280
	GTGGTGTGTC	TAGTCTCTAC	AAAGCTCTGG	AGGCGGACTG	TTGGGAAAG	ACTGAGTCGG	2340
	GATGACAAGG	CCACCATCAT	CCGCGTGGGG	AAGAGCCTCC	TCACTCTGAC	CCCTCTGCTA	2400
	GGGCTCACCT	GGGGCTTTGG	AATAGGAACA	ATAGTGGACA	GCCAGAATCT	GGCTTGGCAT	2460
	GTTATTTTGT	CTTACTCAAA	TGCATTCCAG	GGATTTTTAA	TCTTATGCTT	TGGAATACTC	2520
20	TTGGACAGTA	AGCTGGGACA	ACTTCTGTTC	AACAAGTTGT	CTGCCCTAAG	TTCTTGGGAG	2580
	CAAAACAGAAA	AGCAAAACTC	ATCAGATTTA	TCTGCCAAAC	CCAAATTTCT	AAAGCCTTTC	2640
	AACCCACTGC	AAAAACAAAG	CCATTATGCA	TTTTCTCATA	CTGGAGATTC	CTCCGACAAAC	2700
	ATCATGCTAA	CTCAGTTTGT	CTCAAAATGAA	TAA			

Seq ID NO: 175 Protein sequence  
Protein Accession #: Eos sequence

30	1	11	21	31	41	51	
	MKVGVLNLIS	FFTFDTHGGG	FLGKNDGIKT	KKELIVNKKK	HLGPVEEYQL	LLQVITYRDSK	60
	EKRDLRNLFLK	LLKPLLLWSH	GLIRIIRAKA	TTDCNSLNGV	LQCTCEDSYT	WFPPSCLDFQ	120
	NCYLHTAGAL	PSCECHLNLL	SQSVNFCERT	KINGTFKINE	RFTNDLLNSS	SAIYSKYANG	180
	IEIQLKKAYE	RIQGFESVQV	TQFRNGSIVA	GVEVVGSSSA	SELLSAIEHV	AEKAKTALHK	240
	LFPLEDGSPR	VFGKAQCNDI	VFGFGSKDDE	YTLPCSSGYR	GNITAKCESS	GWQVIRETCV	300
35	LSLLEELNKN	FSMIVGNATE	AAVSSFVQNL	SVIIRQNPT	TVGNLASVVS	ILSNISSLSL	360
	ASHFRVSNST	MEDVISIADN	ILNSASVTNW	TVLLREEKYA	SSRLLETLEN	ISTLVPPPTAL	420
	PLNFSRKFID	WKGIPVKNKQ	LKRGYSYQIK	MCPQNTSIPI	RGRVLIGSDQ	FQRLPETII	480
	SMASLTILNI	LPVSKNGNAQ	VNGPVISTVI	QNYISINEVFL	FFSKIESNLS	QPHCFVWDFS	540
	HLQWNDAGCH	LVNETQDIVT	CQCTHLTSFS	ILMSPEVPST	IFPVVKWITY	VGLGISIGSL	600
40	LLCLYIEALF	WKQIKKSQTS	HTRRICMVNI	ALSLLIADWV	FIIVGATVDTT	VNPSGVCTAA	660
	VFFTHFFYLS	LPFWMMLMGI	LLAYRIILVF	HHMAQLHMA	VGFCLGYGCP	LIISVITIAV	720
	TQPSNTYKRK	DVCMWNWSNG	SKPLLAFFVP	ALAIIVAVNFV	VLLVLTKLW	RPTVGERLSR	780
	DDKATIIIRVG	KSLLILTPLL	GLTWGFGIGT	IVDSQNLAWH	VIFALLNAFQ	GFFILFCGIL	840
45	LDSKLRQLLF	NKLSALSSWK	QTEKQNSDDL	SAKPKFSKPF	NPLQNKHYA	FSHTGDSSDN	900
	IMLTQFVSNE						

Seq ID NO: 176 DNA sequence  
Nucleic Acid Accession #: AB035089.1  
Coding sequence: 9845..10219

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	CAGTCTAGT	AAAAGGGAGA	ACATCAATAT	AGGATGTTTC	TTAGCAATAG	AAAAGAAGGG	120
55	CCAAGAGGAA	TTAGGGAGAG	AGTTATAAGA	GATCAGCAAG	GGGACAGGGT	TAGATTGGT	180
	TTGGTTTGAA	AGCATAAGCT	AAATATGATG	CTGTCTCCCTG	GCAAGTGTGG	CAGAGTAGGA	240
	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACCTG	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	TTACTGGAGT	TGTTTTCCTC	CATGAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTCTG	AGGTGTGTCA	ATGTATACAT	ATCTATATCT	420
60	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAA	480
	AATCTCTCTC	ACTAACCAGT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACCTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GGTCCAGGAA	AATCTAGGAG	ATATTCTTTA	ACCAATCTAT	AAAGGCATTA	660
	GTAATGACAG	GATATTTCTT	GAAAGTGTAA	TTTCCCATAG	AGGAATTTGT	TTTAATTTCT	720
65	GGATTCTCTG	AGCCAAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTTGGA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCCTTT	CTAGCCTGTC	TATCAGATGC	900
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCAT	TGAACCTCAT	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCTTTAAG	1020
70	TTCAACCTTC	AGGGCAAAAC	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATCTCTTT	1080
	CCATAGATTG	GTCCCTCTGA	ACCCCGGTTT	GTCTCAGCTT	GTTATCCTGT	TTTTTTCTTC	1140
	CCTCQATTCC	CAGGATGAGC	TTGTTGCTTC	TGTCCTATGA	GACATTAGAT	TCCTTTTCTT	1200
	TGGTACCGGA	GTAATATCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGATGCAG	ACTCAGCTGA	GAAGACCAAT	ATTCAATTTT	GGAATTTCTT	ATCTCAGATA	1320
75	TTTCTCTCTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTTAG	TCCATCAAGC	CCCCATTAGT	1380
	CTATTCCTCCG	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTTCAGA	GACTCAAAAC	1440
	ATATATATTT	ATACAGGAGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
80	GTGAGAAATT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTCAG	1560
	CCTATGTGTT	TCTGCACTCT	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTG	ATGTGCTGAG	1620
	AAAACAAACT	CACGGCTGGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TGGGGAGAAA	1680
	TGTGGAGAAA	TCAGAACTCT	ATTCAAGGTC	GGTTGGAATG	CACACTTGTG	CAGAATTCTA	1740
	TGGAGAAGAG	TCTGGCATTT	CCTCAAAATG	TTAACTTGGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCATTTCAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAAATCAT	TATTCATAAT	AGTAAAGGGA	TGGAACCAAC	ACAAATGTCC	1920
	ATCAACTTAT	GATTAAGAAA	AATCTGGTCT	ATTCTAGAAA	TGGAATATTA	TTGACCACAA	1980

	AAAAGGAATG ATGTACTGAT CCATGCAATG ATGTGGACAA ACCATGAAAA TAACACTAGA	2040
	TTAAAGAAGC CAGTCACAAA AGGACTTACT GTATGATTCC ATTTACCTGA AATGTTTGA	2100
	ATAGGCAAT CCATAGAAAC AGGAGGTAGA TTCTCGTTT CCAGGGTCTC CAGGAAGGGA	2160
5	AGAAATGAAT ACAAGATTTC TTTGGAGGT AGTGAAATTG TTGTGAATG AGATCATGAT	2220
	GATGATAGCA CAACTTTGTG AATATAATAA AATCATTGAA TTGTACAGT GAATTTATGG	2280
	TATATAAAT ATATGTTAAT AAAAAGGGGG TCCACAAAAC AAACAGCCCC CCACTCTGGT	2340
	TGTCAGGGAG ATATTGGATT AAATGGCCTT GGACAACAAC CCCCTCCCT GGGCCACAGC	2400
	ATTCTTCAGA TTACAGATA TTCCAGGGGA AACACTGGAA TGAGTCTGAA GCCAGGTGCT	2460
10	AAACAGAAG ACCATTGAGA AATGTTGTGA TCCTGACAG TCAAGCAAT TATTTTCGG	2520
	CTTCATTTT AAATGTAAAA TTAGAAAGCT GCCATTAA ATGGCCCGTC TGTTTCAAT	2580
	GCTCTTCTCA GTGTAGCCCT GTTAACCTAA TGTGTTAGTC TGTTTTCATG CTGCTGATA	2640
	AAACATACCT GAGACTGGCA AGAAAAAGAG GTTTAATTGG GCTTAGAGTT CCACGTGATT	2700
	GGGAGGCCCT CAGATCACA GTAGGAGGCA AAAGTTATTC TTACATGGTG GCTGCAAGAG	2760
15	AAGATGAGGA AGAAGCAAAA GAAGAAACCC CTGATAAAC CATCGATCT CCTGAGGCTT	2820
	ATTAACATATC ATGAGAAATG CACAAGAAAG ACCGCCCCCC ATGATTCAAT TACCTCTACC	2880
	TGGGTCCCTC CAATAACATG TGGAAATCT GGTAGATACA ATTCAGTGT AGATTGGGT	2940
	GGGAACACAG CCAAAACCATA TCACCTAGCA AGGCAGATAA CTTTCTCACT GAGCCTATGC	3000
	AACAGAAAAC CATCTGGGAT GGTGTGAAG GGCACAGGAA GTGACTGGTA GGATCACTGC	3060
20	CAAAGCTGAG CACTCAGGAG AAGGCAATAG AATCCTATTC TCCATAGTAT GCTATAAGAT	3120
	ACTGAAGTAC ACTTCTTCAC TATCTCTTTG GACTTAGAAT TAGCACTACA TTCTTGTITA	3180
	TACAGAAAA TTACTAAGGA AATTCATAGG ATGCAAAAA CTTTCAGAAC TGAAAAACAG	3240
	GAAATGTAA CTTTTAGTT CTTTGGTATT CGAAGTATGC CTAAGAGACA ATGCAAAATC	3300
	CAAGAAAGA ATGGTGGGT TTTGTTTGT TTGTTTGT TTTGTTTGA CAGCTGGAGT	3360
25	AGAATACAA GGGATGGAT TGAACAAAT GAGAGGAAAT TGAATCTTA AACTTATTCT	3420
	CATTGGCATT AGAAGGCCAC CTACATGTAT TTCATAGAG CCGGTGACTG CTGACTGCA	3480
	TTCTTATTT TTCCCTATAG ATTAAGAGG AGGTACAATG GTAGAAGTGT AATCTGTCC	3540
	TTGTCTATA ATTTCATAT TCATAAGGT GAGTGTAGC CCGCTGTGA AATCTGAAGT	3600
	TGAGTAACT CAAATCTAA CACACAGGG AAAGGCAGCA AGAGGAGAGG CATAAATTTA	3660
30	GGATCTCACC CTTCATTTCA CAGACACA CAGCTCTCT GCCCACTCT GCTTCTCTA	3720
	GGAAACACAG TAAGAGCTTC AAGCCTCTCC AGCTTAATA CATGAATTAT TTTTGAGAA	3780
	AATAATGATA CTGTGTTCTA TATCATGCAT CTCTGCTATT CTGTCTGATT ATATTTTACT	3840
	TATCTGCCA GAGCAAAAT AAAATACCTA TTTCTCTGA TTTGTCCTTT ATCTAAATG	3900
	CTTAGTTCCA AGTAACCAAA GGCATTTTA GGAACACAGA GGGAGAGTGC CTTGCAGCA	3960
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40	TTTAAGAAAA TTGTACTACA AAATACCATT CCAATTATTA AAGTCATTCT GACAGGAATC	4320
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	CAACACCAAG TTCATGTTG ATCTGTTCCA ACAGTTCAGA AAATCAAAAG AGAACAACAT	4440
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5 AAGTCGAAAG AAGATTAACT CCTGGGTGGA AAGTCAAACG AATGGTAGGA GAGCCACCCA 7080  
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Seq ID NO: 177 Protein sequence  
 Protein Accession #: BAB21525.1

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 QVTENTTEKA ATYHVDRSGN VHQFQKLLT EPNKSTDAYE LKIANLKFE KYQFLQEYL 120

DAIKKFYQTS VESTDFANAP EESRKKINSW VESQTNKIK NLFPDGTIGN DTLVLVNAI 180  
YFKGQWENKP KKENTKEEFK WPNKNTYKSV QMRQYNSFN FALLEDVQAK VLEIPYKGD 240  
LSMIVLLPNE IDGLQKLEEK LTAEKLMEMT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300  
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Seq ID NO: 178 DNA sequence

Nucleic Acid Accession #: NM\_001910.1

Coding sequence: 50..1240

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GTTCTGGAAG TCCCATTAAT TGACATGAT CCACTTACCC GAGTCTCTCT CAATGGACCA 240  
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CGTGGATGGA ATGCACTTCT GCAGCAGTGG CTTTCAAGGA CTGACATCC ACCTCCAGC 1140  
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CTTGTGTCAT CTTGTACAGA GGCAGATAAT GCTGGTGCCT CTCTATTGGT AATGTTAAGA 2100  
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Seq ID NO: 179 Protein sequence

Protein Accession #: NP\_001901.1

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QPSQSSTYSQ PGQSFSIQYG TGSLSGIIGA DQVSVEGLTV VGGQFGEBSV EPQQTFFVDAE 180  
FDGILGLGYP SLAVGGATPV FDNMMAQNLV DLPMPFVYMS SNPEGGAGSE LIFGGYDHS 240  
PGSSLNWVFP TKQAYQIAL DNIQVGGTVM FCSGGCAIV DTGSLITGP SDKIKQLQNA 300  
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Nucleic Acid Accession #: NM\_018058.1

Coding sequence: 319..1575

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GGGCTTTGTC AACACGTG

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Seq ID NO: 181 Protein sequence  
Protein Accession #: NP\_060528.1

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FRDIASPKFS MPSPVRVTIT ADFDNDQELE IFFNNIAYRS SSANRLPRVI RREHGDPLIE 180
ELNPGDALEP EGRGTGGVVT DFDGDMIDL ILSHGESMAQ PLSVFRGNQA FNNWLRVVP 240
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KMVSRNVASG ENNSVLEILY PRDEDTLQDP APLETMPNAS SSHSCALET PYVSTPMEAT 360
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Nucleic Acid Accession #: AJ279016  
Coding sequence: 1..1962

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TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
CAGAAGCGGC TGGTGAAACAT CGCGGTGATG GAGCGCAGCT CACCCCTACTA CGCGCTGCGG 300
GACCGGCAGG GGAACGCCAT CGGGGTCACT GCCTGCGACA TGACACGGGA CGGCGGGGAG 360
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Seq ID NO: 183 Protein sequence  
Protein Accession #: CAC08451

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GRYSIIYANY AYGNVGPDAL IEMDFEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
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Seq ID NO: 184 DNA sequence  
Nucleic Acid Accession #: FGENESH1  
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TCACCCTACT AGCGCTGGG GAGCGGCGAG GGGAAAGCCA TCGGGTCAC AGCCTCGGAC 240
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30     CCACCTACAA CCCTGTCAGG CCTCTCTGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC 420
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TGTCGGGGTG GACTGAGACC TACCCATGAA CCAGAACCAT TTCTCTGAG ACCCAATCA 540
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Protein Accession #: FGENESHH

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 Protein Accession #: NP\_000575.1

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 GTGCTTGTGG TGATTGTGGT GTGCAGTATC CGGAAAAGCT CGAGGACTCT GAAAAGGGG 1140  
 80 CCGCGGAGG ATCCAGTGC CATTTGTGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA 1200  
 ACCCAGAAC GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATCGA TATCCTGAAG 1260  
 CTTGTAGCAG CCCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC 1320  
 AGTGAGAGGG AGGTTGCTGC TTTCTCAAT GGGTACACAG CCGACCACGA CGGGGCTTAC 1380  
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 GCCCTGCGCC AGCACCGGAG AAACGATGTT GTGAGAGAAGA TCGTGGGCT GATGGAAGAC 1500  
 ACCCCCCAGC TGGAACTGA CAACTAGCT CTCCGATGA GCCCAGGCC GCTTAGCCCG 1560

5 AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCOG CTCTCCTGAC GGTGGAGCCT 1620  
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 GACTCTACAT CCAGCGGCTC CTCGCGCTG AGCAGGAACG GTTCCTTAT TACCAGAGAA 1740  
 AAGAAGGACA CAGTGTGCGC GCAGGTACGC CTGACCCCT GTGACTTGCA GCCTATCTTT 1800  
 GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG 1860  
 GCTGAGGACA AACTAGACCG GCTATTGCAA ATTATTGAG TCAAGAGCCA GGAAGCCAGC 1920  
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10 Seq ID NO: 191 Protein sequence  
 Protein Accession #: NP\_055267.1

1 11 21 31 41 51  
 15 MGTSPSSSTA LASCRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTYRHVDRA 60  
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 LPCAALDRE CTCPPFMFOS NATCAPHTVC PVGWGVRKKG TETEDVRCKQ CARGTFSDVP 180  
 SSVMKCKAYT DCLSNLVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPERMETHE 240  
 VPSSTYVPKG MNSTESNSSA SVRPKVLSSI QEGTVFDNTS SARGKEDVNK TLPNLQVNH 300  
 20 QQGPHRHIL KLLPSMEATG GEKSSTPIKG PKRGHPRNL HKHFDINEHL PWMIVLFLL 360  
 VLVVIVVCSI KRSSRTLKKG PRQDPSAIVE KAGLKSMTP TQNREKIYY CNHGIDILK 420  
 LVAAQVGSQD KDIYQFLCNA SEREVAASN GYTADHERAY AALQHWITRG PEASLAQLIS 480  
 ALRQHRNDV VEKIRGLMED TQLETDKLA LPMSPSPLSP SPIPSNAKL ENSALLTVEP 540  
 SPQDNKNGFF VDESEPLLR DSTSSGSSAL SRNGSFITKE KEDTVLRQVR LDPCLQPIF 600  
 25 DDMHLHFNPE ELRVIEEIPQ AEDKLDRLPE IIGVKSQEAS QTLLDVSVYSH LPDLL

Seq ID NO: 192 DNA sequence  
 Nucleic Acid Accession #: XM\_044533  
 Coding sequence: 238..2751

30 1 11 21 31 41 51  
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 AGCGGCGTCA GCTGTTTCA CTTGTGGACA GCAGCCTTCA GCGCCATGTG TACCTACATC 720  
 45 AACATGGAGA ACTTACCCTT GGCAAGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780  
 AAGGGCGGTT GTCCCTTCGA CCGCAATTTT AAGTCCACTG CCCTGGTGGT TGATGGGGAG 840  
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 CCCATGGCCA ACTGCAGCT GTACAGGAGC TGTGGGACT GCGCTCTGCG CCGGACCCCG 1860  
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 70 GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGACGG GGTGGCAGAC 2280  
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 75 CCTGTGTGTC TGCCCCCTGA GACCCGCCCA CTCACCGGCC TAGGGCCCCC TAGCACCCCG 2580  
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 TGCTCTTAT GTAACTGAG CCCTTTGTTT AAAAAAAT TCCAAATGTG AAATAGAAAT 3060  
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 GGGGTGCTGG GGATGCATCC AAAGTGGTGT TGTGAGACAG AGTTGGAAC CCTCACCAAC 3180

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10  
TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCTGTCTC ACTGCAGATT 3240  
CAGGACCAGC TTGGGCTGCG TGCGTCTGTC CTGCGCAGTC AGCCGAGGAT GTAGTTGTGT 3300  
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GGTCTGGGC TCGGACCCAA CTCTGGACC TTTCAGCCT GTATCAGGCT GTGGCCACAC 3420  
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CAGGGAAGAG ACTGTGCGCT GCCTTCTCC GTTGTTCGT GAGAACCCT GTGCCCTTTC 3540  
CCACCATATC CACCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACATA CTGCACCCCTG 3600  
GTCCTCTCCC CAGTCCCAGG TTCACCTCC ATCCCTCACC TTCTCCACT CTAAGGGATA 3660  
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720  
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Seq ID NO: 193 Protein sequence  
Protein Accession #: XP\_044533.3

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30  
1 11 21 31 41 51  
MLRTAMGLRS WLAAPWALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60  
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SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180  
GKGRCPFFPN FKSTALVVDG ELYTGVSSF QGNDPAISRS QSLRPTKTES SIWLQDPAF 240  
VASAYIPESL GSLQDDDKI YFFSETGQE FEFFENTIVS RIRICKGDE GGERVLQQRW 300  
TSFLKAQLLC SRPDGFPFN VLQDVFTLSP SPQDWRDLTF YGVFTSQWRH GTTEGSACV 360  
FTMKDVQRVF SGLYKEVNR TQQWYVTHP VTPRPGACI TNSARERKIN SSLQLPDRVL 420  
NFLKDHFLMD GQVSRMRLLL QPQARYQVVA VHRVPLGHT YDVLFLGTGD GRLHKAVSVG 480  
PRVHIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540  
PYCAWSGSSC KHVSLYQPL ATRPWIQDIE GASAKDLCAS SSVVSPSPFP TGEKPCQVQ 600  
FQPNVTNTLA CPLLSNLATR LWLNRGAPVN ASASCHVLP GDLLLVGTQQ LGFEQCWSLE 660  
EGFQQLVASV CEPVEDGVA DQTEGGGSP VIISTRVSA PAGGKASWGA DRSYWKFLV 720  
MCTLFLVAVL LPVFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPEPR PLNGLGPPST 780  
PLDHRGYQLS SDSPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 194 DNA sequence  
Nucleic Acid Accession #: NM\_022819.1  
Coding sequence: 1..635

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AGCCTGGGTA TGAAGAAGTT CTTACCGTG GCCATCCTGT CTGGCAGCGT TCTGTCCACA 180  
GCTCAGCGCA GCCTGCTCAA CCTGAAGGCC ATGCTGGAGG CCGTCACAGG GAGGAGCGCC 240  
ATCCTGTCCT TCGTGGGCTA CGGTGCTAC TGTGGGCTGG GGGGCGGTGG CCAGCCCAAG 300  
GATGAGGTGG ACTGGTGTCTG CCACGCCAC GACTGCTGCT ACCAGGAAC CTCTTGACCA 360  
GGCTGTACCC CCTATGTGA CCACTATGAT CACACCATCG AGAACACAC TGAGATAGTC 420  
TGCAGTGACC TCAACAGAC AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480  
GTCTGTGACC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCCT CAATGTCTAC 540  
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AGTACCAAT CCCACGCCC CCCCGCCCT CCCTAG

50  
Seq ID NO: 195 Protein sequence  
Protein Accession #: NP\_073730

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60  
1 11 21 31 41 51  
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GCHPYVDHYD HTIENNTIEV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EBYRGLFNVY 180  
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Seq ID NO: 196 DNA sequence  
Nucleic Acid Accession #: XM\_028196.1  
Coding sequence: 1315..1791

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CGCCCGCCCC ACCTTCTCTC CCACCCACAT GCCGAAGGGT GGCCAGGCG GCAGGTGGAC 540  
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CTCCGCCCAT GAGCTCTCCG ACCCTCTGG GCTTCCAGT TCTTGGGGC TGCAGTGAAC 780  
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AGGAGGAGCC CAGGTCACAG GGCCAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCTCTG 960  
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5 CTCTCTGCTG CACAGAACCCT TCGCCCTGCG CCACCCCGTG CTGCCTCCTT GCCCTGGCAG 1200  
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 15 CTGCGCTGCA GCGCGGGGGT CTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCAGGG 2040  
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 20 TGGGGAGCTG ACAGGGCAGG GGGCCTTGGC TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340  
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 30 CTGATGGCGA CCAATTTTCG GGGTCTGAGC CCAACTCGG CAGAAATCAC CTTCCCGGGC 2940  
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 TACGTGCCCA GCTCAGGCGG GCTGACCGTG GTGGTGTGG AGGCTCGAGG CTTGCGTCCA 3060  
 GGAATTGAGC AGCCCTACGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG 3120  
 35 AGAAGACAG CCACCAAAAA GGGCAGCGCG GCCCCTACT TCAATGAGGC CTTCACCTTC 3180  
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 CCGCTGCAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGGCCATTGC CCAGCGGCAC 3360  
 CCGCTGCCGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCCG CCTTCGCTCG 3420  
 40 CGCCTGCCCT TGCCCACTC CTGAATGCAC CACATGCCCT TGCTCTCCCG CTGAGCCACG 3480  
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Seq ID NO: 197 Protein sequence

Protein Accession #: XP\_028196.1

45 1 11 21 31 41 51  
 MGHPPVSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQBG CGDNPAKWGL QLSTDALSLA 60  
 STPGPRWALI AGALAAAGVLL VSCLLCAACC CRRHRKKPR DKESVGLGSA RGTITTHLVR 120  
 50 SGLLTQSRRE GLKSLRLQSPG QRGEPSPRDG LTPTEAGR

Seq ID NO: 198 DNA sequence

Nucleic Acid Accession #: NM\_000612.2

Coding sequence: 553..1095

55 1 11 21 31 41 51  
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 60 TTCTGTTTCT CTCGTGCTGT TTCTCTCCCG CTGTGCGCCT GCGCGCCTCT CGCTGTCTCT 180  
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 65 ACATTGCGCC CCGCGACTC GCGCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG 480  
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 75 CCGCTGATTG CTCTACCCAC CCAAGACCCC GCGCCCGGGG GCGCCCGCCC AGAGATGGCC 1080  
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 CTCTCTCTGA CACGAGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACGT 1200  
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 80 CCTCGGCCCC CTCCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC 1320  
 GATTGGCTTT AAACACCTTT CACATACCTT CCCCCC

Seq ID NO: 199 Protein sequence

Protein Accession #: NP\_000603.1

1 11 21 31 41 51

MGIPMGKSM L VLLTFLAFAS CCIAAYRPSE TLGGELVDT LQFVCGDRGF YFSRPASRVS 60  
 RRSRGIVEEC CFRSCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPYPYV GKFFPYDTWK 120  
 QSTQRLRRGL PALLRARRGH VLAKELEAFR EAKRHRPLIA LPTQDPAHGG APFEMASNRK

Seq ID NO: 200 DNA sequence  
 Nucleic Acid Accession #: AK057131.1  
 Coding sequence: 61..1146

1 11 21 31 41 51  
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 GAGGTTTATG GCTAGCAATC CCTTAACCAA TGCAATAATC AGGACCACCA CGGCACTCAC 1020  
 CATATTCAA GCGAGGGTCA AGTTCAATGT CATCCCCCA GTGGCCGAGG CCACAGTCAA 1080  
 TCTCCGGAT CACCTGGAG AGACAGTCCA AGAGGTCTTA GAACTCAGCA AGAATCTGT 1140  
 GGCTGATAAC AGAGTCCAGT TCCATGTGTT GAGTGCTTTT GACCCCTCC CCGTCAGCCC 1200  
 TTCTGATGAC AAGGCTTGG GCTACCAGCT GCTCGGCCAG ACCGTACAGT CCGTCTTCCC 1260  
 GGAAGTCAAT ATTACTGCCC CAGTTACTTC TATTGGCAAC ACAGACAGCG GATTCTTTAC 1320  
 AAACCTCACC ACTGGCATCT ACAGGTTCTA CCCCATCTAC ATACAGCCTG AAGACTTCAA 1380  
 ACGCATCCAT GGAGTCAACG AGAAATCTC AGTCCAAGCC TATGAGACCC AAGTGAAT 1440  
 CATCTTTGAG TTGATTGAGA ATGCTGACAC AGACCAGGAG CCAGTTTCTC ACCTGCACAA 1500  
 ACTGTGAGGT CAAGGGGCTT GCTGGGTTAG GCATGCCCGA CCGCGGACA GGACTAACCC 1560  
 AAGGGGGAAA GCTAGTGTG ATGAACTTT TGATCAAAAC CACATTGTAA AACATTGCC 1620  
 ATCTGCTTG CTCACCTTAA AACTCTCCCA AGAACCAAGG CCGGGTAAGG TAAAGTCAGC 1680  
 AGAAATCTG CTCTCCCTT CTCTCCGACA TCTGCATCCC TTGATCCACT GGCATTGTCT 1740  
 GCGCTCTGT CCCTTATCTG TCTTATGCTG GTTATTTTAC TGCTTCACCT TCCAGGCTTG 1800  
 ACTTAACAAA TGTAGATTGG AGAAATCTCA ACCAGTTGTT ACCTGATAGG AGTCTTTAAT 1860  
 TTAGGCGACT TTGCTGGGGA TGCTTTCTCC AGAGCTTATA TATTCTTCT TACTAGAACT 1920  
 TTCTTCCCC TTTTATTTCC CTCTCTTCTT GGACTCATGA GCTGCTCTT CATCTCTCT 1980  
 CTCTCTCTG CATCTCTCC CTTACTCTTC AATTATTCT ACTTCTGGAC CTGGAATTAC 2040  
 CCAAAGTGTG ATACTACCAT AATTGTCCAC ATAATCAGTC AAATAAAGTG ATCTGTGCAT 2100  
 C

Seq ID NO: 201 Protein sequence  
 Protein Accession #: BAB71368.1

1 11 21 31 41 51  
 MAQRVCVLA LVAMLLVFP TVSRSMGPRS GEHQASRIP SQFSKEERVA MKEALKGAIQ 60  
 IPTVTFSSEK SNTTALAEPG KYIHKVFTV VTSFQIHEV VEEYSHLFTI QGSDPSLQPY 120  
 LLMAHFDVVP APEGHEVPP FSGLERDGI YGWTGLDDKN SVMALLQALE LLLIRKYIPR 180  
 RSEFFISLGH EESSGTGAQR ISALLQSRGV QLAFIVDEGG FILDDFIPNP KKPIALIAVS 240  
 EKGSMMLMQ VNMTSGHSA PPKETSIGIL AAASRLQET PMPIIFGSGT VVTVLQQLAN 300  
 EVYGEKSLAQ CNQDHHGTH HIQSRGQVQC HPPSGPGHSQ LPDSFPWTDSP RGPRTHEHC 360  
 G

Seq ID NO: 202 DNA sequence  
 Nucleic Acid Accession #: NM\_004217.1  
 Coding sequence: 58..1092

1 11 21 31 41 51  
 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCTCT CCCCCTTCTC TCTAAGGATG 60  
 GCCCAGAAAG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120  
 AGCACCTTGC CCCAGGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180  
 ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCTGGCC AGAAGGTGAT GGAGAATAGC 240  
 AGTGGGACAC CCGACATCTT AACCGGGCAC TTCACAAATG ATGACTTTGA GATTGGGCGT 300  
 CCTCTGGGCA AAGGCAAGTT TGGAAACGTC TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360  
 ATCGTGGCCG TCAAGTCTCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420  
 CTGCGCAGAG AGATCGAAAT CCAGGCCAC CTGACCATC CCAACATCTT CGCTCTCTAC 480  
 AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540  
 CTCTACAAGG AGTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG 600  
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660  
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG 720  
 TCTGTGCATG GCGCTCTCTT GAGGAGGAAG ACAATGTGTG GCACCTGGA CTACCTGCC 780  
 CCAGAGATGA TTGAGGGGCG CATGCACAA GAGAAGGTGG ATCTGTGGTG CATTGGAGTG 840  
 CTTTGCTATG AGTGTCTGGT GGGGAACCCA CCTTTGAGA GTGCATCACA CAACGAGACC 900  
 TATCGCCGCA TCGTCAAGGT GGACCTAAG TTCCCGCTT CTGTGCCAC GGGAGCCGAC 960  
 GACCTCATCT CCAAACTGCT CAGGCATAAC CCTCGGAAC GGCCTGCCCT GGCACGAGTC 1020

TCAGCCACC CTGGGTCG GGCACACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA 1080  
 TCTGTGCGCT GATGGTCCCT GTCACTTCACT CGGGTGGCGT TGTITGTATG TCTGTGTATG 1140  
 TATAGGGGAA AGAAGGGATC CCTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200  
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 203 Protein sequence  
 Protein Accession #: NP\_004208

1 11 21 31 41 51  
 MAQKENSYPW PYGRQTAPSG LSTLPQVRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60  
 SSGTDPILTR HFTIDDFEIG RPLGKGFN VYLAREKSH FIVALKVLFK SQIEKEGVEH 120  
 QLRREIEIQA HLHHPNLR YNYFYDRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180  
 MEELADALMY CHGKKVHRD IKPENLLGL KGELKIADFG WSVHAPSLRR KTMCGTLDYL 240  
 PPEMIEGRMH NEKVDLWCIG VLCYEYLLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA 300  
 QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPSPAL QSVQ

Seq ID NO: 204 DNA sequence  
 Nucleic Acid Accession #: AK055663  
 Coding sequence: 38..1423

1 11 21 31 41 51  
 AGAACGGCTT CCGCGGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTG 60  
 AAAACACCAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120  
 CCGAAGGTCC TGGAAGATAC TGCTCTTTGG TGTAAATAAC TTGATATGTA CTGGCTTCT 180  
 GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT 240  
 TTTTGATCTT TTTTATTTAA TGACATGTTT AATAAGTTAC TGGGTAACTT TGAGGAAACC 300  
 TAGCCCTGTC TATTCATTGG GGTITGAAAG ATTAGAAGTC CTGGCTGTAT TTGCTCCAC 360  
 AGCTCTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAAAGAA AGTGCAGAAC GCTTTTGGGA 420  
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTGGTACT TTTGTGGCTC TTTGTTTCAA 480  
 CCTGTTCAGC ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540  
 TACGAGCTGG CTTCAGAGC ATGTTGCAGA TCTTAGTCGA AGCTGTGTG GAATTATTC 600  
 GGGACTTAGC AGTATCTTCC TTCCCGCAAT GAATCCATTT GTTTGTATG ATCTGTCTGG 660  
 AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCGGTAGA 720  
 CACTGCCTCT GCTATAGCTA TTGCCTTGAT GACATTGGGC ACTATGTATC CCATGAGTGT 780  
 GTACAGTGGG AAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATGTGCT AGTGGACAA 840  
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTATGAA GTCCGAAATG AACATTTTG 900  
 GACCTAGTGT TTTGGCTCAT TGGCTGGATC AGTGCAATGA AGAATTGCGA GAGATGCCAA 960  
 TGAACAAATG GAGTCTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC 1020  
 TGTTCAAATT TTCAAGGATC ACTGGATTAG GCCTGCCTTA TTGTCTGGGC CTGTGTCAGC 1080  
 CAATGTCCTA AACTTTTCAG ATCATCAGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140  
 TGAATTGAAC CAGTTTACAT CAACCTCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200  
 ATTTAACACT CCTGGGAAAT ATGTGAACCC AGTATTCTT CTAAACACAC AAACAAGGCC 1260  
 TTATGCTGCT GGTCTCAATC ATGGACACAC ACCCTACAGC AGCATGCTTA ATCAAGGACT 1320  
 TGGAGTTCCA GGAATTGGAG CAATCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380  
 TAGATATGGA ACTAATAATA GAATGGGACA ACCAGACCA TGATAGACTC TAATTTATT 1440  
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTAG TAATCCAAT TTGCATTGAC 1500  
 TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC 1560  
 TATGAAACTA TTTTGTGTA AAATGTATT GTGACAGTGA AATCCTCGTA AATGTTAAG 1620  
 GCTTTAATAA GGCTCTCTTT AGAAAATGTG TTTCTTTAAA TTTGATTTT GGTATCTTTG 1680  
 GTTTTGTAGT TGACTGCAGT GTGATGTGAC CTACCTTTA TAAGAGCCAC TTGATGGAGT 1740  
 AGATCTGTA CATTACTAAG ATACGATATT TCTTTTTTTT TCCGAGACGG AGTCTGTCTC 1800  
 TGCCACTGTG CCCGGCCAAT ACATTATAT TAACCTAAGG CTGACTTTA TTAAGGCTTC 1860  
 CTTAGTTTTT GTTTTGTGTT GTTTTTGAG ATGGAGTCTC ACTCTGTGCG CCAGGCTGGA 1920  
 ATGCAGTGGC ATGATCTCAG CTCACCTGCA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC 1980  
 TGCCCTAGCC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCAAGCCC AGCTAATTTT 2040  
 TGTATTTTGA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAATCCTCG 2100  
 ACCTCATGAT CCACCCCACT TAGCCTCCCA AAGTGTCTGG ATTAGGTGTG AGCCACCGCA 2160  
 CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATA TACACATTTT 2220  
 GGGAAAGGGA AAAATGTCTG TTCAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT 2280  
 AATTGCTAAA TTTTCTTTG AGGTTCTCT GAATTATGTC TTCAAACTA AAAGCAAAAA 2340  
 TTTTATGACA AAATTTTGA ATACATTCTA TCTAGCACAA TTTGAATTT TAATTATCAA 2400  
 GATTTTGTG AAAGTTTCTC TCCTTTAAAA ATTTAGTAC ATTTGTAAT

Seq ID NO: 205 Protein sequence  
 Protein Accession #: BAB70980.1

1 11 21 31 41 51  
 MGTIHLFRKP QRSFFGKLLR EPRLVAADRR SWKILLFGVI NLICTGFLM WCSSTNSIAL 60  
 TAYTYLTIFD LPSLMTCLIS YWVTLRKPS VYSFGERLE VLAVFASTVL AOLGALFILK 120  
 ESAERFLQEP EIHTGRLLVG TFVALCFNLF TMLSIRNKP AYVSEAASTS WLQEHVADLS 180  
 RSLCGIIPGL SSIFLPRMNP FVLIDLAPAG ALCITYMLIE INNYFAVDTA SAIAIALMTF 240  
 GLTMYPMSVYS GKVLQITTP HVIGQLDKLI REVSTLDGVL EVRNEHFVTL GFGSLAGSVH 300  
 VRIRRDANEQ MYLAHVNTNRL YTLVSTLTIV IFKDDWIRPA LLSGPVAANV LNFSDHNVIP 360  
 MPLLKGTDDL NPVTSTPAKP SSPPPPEFSN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY 420  
 SSMLNQGLGV PGIGATQGLR TGFTNIPSRV GTNNRIGQPR P

Seq ID NO: 206 DNA sequence  
 Nucleic Acid Accession #: NM\_016361.1  
 Coding sequence: 397..1662

1 11 21 31 41 51



5  
10  
15  
20  
25  
30

GGAACTCAGG	GCCGGCTCCT	GTTCCTTCAA	GAGTGTCTGA	GGCCAAACTT	GAATACAAG	60
TTTAATGTTT	CTCGTCGGGC	AAAAGATAAG	GATCCGATCT	CCCCCGGCC	GGTGTGCAGC	120
AGGAGCGACC	AACCCCGACC	CGGGTTAAAA	CTCCAGGGA	CTCTCGCTG	CTGCCACCTC	180
TTGTTCTCTC	CCCCGTTCCC	ACTCGGGGTC	TCCCTCAGGG	CGGGAGGCA	CAGCGGTCCC	240
TGCTTGCTGA	AGGGCTGGAT	GTACGCATCC	GCAGGTTCCC	GCGGACTTGG	GGGCGCCCGC	300
TGAGCCCGGG	CGCCCGCAGA	AGACTTGTGT	TTGCCTCTG	CAGCCTCAAC	CCGGAGGCGAG	360
CGAGGGCTTA	CCACCATGAT	CACTGGTGTG	TTCAGCATGC	GCTTGTGGAC	CCCAGTGGGC	420
GTCTGACCTT	CGCTGGCGTA	CTGCCTGCAC	CAGCGCGGGG	TGGCCTGGC	CGAGCTGCAG	480
GAGGCGGATG	GCCAGTGTCC	GGTCGACCGC	AGCCTGTCTG	AGTTGAAAT	GGTGCAGTTC	540
GTGTTTCGAC	ACGGGGCTCG	GAGTCTCTTC	AAGCCGCTCC	CGCTGGAGGA	GCAGGTAGAG	600
TGGAACCCCC	AGCTATTAGA	GGTCCCACCC	CAAACTCAGT	TTGATTACAC	AGTCACCAAT	660
CTAGCTGGTG	GTCCGAAACC	ATATTCTCCT	TACGACTCTC	AATACCATGA	GACCAACCTG	720
AAGGGGGGCA	TGTTTGTCTG	GCAGCTGACC	AAGGTGGGCA	TGCAGCAAT	GTTCGCTTGT	780
GGAGAGAGAC	TGAGGAAGAA	CTATGTGGAA	GACATTCCCT	TTCTTTCACC	AACCTTCAAC	840
CCACAGGAGG	TCTTTATTGG	TCCCACTAAC	ATTTTTCGGA	ATCTGGAGTC	CACCCGTTGT	900
TTGCTGGCTG	GGCTTTTCCA	GTGTCAAGAA	GAAGGACCCA	TCATCATCCA	CACGTGATGA	960
GCAGATTTCG	TGGCTTTGTA	TCCCAACTAC	CAAGCTGCT	GGAGCCTGAG	GCAGAGAACC	1020
AGAGGCCCGA	GGCAGACTGC	CTCTTTACAG	CCAGGAATCT	CAGAGGATTT	GAAGAGGTG	1080
AAGGACAGGA	TGGGCATTGA	CAGTAGTGAT	AAAGTGGACT	TCTTCATCCT	CCTGGACAAC	1140
GTGGCTGCGG	AGCAGGCACA	CAACCTCCCA	AGCTGCCCA	TGCTGAAGAG	ATTGTGACCG	1200
ATGATCGAAC	AGAGAGCTGT	GGACACATCC	TTGTACATAC	TGCCCAAGGA	AGACAGGGAA	1260
AGTCTTCAGA	TGGCAGTAGG	CCCATTCCTC	CACATCCTAG	AGAGCAACCT	GCTGAAAGCC	1320
ATGAGACTCTG	CCACTGCCCC	CGACAAGATC	AGAAAGCTGT	ATCTCTATGC	GGCTCATGAT	1380
GTGACCTTCA	TACCGCTCTT	AATGACCCCTG	GGGATTTTGT	ACCACAAATG	GCCACCGTTT	1440
GCTGTGTACC	TGACCATGGA	ACTTTACCGA	CACCTGGAAT	CTAAGGAGTG	GTGTGTGCAG	1500
CTCTATTACC	ACGGGAAGGA	GCAGGTGCCG	AGAGGTTGCC	CTGATGGGCT	CTGCCCCCTG	1560
GACATGTTCT	TGAATGCCAT	GTCAGTTTAT	ACCTTAAGCC	CAGAAAAATA	CCATGCACTC	1620
TGCTCTCAAA	CTCAGGTGAT	GSAAGTTGGA	AATGAAGAGT	AACGTATTTA	TAAAAGCAGG	1680
ATGTGTTGAT	TTTAAATATA	AGTGCCTTTA	TACAAAAAAA	AAAAAATAA	A	

Seq ID NO: 207 Protein sequence  
Protein Accession #: NP\_057445.1

35  
40  
45

1	11	21	31	41	51	
MRLWTFVGL	TSLAYCLHQ	RVALAELQEA	DGQCPVDRSL	LKLKMQVQVF	RHGARSPLKP	60
LPLEEQVENN	PQLEVPPT	QFDYTVNL	GGPKPYSPYD	SQYHETTLKG	GMFAGQLTKV	120
GMQMFALGE	RLRKQYVEDI	PFLSPTNPQ	EVFIRSTNIF	RNLESTRCLL	AGLFQCCQKEG	180
PIIIHTDEAD	SEVLVYNYQS	CNSLRQRTRG	RQQTASLQPG	ISEDLLKVKD	RMGIDSSDKV	240
DFPILLDNVA	AEQAHLNLPSC	PMLKRFARMI	EQRAVDTSLY	ILPKEDRESL	QMAVGPFLHI	300
LESNLLKAMD	SATAPDKIRK	LYLYAAHDVT	FIPLMLTGI	FDHKWPPFAV	DLTMELYQHL	360
ESKEWFQVLY	YHKEBQVPRG	CPDGLCLPDM	FLNAMSVTYL	SPEKYHALCS	QTQVMEVGNE	420
E						

Seq ID NO: 208 DNA sequence  
Nucleic Acid Accession #: CAT cluster

50  
55  
60

1	11	21	31	41	51	
TTTGAGGGGG	TGGTGGGGCG	AGTTTAATTC	ATAAAGAAGC	CTCCTGATCA	GAAGGGGGCC	60
TAAACAGCTG	CCCTTGAGGA	GAAGTCCTTC	CTTGAGGATA	AGGCCTCCCA	GGGAGGAGGG	120
TGCTGGGGGC	CAGTGTAGG	CTTCAGGCCA	TCCCTGGAGG	CCAGTCCTGT	GCTCAGCAAG	180
TAGTGGCAGA	GCCTGGAGTG	ATGAGTGGGA	TGGCCTTCTC	AGGTACAGGA	CTGTGCTGCT	240
TCTGGCTGCT	CTTGCAATTG	CATTTGCCAC	TCAGAACTGC	CGCATCCCA	GCAATGGCCA	300
GAGGCCCTCC	GCAGATCAGT	CCGCTCAGT	GCAGGTTTTT	CCAGTCATAG	TAGAAGGGAT	360
CGTCTTTATT	GGCAAAATGG	TCATTGGCTT	CCAAGGCAGT	CAGGCCAACT	GTGTGACTCT	420
GCAGGTTCTT	CACTGCTCCT	TCACCAGTGT	CCTGCGAGGT	CACCTTGGCG	AGGGCTCACC	480
TGAGCTGGCA	GCGCAG					

Seq ID NO: 209 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..564

65  
70  
75  
80

1	11	21	31	41	51	
ATGGAGCCCT	GGGCGTGCTT	GCAGGGTTTA	AAGAGCCGAC	CCACGTGCCC	AGCAGCCTCC	60
TCAGATCCGT	TCTCTGCGCT	GCCAGCTCAG	GACACTGGTG	AAGGAGCAGT	GAGGAACCTG	120
CAGAGTCACA	CAGTTGGCCT	GACTGCCTTG	GAAGCCCAATG	ACCCATTGTC	CAATAAAGAC	180
GATCCCTTCT	ACTATGACTG	GAAGAACCTG	CAGCTGAGCG	GACTGATCTG	CGGAGGGCTC	240
CTGGCCATTG	CTGGGATCGC	GGCAGTTCTG	AGTGGCAAAT	GCAATGCAAA	GAGCAGCCAG	300
AAGCAGCACA	GTCTGTATCC	TGAGAAGGCC	ATCCCACTCA	TCACTCCAGG	CAGATTCTCT	360
ACCTTGGCCA	AATCAAAATA	ACCTTTATCT	CCAAGCACCT	TTGTCTTGGT	GTTTGGCATC	420
AGCTACACAT	CAGTCTTCOG	AGTGCCTCTT	TCTGCGTCCC	TGTACCCCTG	CATTCTCTGT	480
GATGCTGCTG	CCCTCACATC	AGGCCATCCA	AGCATGACA	ACATAAGCAT	GCAGAACACT	540
GGAACGAAGG	GCTGTACCTA	ATGA				

Seq ID NO: 210 Protein sequence  
Protein Accession #: FGENESH predicted

1	11	21	31	41	51	
MEPWANLQGL	KSRPTCPAAS	SDPFSALPAQ	DTGEGAVRNL	QSHTVGLTAL	EANDPFANKD	60
DPFFYDWKNL	QLSLGICGGL	LAIAGIAAVL	SGKCKCKSSQ	KQHSFVPEKA	IPLITPGRFL	120

TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSGHP SMQNISMQNT 180  
GKKGCT

5 Seq ID NO: 211 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..318

1	11	21	31	41	51	
10	ATGCCCGGCC	ACCCCGTCTG	TGAAGTGAGG	AGCACCTCTG	CCGGCTGCC	CCGCTGGGA 60
	AGTGAGGAGC	GGCTCTGCC	GGCTGCCACC	CCGTCTGTGA	GTGCCTGCTG	CGCTGGGCC 120
	AGGCGCGCCG	TGCCCTGCCA	GGCCCTCCGG	CCCCCACCT	TCCACCCAG	GGCTGTCTCC 180
	TCACCCAGG	GTTCCTCTC	CCTAGTTTCC	ACCAGAGACT	GGGTCTTCAT	TCTCACCTCG 240
	CTACACAGCC	CCTACCAGAA	CGTTCTGAAA	TGCAAACTTA	ACAACTGTCT	CACCCAGCA 300
15	GGAAACTCCC	CAGGCTCCCG	GGCCCCCTGC	GGGGTTGCAG	GCCTCACTCT	TCGCGCCAT 360
	CCCTCGCCCC	TGACCGCCCT	GAGCTCGCCC	CCAGTGCTGG	CCCTTCAGCT	CCAGTTATCC 420
	CTCCAGCCT	CCAAGGTCCC	CGTTACCGAA	GACCGCCACC	ATCAACGACAT	AGCGCAGCAC 480
	ATATGGGACA	CTGGTGAAGG	AGCAGTGAGG	AACCTGCAGA	GTCAACAGCT	TGGCCTGACT 540
	GCCTTGAAG	CCAATGACCC	ATTGCAAT	AAAGACGATC	CCTTCTACTA	TGACTGAAA 600
20	AACCTGCAGC	TGAGCGGACT	GATCTGCGGA	GGGCTCCTGG	CCATTGCTGG	GATCGCGGCA 660
	GTTCTGAGTG	GCAAATGCAG	ATGCAAGAGC	AGCCAGAGC	AGCACAGTCC	TGTACCTGAG 720
	AAGGCCATCC	CACCTATCAC	TCCAGGCAGA	TTTCTCACCT	TGGCCAAATC	AAATAAACCT 780
	TTATCTCAA	GCACCTTTGT	CTTGTGTTT	GGCATCAGCT	ACACATCAGT	CTTCCGAGTG 840
25	CCTCTTTCTG	CGTCCCTGTA	CCCTGCCATT	CCTGGTGATG	CTGCTGCCCT	CACATCAGGC 900
	CATCCAAGCA	TGCAGAACAT	AAGCATGCAG	AACACTGGAA	CGAAGGGCTG	TACCTAA

Seq ID NO: 212 Protein sequence  
Protein Accession #: FGENESH predicted

1	11	21	31	41	51	
30	MPGHPVCEVR	STSARLPRLG	SEERLCPAAT	PSVSACCAGP	RPPVPCQALR	PPTFHPRACS 60
	SPQGSISLVS	TRDWFILTL	LHSPYQNVLK	CKENNLCTFA	GNSPGSRAPC	GVAGLTILRAH 120
35	PSALTALSSP	PVLALHVQLS	LPASKVPVTE	DRHHHDIAQH	IWDTGEGAVR	NLQSHTVGLT 180
	ALEANDPFAN	KDDPFYYDWK	NLQLSGLICG	GLLAIAAGIAA	VLSGKCKCKS	SQKQHSVPVE 240
	KAIPILITPGR	FILTLAKSNKP	LSPSTFVLVF	GISYTSVFRV	PLSASLYPAI	PGDAAALTSG 300
	HPSMQNISMQ	NTGTRKGT				

40 Seq ID NO: 213 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1758

1	11	21	31	41	51	
45	ATGATGGGGT	CTCATGTTGC	CCAGGCTGGT	CTTGAACCTC	TGGGCTCGAG	TGACCCTCCT 60
	GCCTTGGCCT	CCGAAAGTGC	TGGGATTACA	GGACTGTTAT	TACAGGAATC	CATAACACTG 120
	GAGGATGTGG	CTGTGGACTT	CACCTGGGAG	GAGTGGCAAC	TCCTGGGCGC	TGCTCAGAAG 180
	GACCTGTACC	GGGATGTGAT	GTTGGAGAAC	TACAGCAACC	TGGTGGCAGT	GGGGTATCAA 240
50	GCCAGCAAAC	CGGATGCAC	CTTCAAGTTG	GAACAAGGAG	AACAACCTGTG	GACAATTGAA 300
	GATGGAATCC	ACAGTGGAGC	CTGTTCAGGT	TCTCCAAAGG	TCCCGTTCTC	CATTTTCTCA 360
	TCTGTGCCCT	TCACCTCTCA	AAATTGCCTT	CATTCTAACA	TATGGAAGT	TGATCATGTG 420
	CTGGAGCGCT	TGCAGAGTGA	AAGCCTGGTG	AACAGAAGGA	AACCATGTCA	TGAACATGAT 480
	GCATTTGAAA	ATATTGTTCA	TTCAGCAAAA	AGTCAGTTTC	TGTTAGGGCA	AAATCATGAT 540
55	ATATTGACT	TACGTGGAAA	AAGTTTGAAA	TCCAATTAA	CTTTAGTTAA	CCAGAGCAAA 600
	GGCTATGAAA	TAAAGAATCT	TGTTGAGTTT	ACTGGAATG	GGGACTCCTT	TCTTCATGCT 660
	AACCATGAAC	GACCTCATAC	TGCAATTAAA	TTCCTGCAA	GTCAAAAAC	CATCAGCACT 720
	AAGTCCCAAT	TCATCAGTCC	CAAGCATCAG	AAAAACAGAA	AATTAGAGAA	GCATCATGTG 780
	TGCAGTGAAT	GTGGGAAAGC	CTTCATCAAG	AAGTCTTGGC	TAACTGATCA	CCAGGTAATG 840
60	CATACAGGAG	AGAAACCCCA	CAGATGTAGT	CTATGTGAGA	AAGCCTTCTC	CAGAAAGTTC 900
	ATGCTTACTG	AACATCAGCG	AACTCATACA	GGAGAAAAAC	CATTATGAATG	CCCTGTAATG 960
	GGCAAGCCCT	TTCTCAAGAA	ATCAGGCTC	AACATACATC	AGAAAACACA	TACCGGAGAG 1020
	AAACCCCTATA	TATGCAGTGA	ATGTGAAAAA	GGCTTCATCC	AGAAAGGAAA	TCTCATTGTA 1080
	CAACAGCGAA	TTATACAGG	TGAGAAACCT	TATATATGCA	ATGAATGTGG	AAAAGGCTTC 1140
65	ATTGAGAGA	CGTGTCTCAT	AGCATCATCAG	AGATTTCACA	CAGGAAAGAC	GCCTTTTGTG 1200
	TGCAATGAAT	GTGAAAAATC	CTGTTCTCAG	AAATCAGGTC	TCATTAAACA	TCAAAGAAAT 1260
	CACACAGGAG	AGAAACCCCT	TGAATGTAGT	GAATGTGGGA	AAGCCTTTAG	CACAAAGCAA 1320
	AAGCTCATTT	TCCATCAAAG	GACTCATACA	GGAGAGAGAC	CCTATGGCTG	TAAAGAGTGT 1380
	GGGAAAGCGT	TTGCGTATAT	GTCGTGTCTG	GTTAAGCATA	AGAGAATACA	CACAAGGGAG 1440
70	AAACAAGAGG	CAGCCAAGGT	GGAAATCCT	CCTGCAGAGA	GGCAGAGCTC	ATTACACACC 1500
	AGTGATGTCA	TGCAGGAGAA	AAACTCTGCT	AACGGGGCGA	CTACACAAGT	GCCTTCTGTG 1560
	GCCCCCTCAG	CATCATTAAG	CATCAGCGGC	CTCCTGCAAA	ACAGGAACGT	AGTCTTGTG 1620
	GGACAGCCAG	TGGTCAGATG	TGCAGCCTCA	GGAGATAACA	GAGGATTTCG	ACAGGACAGA 1680
75	AACCTTGTGA	ATGCAGTGAA	TGTGGTTGTG	CCTTCGGTGA	TCAATTATGT	CTTATTTTAT 1740
	GTTACAGAAA	ACCCATAG				

Seq ID NO: 214 Protein sequence  
Protein Accession #: FGENESH predicted

1	11	21	31	41	51	
80	MMGSHVAQAG	LELLGSSDPP	ALASESAGIT	GILLQESITL	EDVAVDFTWE	EWQLLGAAQK 60
	DLYRDVMLEN	YSLNVAVGYQ	ASKPDALFKL	EQGEQLWTIE	DGIHSGACSG	SPKVPFSIFS 120
	SVPPTLQNC	HSNIKWVDEH	LERLQSESLV	NRKPKCHEHD	AFENIVECSK	SQPLLQNHND 180
	IFDLRGKSLK	SNLTLVNQSK	GYEIKNSVEF	TGNGDSFLHA	NHERLHTAIK	FPASQKLIST 240

KSQFISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQM HTGEKPHRCS LCEKAFSRKF 300  
 MLTEHQRTHT GEKPYECPEC GKAFLEKSRK NIHQKTHGE KPYICSECGK GFIOKGNLIV 360  
 HQRIHTGEKP YICNECGKGF IQKCLIAHQ RFHTGKTPFV CSECGKSCSQ KSGLIKHQRI 420  
 HTGEKPFECB ECKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VKHKRIHTRE 480  
 KQEAARKVENP PAERHSSLHT SDVMQEKNSA NGATTQVPSV APOTSLNISG LLANRNVVLV 540  
 GQPVVRCAS GDNRGFAQDR NLVNAVNVVV PSVINYLFI VTEMP

Seq ID NO: 215 DNA sequence  
 Nucleic Acid Accession #: NM\_032190.1  
 Coding sequence: 502..1332

1 11 21 31 41 51  
 GATTCCGTGT TCTTGGCCAT GTTAGCCATA ATATCCTGTG CAGTATGTTT TTCTGTGCA 60  
 GAGGCAAAAA CATATTGGGC ATATGTTCCC AAGCCCCCAG CAGTATGACC CATACTTTGG 120  
 AGTGACACTC CTCCTAAGAT TTATCATGAT TAAGGAGCAT GGGCTCCAGG ACCCTTAACT 180  
 CCACCTGACA TAGAACAGTT AGACTCTCAG AATAATGTCA TTAATTATAC CGCTCCATTG 240  
 GAAGGACTTC CTTTGTGTGT CACCACAAAG ACATCACTCA GCCATAGCTG TCTTACAGTT 300  
 CAAGCTCACA CATGGTTGAG TCACTATGGG AAAATCATGT ACTTATTAAG TCTTGGTTAT 360  
 ATTAATGTAA CCGGTGTGCT AACCAACCAT TCCTGGCCCA ATCGCCTTCA TTGTGCTGAC 420  
 TATACAGAAT GGATTCCCTT CAATAGTTC TACCCCCCTC CATAGACCCA GTGTCTTGGC 480  
 CCACCTGGTA GAAACAAATC TATGTTAACT GGAGACATTG TGGATTGGGG ACCTAAAGGC 540  
 CAATTAGATG GAAAGAAAGA AAATCAGAAA TCGTGGCACA AACTTTGCTG GCATTGGTGG 600  
 CAAGCTTTTA ATGCTTCTTC TTTATATAAC ACTGGGATCC AATCCAGTGC GGCCGCCCAG 660  
 ATTGCTTGGC ATGGAGCAGG CTTTAGCCCG CCTCTCTCTC AGTGGCATT TCTAGGAGG 720  
 AAAGGACCAA TTCAAAAGAT GATATGGAAG GCAGCATTCC CATTATGAA TGGCAACATC 780  
 TGGGTGCCA TAATACTATC CAATAATAGC AATAGTAAGC AACACAGTCT TAATGTTACA 840  
 TTTGTAAGA ATATCACACC TCAATTTACA GTTTGTGTTT TTAATCCTTA TGTGTTTTTG 900  
 GCAGCTAAGA AGGACCAGCT CCAGGTAAAC AATACCCAAAT TGACCTGTAA ATCTTGCCAG 960  
 TTATATCATC GCATTAATCA TAGCATTG CAAACACATA ATATCTCTAC TTTGATGATT 1020  
 TTAGTTGCA TCCCTGGGCT ATGGATTCTT GTTAATCTGT CTGAGCCATG GGCTGCCACA 1080  
 ATTGCTTAC ATTTGTGAA ACTTCTCTA ACTCAGTTTA CTCATTGTGT CCGTAGAGGC 1140  
 TTAGGCATGA TAATTTTGTG TATTGTTTAC TTGGTCACAC TAATAATTTC TGTGTTGATG 1200  
 TCCTCTGTAG CTTTGCATAG TTCTATTCAA ACAGCTCAGT ATGTGGAGAA CTGGACACGC 1260  
 ACAGTCAACC AAGGCTGGCT ACTTGAGAAT AAAATTAACA CTGAGTTACA AACTGAAGTG 1320  
 GCAGTGTAT AATCCACGAT TCTATGGTTA GGGGAACAAAG TACAAGCTT GCAATGTCAG 1380  
 CAGTAATTGT GTTGTCAATT TAATCACACT CATATTTGTG TAACCAACTT AGAATATAAC 1440  
 CAAAGTAGAT ATCCATGGGA TCTTGTGAAA GCCCATTGCG AGGGAGCTTT CACATCCGAG 1500  
 ATCACCTTTG ATATTTGGTA ATTACAAAC AAAATCTCTG ATTTAAATAA ACAAAATCCA 1560  
 GAGTTTCAGC CTTCTTTAGA AGACTGACT GAATTCACGC AAGGCCTGGA GAGCGTCAAC 1620  
 CCTGGACCTT ACTTAAAGCA CCACATTAACT ATCTTATATA TAGTCTCTGG AATAATGTTG 1680  
 TTTGTCTCT GTCTCTCTGT CATAGTCTGT AAAATCGGAT GGACTGCCAA TCGGAGAAATG 1740  
 AAAGCTACCC AGCCTGGCCT TACATCTCTT CACTTAATAC ATAAACAAGA AGGGGGAAT 1800  
 GTTGGGAGCC AAAAGGCCA AAGGATGTT GACCAACTCA GCATTCACCT GGAGGCTACA 1860  
 TGATCAACA GCAAACTGTT TATCATGAAT ACAGAAATGTG GGCAAACTCG CTTCTGTGCC 1920  
 TGCCAGAAAG GTTGTCTGAG GGCCATGCT CCTGGCCCC GGCTCCTTGA GGTATCTAC 1980  
 TGGGACATCT AGAGCTATT GTTCAGGAA TGCAGTCTTG CAAGCCTACT CTGGACGAG 2040  
 CAGCTGACCT CTTCTTCCAC ACCCTTCTC ACTATCTCTT TTGCCATAA AATATGGAGG 2100  
 GCTGTGTAAA GCTCAGGGCC CTTGTCCACT AGAGGCAAGG TGTCCCTGA CCCTTCTTCC 2160  
 AAACAT

Seq ID NO: 216 Protein sequence  
 Protein Accession #: NP\_115566.1

1 11 21 31 41 51  
 MLTGDIVDWG PKGQLDGKEE NQKSWHKLW HWWQAFNASS LYNTGIQSQS AAQIAWHGAG 60  
 FSPFLQWHY LGRKGPQK IWKAAFFPMN GNIWVAILLS NNSNSKQHS NVTVPVKNIT 120  
 QFTVCFNFPY VFLAAKDKQL QVNTQLTCK SCQLYHCINH STLQENIST LMILGCIPLG 180  
 WIPVNLSEPW AATIALHFVK LLLTQFTHCV RRLGMIIFA IVYLVTLIIS VVMSSVALHS 240  
 SIQTAYVEN WRTVNGGWL LENKINTELQ TEVAVL

Seq ID NO: 217 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1566

1 11 21 31 41 51  
 ATGGTGAACC CCAATCCAC TTCTCCCTC TTCAGGTTAT GTTTTTGCT CCTGAGGAGT 60  
 CAGAACCTGT GGGTTGAAGA GCAAATTCAA TGCAAAAACA TATTGGGCAT ATGTTCCCAA 120  
 TCCCCAGCA GTATGGCCTA TACTTTGGAG CTCACCTCTC CTGAGATTGA TCACGATCAG 180  
 GGAGAGTGGG CTCAGGAGC CCTAATCCCT CGTGACATAG AAAAGTTAGA CTCTCAGAAC 240  
 AATGTCAATTA ATTATACCAC TCCACTGGAA GGACTCCCTT TGTTTATCAC CACAAGAACG 300  
 TCGTCAAGCC ATAGCTGTCT TGCAATTCAA GCTCAAAACAT GGTGTAGTCA CTATGGAAAA 360  
 ATTATGTACT TATTAGGTCT TGGTCTATT AATGTAACGT GTGTGCTAAC CAATCATTCC 420  
 CAGTCCAGTC ACCCTAATTC TGCTGATTAT ACAGAAATGA TTCCATTCAA TAGTCTCTAC 480  
 CCCACTCTGT GGACCCAGTG TCTTGATCCA CTGGCTAGTA AACAATATAT GTCAACTGAA 540  
 GACACTGTGG ATTGGGAACC TAAAGGTCAA TTAGATGGAA AAGGTGAAAG TCAGAAATCA 600  
 TGGCACAAC TTCCTGGCA TTGGCGCAA GCTTTTAATG CTTCTCTTCT ATACAACAGC 660  
 AGAATCCAAT CCCAGTCTGC TGCTCAGATT GCTTGGCATG GAGCAGGCTT TAGCCACCT 720  
 CTTCTCAGT TGCATTATCT GGGGAGGAAA GGACCAATTC AAGAACTAT ATGGAAGGCA 780  
 GCATCCCAT TTATGAATGG CAACATCTGG ATTGGAAAC TGCTAATATA TAGCAATAGT 840  
 AAGCAACACA GTCTTAATGT TGCAATTGTA AAGAATATCA CCACTCAGTT TACAGTTTGT 900  
 GTTTTTAATC CTTATGCCTT TTTGGCAGCT AAGAAGAACC AGCTTCAGT GGAGAACTGG 960

5  
10  
ACACGCACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020  
GAAGTGGCAA TGTGTAAATC CATGGTTCTG TGGTTAGGAG AACAGGTACA AAGCTTGCAG 1080  
TTGCAGCAGC AATTCGGTCA TCATTTTAAT CACATTCTATA TTTGCGTAAC TAACTCAGAA 1140  
TATAACCAA GTGAGTATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTCACA 1200  
TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAA TTATTGATT AAATAGGCAA 1260  
ACTCAAGAA TTCAGCCTTC TTTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC 1320  
CTCAACCCCT GGACCTATCT AAGGCACCAC ATTAACATCT TATATGTAGT TCTTGGAATA 1380  
ATGTTGTTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440  
AGAATGAGAG CCTCCAGCC CAGCCTTACA TTCTTTCAAT TAATACATA ACAGAAAGGG 1500  
GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATTCT GCTGGAGGCT 1560  
ATATGA

Seq ID NO: 218 Protein sequence  
Protein Accession #: FGENESH predicted

15  
20  
25  
1  
11 21 31 41 51  
MVNPKSTSSL FRLCFLLLRS QNLWVEEQIQ CKNILGICSG SPSSMAYTLE LTFPEIYHDO 60  
GEMAPGLTP RDIEKLDSON NVINYTTPL E GLPFIITKT SLSSHCLAIO AQTWLSHYGK 120  
IMYLLGLGSI NVTGVLINHS QSSHPNCADY TEWIPFNSSY PTLWTQCLDP LASKQYMSTE 180  
DTVDWEPKQG LDGKGESQKS WHKLHWHWRQ AFNASSLYNS RIQSQSAAQI AWHGAGFSPP 240  
LPQLHYLGRK GPIQETIWK A ALPFMNGNIW IGTLSNNSNS KQHSLNVAIV KNITTQFTVC 300  
VENPYAFLLA KKNQLQVENW TRTADQARLL QNKINTELQT EVAMLSKSMVL WLGEQVQSLQ 360  
LQQQLRHHFN HIHICVTNSE YNQSEYPWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNRO 420  
TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW 480  
RMRASQPSLT FQLIHKQKG GYAGSQRPVG RDQLSILLEA I

Seq ID NO: 219 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..900

30  
35  
40  
45  
50  
1  
11 21 31 41 51  
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60  
CCGCGGGCGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGCGACGGC 120  
GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180  
CGGCCCACTG CGCTGGACAC CTCTCTCTGT ACGTACGTTT AATCGCCCGT CGCGCGCGCT 240  
GGCTCGGCGG GGGCTGTGCA CCGGGGAGCT GGGGCGGGCG TCTCGGCGGG AGGGCGCAGA 300  
GGACCCCGGG GAGGAGACTG GAGCAGGCCG CGAGGTGGCG CTGTTGCGGC CCAGGACGCT 360  
CTTCTAACT CAGGCTCTCC CCGCCCCGCC CCTGCAGTGC AAGTCTGTGT GGATGGAGCT 420  
CCGGTGGGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTCTC 480  
CTTTGTACCC CGGATACCGA TGTCTTCTGT GCGTGTCTCA GCGTGGTGCA GCCCAGCTCC 540  
TTTCAAAAC TACAGAGAA ATGGCTGCCG GAGATCCGCA CGCACAAACC CCAGGCGCCT 600  
GTGCTGCTGG TGGGCACCCA GCGCGACCTG AGGGACGATG TCAACGTACT AATTCACTG 660  
GACCAAGGGG GCGGGGAGGG CCCCGTGCCC CAACCCAGG CTCAGGCTCT GCGCGAGAAG 720  
ATCCAGCCTT GCTGTCTACT TGAGTGCTCA GCGTTGACGC AGAAGAACTT GAAGGAAGTA 780  
TTTGAATCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840  
GCCAAGGTG TGGCACCCCT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA

Seq ID NO: 220 Protein sequence  
Protein Accession #: FGENESH predicted

55  
60  
1  
11 21 31 41 51  
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60  
RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120  
LPNKGSPRPA PAVQVLVDGA PVRIELMDTA GQEDFDRLRS LCYPDTDVFL ACFSVVQPSS 180  
FQNIKEKWL EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGFVP QPQAQGLAEK 240  
IRACCYLECS ALTQKNLKEV FDSAILSABE HKARLEKLN AKGVRTL SRC RWKKFFCFV

Seq ID NO: 221 DNA sequence  
Nucleic Acid Accession #: XM\_063832.2  
Coding sequence: 1..711

65  
70  
75  
80  
1  
11 21 31 41 51  
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60  
CCGCGGGCGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGCGACGGC 120  
GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180  
CGGCCCACTG CGCTGGACAC CTCTCTCTGT CAAGTCTTGG TGGATGGAGC TCCGGTGGCG 240  
ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTITGACC GACTTGTGTC CCTTTGCTAC 300  
CCGGATACCG ATGTCTTCTT GCGGTGCTTC AGCGTGGTGC AGCCAGCTTC CTTCACAAAC 360  
ATCACAGAGA AATGGCTGCG CGAGATCCGC ACGCACAAAC CCAGGCGGCC TGTGCTGCTG 420  
GTGGGCACCC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTCACTG GGACCGAGGG 480  
GGCGGGGAGG GCGCCGTGCC CCAACCCAG GCTCAGGTC TGGCCGAGAA GATCCGAGCC 540  
TGCTGTACCC TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600  
GCTATTCTCA GTGCCATTGA GCACAAAGCC CGCTGGAGA AGAAACTGAA TGCCAAAGGT 660  
GTGGCACCCC TCTCCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTCGTTTG A

Seq ID NO: 222 Protein sequence  
Protein Accession #: XP\_063832.1

1  
11 21 31 41 51

MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60  
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRRLSLCY PDTDVFLACF SVVQPSSEFN 120  
 ITEKWLPEIR THNQAPVLL VGTQADLRDD VNVLIQLDQG GREGVPVQPQ AQGLAEKIRA 180  
 CCYLECSALT QKNLKEVFD S AILSAIEHKA RLEKKNLAKG VRTLSRCRWK KFFCFV

Seq ID NO: 223 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1161

10 1 11 21 31 41 51  
 | | | | |  
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 60  
 TTCGAGATG ACTTCATTGC CAAGGTGTG CCGCGGTGT TGGGGCTGGA GTTTATCTTT 120  
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTGGAAA 180  
 15 TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCCTG 240  
 CGTTCTGTGA TGGACTACTA TGTGGGGGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC 300  
 CGGCTGTGTC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCAGCGTG 360  
 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420  
 AATTGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTGTGG CCTAACAGTC 480  
 20 CACCTCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540  
 AGCATCTGCC ATACCTTCCG GTGGCAGGAA GCTATGTTCC TCCTGGAGTT CCTCTGCCC 600  
 CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660  
 GACCGGATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720  
 25 GTCATCTGCT TCCTTCCAG CGTGGTGTG CGGATCCGCA TCTTCTGGCT CTGCACACT 780  
 TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840  
 AGCTTCACCT ATCATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900  
 TTTCCCAACT TCTTCTCCAC TTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960  
 CCAGATAATA ACCGAGCAC GAGCGTGGAG CTCACAGGGG ACCCAACAA AACCAGAGGC 1020  
 30 GCTCCAGAGG CGTAAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080  
 ACCTCAAATA ACCATTCCAA GAAGGACAT TGTACCAAG AACCAGCATC TCTGGAGAAA 1140  
 CAGTTGGGAT GTTGATCGA G

Seq ID NO: 224 Protein sequence  
 Protein Accession #: Eos sequence

35 1 11 21 31 41 51  
 | | | | |  
 MNRHHLQDHF LEIDKKNCV FRDDFIKVL PPVLGLEFIF GLLGNLALW IFCFLKSWK 60  
 SSRIPLFNLA VADFLLIICL PFVMDYVRR SDWKFGDIPC RLVLFPFAMN RQGSIIPLTV 120  
 40 VAVDRYFRV HPHALNKIS NWTAAIISCL LWGITVGLTV HLLKKLLIQ NGPANVCISF 180  
 SICTHFRWHE AMFLLEFLLP LGIILFCSAR IISLRQRQM DRHAKIKRAI TFIMVVAIVF 240  
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNMLD PVVYFSSPS 300  
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV L TGDPNKTGR APEALMANS EPWSPSYLGP 360  
 45 TSNHSHKXGH CHQEPASLEK QLGCIE

Seq ID NO: 225 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1092

50 1 11 21 31 41 51  
 | | | | |  
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 60  
 TTCGAGATG ACTTCATTGT CAAGGTGTG CCGCGGTGT TGGGGCTGGA GTTTATCTTC 120  
 55 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTGGAAA 180  
 TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTGGCTGACT TTCTACTGAT CATCTGCCCTG 240  
 CCCCTCTGGA TGGACAACTA TGTGAGCGT TGGGACTGGA AGTTTGGGGA CATCCCTTGC 300  
 CGGCTGATGC TCTTCATGTT GGCTATGAAC CGCCAGGGCA GCATCATCTT CCTCAGCGTG 360  
 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420  
 60 AATCGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTATTGG CCTGACAGTC 480  
 CACCTCTGA AGAAGAAGAT GCCGATCCAG AATGGCGGTG CAAATTTGTG CAGCAGCTTC 540  
 AGCATCTGCC ATACCTTCCA GTGGCAGGAA GCCATGTTCC TCCTGGAGTT CTCTGCCC 600  
 CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660  
 GACCGGATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720  
 65 GTCATCTGCT TCCTTCCAG CGTGGTGTG CGGATCCGCA TCTTCTGGCT CTGCACACT 780  
 TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840  
 AGCTTCACCT ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900  
 TTTCCCAACT TCTTCTCCAC TTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960  
 CCAGATAATA ACCGAGCAC GAGCGTGGAG CTCACAGGGG ACCCAACAA AACCAGAGGC 1020  
 70 GCTCCAGAGG CGTAAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080

Seq ID NO: 226 Protein sequence  
 Protein Accession #: Eos sequence

75 1 11 21 31 41 51  
 | | | | |  
 MNRHHLQDHF LEIDKKNCV FRDDFIVKVL PPVLGLEFIF GLLGNLALW IFCFLKSWK 60  
 SSRIPLFNLA VADFLLIICL PFLMDYVRR WDWKFGDIPC RLMLFPLAMN RQGSIIPLTV 120  
 80 VAVDRYFRV HPHALNKIS NRTAAIISCL LWGITIGLTV HLLKKMPIQ NGGANLCSF 180  
 SICTHFRWHE AMFLLEFLFP LGIILFCSAR IISLRQRQM DRHAKIKRAI TFIMVVAIVF 240  
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNMLD PVVYFSSPS 300  
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV L TGDPNKTGR APEALMANS EPWSPSYLGP 360  
 TSP

Seq ID NO: 227 DNA sequence  
Nucleic Acid Accession #: NM\_006018  
Coding sequence: 61..1224

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
CGCCACTTTG CTGGAGCATT CACTAGGCGA GCGCTCCAT CGGACTCACT AGCCGCACTC 60
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 120
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGCTGGA GTTTATCTTT 180
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTGGAAAA 240
TCCAGCGCGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCGTG 300
CGGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 360
CGGCTGTGTC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCAGGGTG 420
GTGGCGGTAG ACAGGTATTT CCGGTGCTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 480
AATTGACAGC CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTGTGTG CCTAACAGTC 540
CACCTCACTA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 600
AGCATCTGCC ATACCTTCGG GTGGCAGCAA GCTATGTTC TCCTGGAGTT CCTCCTGCCC 660
CTGGGCATCA TCCGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGGGCA GAGACAAATG 720
GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 780
GTCACTGTCT TCCCTCCAGC CGTGGTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 840
TCGGGACGCG AGAATTGTGA AGTGTACGCG TCGGTGGACC TGGCGTCTCT TATCACTCTC 900
AGCTTCACCT ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTCTC CAGCCCATCC 960
TTTCCCAACT TCTTCTCCAG TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 1020
CCAGATAATA ACCGCGACAC GAGCGTCGAG CTCACAGGGG ACCCAACAA AACCAGAGGC 1080
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1140
ACCTCAATAA ACCATTCCAA GAAGGGACAT TGTACCAAG AACCAAGCAT CTCGGAGAAA 1200
CAGTTGGGCT GTTGATCGA GTAATGTGAC TGGACTCGGC CTAAGGTTTC CTGGAACCTC 1260
CAGATTGAGA GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG 1320
GTGTGACCAC AGGAATCTCT GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAACCTTGC 1380
TTCACTCTCT AGCTTCGCG GACTGAAGAT GGGCAAATTC TAGGCGTTTC TGCTGAGCAG 1440
AGTTGGAGCC AGAGATCTAC TTGTGACTTG TTGGCTTCT TCCACATCT CCTCAGACT 1500
GGGGGGGGCT CAGCTCCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG 1560
GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCCTGGAGGA AGCCAGGCA TCATTAAACA 1620
AGCCAGTAGG TCACCTGCTC TCCGTGGACC AATTCATCTT TCAGACAAGC TTTAGAGAAA 1680
TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCGG TGGGTGTAAT 1740
AGGGGATTAG CCCCAGAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAAATGGCA 1800
TTGCTGCTTT CAACAGCGA CTAATGCAAT CCATTCCTCT CTGTTTATA GTAATCTAAG 1860
GGTTGAGCAG TTAACAACGG TTCAGGATAG AAAGCTGTTT CCCACCTGTT TCGTTTACC 1920
ATTAAAGGG AAACGTGCCT CTCGCCACG GGTAGAGGGG GTGCAGTTC CTCCTGGTTC 1980
CTTGCTGTGT GTTCTGTGAC TTACCAAAAA TCTACCACTT CAATAAATTT TGATAGGAGA 2040
CAAAAAAAAA A
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Seq ID NO: 228 Protein sequence  
Protein Accession #: NP\_006009.1

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45      1      11      21      31      41      51
      |      |      |      |      |      |
MNRHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
SSRIPLFNLA VADFLIICL PFVMDYYVRR SDWNFGDIPC RLVLFMFAMN RQSSIIFLTV 120
VAVDRYFRV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKLLIQ NGPANVCISF 180
SICHTFRWE AMPLLEFLIP LGIILFCSAR IWSLRQRQM DRHAKIKRAI TFMVVAIVF 240
VICFLPSVVV RIRIFLLLHT SGTQNCVEYR SVDLAFITL SFTYMNMSLD PVVYFSSPS 300
FPNFFSTLIN RCLQRKMTGE PDNNRSTSVB LTGDPNKTRG APEALMANSQ EPWSPSYLGP 360
TSNNHKKKGH CHQEPASLEK QLSCCIE
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Seq ID NO: 229 DNA sequence  
Nucleic Acid Accession #: NM\_014398.1  
Coding sequence: 64..1314

```
60      1      11      21      31      41      51
      |      |      |      |      |      |
GGCACCGATT CGGGGCTGTC CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
CAGATGGGCA GTCAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACCAGC TAAGCAAGCA 240
CCTCACCAA CTTTAGCAGC AAGATTGATG GATGGTCATA TCACCTTTCA AACAGCGGCC 300
ACAGTAAAAA TTCAACAAC TACCCAGCA ACTACAAAAA ACATGCAAC CACCAGCCCA 360
ATTACTACA CCTTGGTCA CACCCAGGCC ACACCCACCA ACTCACACAC AGCTCCTCCA 420
GTTACTGAAG TTACAGTCGG CCTAGCTTA GCCCTTATT CACTGCCACC CACCATCACC 480
CCACGAGCTC ATACAGCTGG AACCAATTCA TCAACCGTCA GCCACACAC TGGGAACACC 540
ACTCAACCCA GTAACCCAG CACCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
ACAACCGGCT AGAAGCTTGA TCAACCCACC CATGCCCCAG GAACAAACGC AGCTGCCAC 660
AATACACCC CACAGCTGCG ACCTGCTTCC ACGTTCTCTG GGCCACCCCT TGCACTCAG 720
CCATGCTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
TACTTCAACA GTAACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CGAAAAATCC 900
AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTACCAA GGATGAAGAA 960
TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
CAAGGAATCA AACATGCGGT GGTGATGTT CAGACAGCAG TCGGCATTC CTTCAGTGC 1080
GTGAGTGAAC AGAGCCTCCA GTTGTGACCC CACCTGCAGG TGAACCAAC CGATGTCCAA 1140
CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTGCTCTGAC 1200
TACACAAATT TGCTTCTGCT GATTGGGGCC ATCGTGGTTG GTCTCTGCTT TATGGGTATG 1260
GGGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAA CTAAATGTGT 1320
CCCCGGGGGA ATGAAATAA TGAATTTAG AGAATCTTT CATCCCTTCC AGGATGGATG 1380
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5 TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440  
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACCTTTT 1500  
 GTTTATTTTA TGAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560  
 GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620  
 AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680  
 ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCTTTG TTATCAAATG GACTTTTCAGT 1740  
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800  
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAC GGAGTTTCAC TCTGTCCACC 1860  
 10 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCCGCTTCC CGGTTTCAAG 1920  
 TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTCG 1980  
 GCTAATTTT GTATTTTAT TATAGACGGG TTCCACCATG TTGGCCAGAC TGGTCTTGAA 2040  
 CTCTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAAA GTGCTGGGAT TACAGGCATG 2100  
 AGCCATTGCG CCCGCCCTTA AATGTTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160  
 GTTGTCTAAG TGTTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220  
 15 CTTGATGACT CCTGCTCCAG AATGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280  
 CTAACCAATA AGCAGAGAG AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340  
 TAGGCTAAGC ACTTTATCTA TATCTCATT CATTCTCACA ACTTATAAGT GAATGAGTAA 2400  
 ACTGAGACTT AAGGGAAGCT AATCATTAA ATGTCACCTG GCTAATCTAT GGCAGAGCCA 2460  
 20 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520  
 CCTACAAGAA CAATGACACC ACACCTCTGC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580  
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640  
 AGCTTTCAG ATACCAAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700  
 TGAGGGGCTT TGTAACACAT TAGTCAGTTG CTCATTTTGA TGGGATTGCT TAGCTGGGCT 2760  
 25 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTTTGA TAATAGAGAA 2820  
 ACTTCGCTAA CCACTCTTTC TTTCTTGAGT GTATAGCCCC ATCTGTGTGT AACTGTCTGC 2880  
 TCTGCACTT CATATCCATA TTTCTTATG TTCCTTTAT TCTGTAGAGC AGCCTGCCAA 2940  
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAG AACTAAGTCA GGATGTTAAC 3000  
 AGAAAAGTCC ACATAACCTT AGAATCTTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060  
 30 CCATGTTGAC TTTCTCATG TGTTCCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120  
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP\_055213.1

35 1 11 21 31 41 51  
 | | | | |  
 MPRLSAAAA LFASLAVILH DGSQMRKAP PETRDYSQPT AAATVQDIKK PVQPAKQAP 60  
 HQTLAARFMD GHITFQTAAT VKIPTTTPAT TONTATTSPI TYTLVTQAT PNNSHAPPV 120  
 40 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNWT QPSNQTLPLA TLSIALHKST 180  
 TQKQPDQPTH APGTAAAHN TTRTAAPAST VPGPTLAPQ SSVKTGIYQV LNSRLCIKA 240  
 EMGIQLIVOD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLFTFKDEES 300  
 YYSISVGYL TVSDPEYVQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTTDVQL 360  
 QAFDPEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMGSM VYKIRLRQCS SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM\_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51  
 | | | | |  
 TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60  
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120  
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180  
 55 TGCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240  
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAAGTGA TTATTACCTT GAAAGAAAAA 300  
 AAGAGCAAC GATGCTTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360  
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420  
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAACTG 480  
 60 AGACTTTTCT ATGGTTTGT GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGST 540  
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA 600  
 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660  
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTTGTATT ATACATTCAT 720  
 GCATTTCTAG CTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780  
 65 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840  
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900  
 CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAAATACAC ACTTCTTTCC 960  
 CCAAAATATC TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT 1020  
 TTTATAACCA ATTCAATAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080  
 70 TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140  
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200  
 TGTACTTTTT GTTTGTATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTTGAAA 1260  
 TACAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320  
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380  
 75 TGTTCATGC CTATATACCTG TAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440  
 GTCATTTTTT TCTTAATAA ACTACCACAA CCTTTCTTTT TTAATAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP\_005400.1

80 1 11 21 31 41 51  
 | | | | |  
 MSVKGMAIAL AVILCATVVO GPFMFKRGRG LCIGPGVKAV KVADIEKASI MYPNNCDKI 60  
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 233 DNA sequence  
Nucleic Acid Accession #: NM\_000577.1  
Coding sequence: 41..520

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5      1      11      21      31      41      51
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GGCACCAGGGG GAAGACCTCC TGTCTATCA GGCCTCCCC ATGGCTTTAG AGACGATCTG 60
CCGACCTCTC GGGAGAAAAA CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACCA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAAATGT 180
10    CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
CATCGCTACA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCGCCTGCC CCGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
15    GGTCTGTCAT ACCAAATCTT ACTTCCAGGA GGACGAGTAG TACTGCCAGC GCCTGCCTGT 540
TCCCATTTCT CATGTGCCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGCTCCCG 600
GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAAACA 660
CTGTGTGACA GAGCTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCAGAAATG 720
GTCCTTTCTA TGTGTGAATC AGAGCACAGC AGCCCTGCA CAAAGCCCTT CCATGTCCGC 780
20    TCTGCATTCA GGATCAAACC CCGACCACCT GCCCAACCTG CTCTCCTCTT GCCACTGCCT 840
CTTCTCCCTT CATCTCCACCT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
ACCAAGTGGC TCCACACCCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
TTTAAGGTTT TGTGGAAAAT GAAAATTAGG ATTTTCATGAT TTTTITTTTT CAGTCCCGT 1020
GAAGGAGAGC CCTTCATTGT GAGATTATGT TCTTCCGGGG AGAGGCTGAG GACTTAAAT 1080
25    ATTCTGTCAT TGTGAAATG ATGGTGAAG TAAGTGGTAG CTTTCCCTT CTTTCTCTT 1140
TTTTTTTGTG ATGTCCCAAC TTGTAATAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
ATTTTTTTT TCCTTTAAAC AACTTCCAT AATCTGGACT CCTCTGTCCA GGCAGTGTCT 1260
CCAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTTCACA GCTGCCTGCA GTACTTTACC 1320
TCCATACAGA AGTTTCTCAG CTCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGTTCTT 1380
30    TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTCTG GCACTTGGAG 1440
ACTTGTATGA AAGATGGCTG TGCTCTGCC TGCTCCCCC ACCAGGCTGG GAGCTCTGCA 1500
GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAAT TCCTACTTTC 1620
35    CTGTGACTTC AGCTCTGTT TACAATAAAA TCTTGAATAA GCCTAAAAAA AAAAAAAA 1680
AAAAAAA AAAA AAAA AAAA
```

Seq ID NO: 234 Protein sequence  
Protein Accession #: NP\_000568.1

```
40      1      11      21      31      41      51
      |      |      |      |      |      |
MALETICRPS GRKSSRMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPFEP 60
HALFLGIHGG KMCLSCVKSQ DETRLQLEAV NITDLSENK QDKRPAFIRS DSGPTTSFES 120
AACPGWFLCT AMEADQPVSL TNMPDEGMV TKFYQDEE
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Seq ID NO: 235 DNA sequence  
Nucleic Acid Accession #: NM\_001840.1  
Coding sequence: 149..1567

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50      1      11      21      31      41      51
      |      |      |      |      |      |
GGGGACTACG GAGAGCTCTG CAGGAGCCCG AGGCCCCCGC CCGGGCCAAG GGAGCTTCTG 60
TCCCGAGGAC CAGGGGATGC GAAGGGATTG CCCCTGTGG GTCACTTTCT CAGTCATTTT 120
GAGCTCAGCC TAATCAAGA CTGAGGTTAT GAAGTCGATC CTAGATGGCC TTGCAGATAC 180
55    CACCTTCCGC ACCATCACCA CTGACCTCCT GTAAGTGGGC TCAAATGACA TTCAGTACGA 240
AGACATCAAA GGTGACATGG CATCCAAATT AGGSTACTTC CCACAGAAAT TCCCTTTAAC 300
TTCTTTTAGG GGAAGTCCCT TCCAAGAGAA GATGACTCGG GGAGACAACC CCCAGCTAGT 360
CCCAGCAGAC CAGGTGAACA TTACAGAATT TTACAACAAG TCTCTCTCGT CCTTCAAGGA 420
GAATGAGGAG AACATCCAGT GTGGGGAGAA CTTCATGGAC ATAGAGTGTG TCATGGTCTC 480
60    GAACCCAGC CAGCAGCTGG CCAATGCACT CCTGTCCCTC ACGCTGGGCA CCTTCACGGT 540
CTGGAGAAC CTCTGGTGC TGTGCGTCAI CCTCCACTCC CGCAGCCTCC GCTGCAGGCC 600
TTCTACCAAC TTCACTGGCA GCCTGGCGGT GGCAGACCTC CTGGGGAGTG TCATTTTTGT 660
CTACAGCTTC ATTGACTTCC ACGTGTTCCT CCGCAAGAT AGCCGCAACG TGTTCCTGTT 720
CAAATCTGGT GGGGTCAAGG CCTCCTTCA TGCCTCGTG GGCAGCTGT TCCTCACAGC 780
65    CATCGACAGG TACATATCCA TTCACAGGCC CCTGGCCTAT AAGAGGATTG TCACCAAGCC 840
CAAGGCCGTG GTGGCGTTTT GCCTGATGTG GACCATAGCC ATTGTGATCG CCGTGTCTGC 900
TCTCTGGGG TGGAACTGCG AGAAACTGCA ATCTGTTTGC TCAGACATTT TCCACACAT 960
TGATGAAACC TACCTGATGT TCTGGATCGG GGTCAACAGC GTACTGCTTC TGTTCATCGT 1020
70    GTATGCGTAC ATGTATATTC TCTGGAAGGC TCACAGCCAC GCGCTCCGCA TGATTCAGCG 1080
TGGCACCCAG AAGAGCATCA TCATCCACAC GTCTGAGGAT GGAAGGTAC AGGTBACCG 1140
GCCAGCCAA GCCGCGATGG ACATTAGGTT AGCCAAGACC CTGGTCTGTA TCCTGGTGGT 1200
GTTGATCATC TGCTGGGGCC CTCTGCTTGC AATCATGGTG TATGATGTCT TTGGGAAGAT 1260
GAACAAGCTC ATTAAGACGG TGTGTGCAAT CTGCAATATG CTCTGCTGCA TGAACCTCAC 1320
75    CGTGAACCCC ATCATCTATG CTCTGAGGAG TAAGGACCTG CGACACGCTT TCCGAGCAT 1380
GTTTCCCTCT TGTGAAGGCA CTGCGCAGCC TCTGGATAAC ACGATGGGG ACTCGGACTG 1440
CCTGCACAAA CACGCAACCA ATGCAGCCAG TGTTCACAGG GCCGCAGAAA GCTGCATCAA 1500
GAGCAGCGTC AAGATTGCCA AGGTAACCAT GTCTGTGTCC ACAGACAGCT CTGCGAGGCC 1560
TCTGTAGACC TATGCTCTCC CTGGCAGCAC AGGAAAAGAA TTTTITTTTT TAAGCTCAAA 1620
80    ATCTAGAAGA GTCTATTGTC TCCTTGGTTA TATTTTTTTA ACTTTACCAT GCTCAATGAA 1680
AAGTGATTG CCACATGTCA CTTATTGTCT TAGTTTCCGT TTGGGCTAAT CTTCCGGGGT 1740
TGTAGGAAA CTTT
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Seq ID NO: 236 Protein sequence  
Protein Accession #: NP\_001831.1



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1      11      21      31      41      51
|      |      |      |      |      |
5  MKSILDGLAD TTFRTITDDL LYVGSNDIQY EDIKGDMASK LGYFPQKFFL TSFRGSPFQE 60
    KMTAGDNPOL VPADQVNITE FYNKLSSEFK ENEENIQCGE NFMIDIECFMV LNPSQOLAIA 120
    VLSLTGTFPT VLENLVLVCV ILHSRSLRCR PSYHPIGSLA VADLLGSVIP VYSFIDFHFV 180
    HRKDSRNVEL FKLGGVTASF TASVGSFLT AIDRYISIRH PLAYKRIVTR PRKAVVAFCLM 240
    WTIAIVIAVL PLLGWNCEKL QSVCSDFPH IDETYLMFWI GVTSVLLLPF VYAYMYILWK 300
    AHSHAVRMIQ RGTQKSIHIIH TSDEGKVQVT RPDQARMDIR LAKTLVLILV VLIICWGPLL 360
10  AIMVYDVFGK MNKLIKTVFA FCSMLCLLNS TVNPIIYALR SKDLRHAFRS MFPSCGTAQ 420
    PLDMSMGDSO CLHKHANNA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL

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Seq ID NO: 237 DNA sequence

Nucleic Acid Accession #: NM\_016083.2

Coding sequence: 64..1482

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1      11      21      31      41      51
|      |      |      |      |      |
20  GATTGCCCCC TGTGGGTCAC TTTCTCAGTC ATTTTGAGCT CAGCCTAATC AAAGACTGAG 60
    GTTATGAAGT CGATCTAGA TGGCCTTGCA GATACCACTC TCOGCACCAT CACCACTGAC 120
    CTCCTGACG TGGGCTCAAA TGACATTGAG TACGAAGACA TCAAGGTGA CATGGCATCC 180
    AAATTAGGGT ACTTCCACA GAAATTCCTT TTAACCTCCT TTAGGGGAAG TCCCTTCCAA 240
    GAGAAGATGA CTGCGGGAGA CAACCCCGAG CTAGTCCCAG CAGACCAGGT GAACATTACA 300
    GAATTTTACA ACAAGTCTCT CTGCTCCTTC AAGGAGAATG AGGAGAACAT CCAGTGTGGG 360
25  GAGAATCTCA TSGACATAGA GTGTTTCATG GTCCTGAACC CCAGCCAGCA GCTGGCCATT 420
    GCAGTCTGT CCTCACGCT GGGCACCTTC ACGGTCTGG AGAACCTCCT GGTGCTGTGC 480
    GTCATCTCC ACTCCCGCAG CCTCCGCTGC AGGCCTTCCT ACCACTTCAT CGGCAGCCTG 540
    CGCGTGGCAG ACCTCCTGGG GAGTGTCAIT TTTGTCTACA GCTTCATTGA CTCCACGTG 600
    TTCCACCGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT CACGGCCTCC 660
30  CTCACCTGCT CCGTGGCAG CCTGTTCTCT ACAGCCATCG ACAGGTACGT ATCCATTAC 720
    AGGCCCTCG CCTATAGAG GATTGTCAAC AGGCCCAAGG CGTGGTGGC GTTTTGCCTG 780
    ATGTGACCA TAGCCATTGC GATCGCGTGC CTGCCTCTCC TGGGCTGGAA CTGCGAGAAA 840
    CTGCAATCTG TGTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT GATGTTCTGG 900
    ATCGGGGTCA CCGAGCTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA TATTCTCTGG 960
35  AAGGCTCACA GCCACGCCGT CCGCATGATT CAGCGTGGCA CCCAGAAGAG CATCATCATC 1020
    CACACGCTCG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG CATGGACATT 1080
    AGGTAGACCA AGACCCCTGT CCTGATCTGT GTGGTGTGTA TCATCTGCTG GGGCCCTTTG 1140
    CTGTCAATCTG TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTA GACGGTGTGT 1200
    GCATTCTGCA GTATGCTCTG CCTGCTGAAC TCCACCGTGA ACCCATCAT CTATGCTCTG 1260
40  AGGAGTAAGG ACCTGCGACA CGCTTTCCGG AGCATGTTTC CCTCTGTGTA AGGCACTGCG 1320
    CAGCCTCTGG ATAACAGCAT GGGGGACTCG GACTGCTGTC ACAACACGCG AAACAATGCA 1380
    GCCAGTGTTC ACAGGGCGCG AGAAGCTGTC ATCAAGAGCA CGGTCAAGAT TGCCAAAGTA 1440
    ACCATATCTG TGTCCACAGA CACGCTCGCC GAGGCTCTGT GAGCCTGATG CCTCCCTGGC 1500
    AGCACAGGAA AAGAAATTTT TTTTAAAGC TCAAAATCTA GAAGAGTCTA TTGTCTCCTT 1560
45  GGTATATATT TTTTAACTTT ACCATGCTCA ATGAAAAGGT GATTGTCAAC ATGATCACTT 1620
    ATCAGTTTGC TAATGTTTCC ATAGTTTAGG TACTCAAACT CCATTCTCCA GGGGTTTACA 1680
    GTGAAGAAAG CCTGTGTTT AAGTGACTGA ACGATCCTTC AAAGTCTCAA TGAATAGGA 1740
    GGGAAACCTT TGGCTACAGA ATTGGAAGTC TAAGAAACCCA TGGAAAAATG CCATCAAATG 1800
    AATAATGCCT TTGTAAACCA AACTTTCACT ATAATGTGAA ATGTAACTGT CCGTAGTATC 1860
50  AGAGATGTCC ATTTTACAA GTTATAGTAC TAGAGATATT TTGTAAAATG TATTATGTCC 1920
    TGTGAGATGT GTATCAGTGT TTATGTGCTA TTAATATTG TTAGTTTCA CAAAACAGAA 1980
    AGGTAGACTT TTATGAGAAC AATGGAACA CAGTGGATAC GTGTCAATGT GTGCACTTTT 2040
    TTTCTATATT ATGCTACTGG ATATAACTTT AGAAATAAAC CTTAATATT CTTCAAATAT 2100
    CTCTATTAA TTTTGACACT GAAATAACCG TAAAGGTTTA TTTTCTGTT ACCTCAACAA 2160
55  GAAGAATTG AGACTTCAA AATATTGAGC AGAATTCATT CATACTTAAA AATTTATTAG 2220
    CCTGCACTT TCATAGGAAG ACACATTATC TTCTGGACTA TAGCTGTTCT AATGGATTAT 2280
    AATCAGAAAG GAAGAGAGAA AGCATATTGA CTTTTTTTGA GCGACATCTC TGACTTTCTT 2340
    TAGTCTTAG CTATTACTGG ATCTCTTAAG ACAGCATGTG TTAATCTTAA TGTATATCGT 2400
    TATCACTGCG CAGTGTCTGT TTAATTGAAT AGTATTGTGT TCCTATATTC CAGGTTTAAG 2460
60  TAGATTTCAT GCCTGGGTGG CCAAACAACA GTCTTCATT TTTTAAATG AAAAGAGTA 2520
    GTGCTGCGAT CAGTAAAATT ATACTGTGTG TGAGTGTGAA TATAAATGTG TGTATGTGTG 2580
    TTTCTGTCGG TAACGTGTAC AGTAATGTCA TAAAGTGAGA AAACGTGAC CAGTATATAA 2640
    CTTTTACCAC TTGCTGCACT CTGCAATG GATTCACTT CTAAAATTGA GTTCTTCTGT 2700
    TAATCTGTGT GATAAAAATA CTGACTCCAA CCATTCAAAA ATTTCAACCC ATCCCTCCTT 2760
65  AAGAGATTGG ATCAAGTATT ACTAAATTGA CCTTAGGTA TTACACAAGA CAGTGCTTAA 2820
    GCAAAAATA ATGACAGGCA TCCAAGGAAG GGATGTATT GTAGTGTAT TGCCAGGAAA 2880
    GGAGAGTACT TTGGTTTCTG AGCACCGAAT ATTGAGCAAT ATGTGAGTCA CTAAAAGGAA 2940
    GACAGTTCTA CAGAAAAACA AATGGTAAAC TTTTCAATA GCGTGTGTAG ATAGTATGCA 3000
    CTATATACAT CACGTTAAAG TAGGACTATC ACACCCAGCC CATGTGGCTA AAAAGCTGA 3060
70  ATCAGACAGT GGATGAGACA CACAACGGCA GTGAAGAACC GATACACTTG CATTGACGT 3120
    CTAGCTATGC TGTATCTGTG CTTTGCCAC ATGCCCTTGG TGACAGCTGA GCACCCAGCT 3180
    CTGTCTGTGT AGGTTTGGCG TAAGGAACAA ATCTCTCCTT TGCTGTGTGT TAGCAAGATA 3240
    CACTCAAGCA TGAAGATAAA CACAGCTGCT TTCTCTTAC ACCCCGGTCT CATGCTCCTT 3300
    AATGGCGCCA TGGGTGCTGT TTGGGCTTT TCCAGTAAG GAATGATATT GCTGAAGAAT 3360
75  CTACTTAACC CTGCAAAATT TTAATTATA TCTCTTCTTA TACAGATAAA ACATGACTCC 3420
    TACAAGGCCC CAGGTTTAC ATAGTCTGAA GTGAAGTACA GAGCTGGCAT CTATCTGGTG 3480
    ATTTCTAGCT CTCGAGATAC CCAAGCAGCC TGATGGGGCA GTTCCCTTTC TTACGGTTCA 3540
    CGCTTAAGG CAGGATGTGG CTTATGAGAT ACTTTGCATT GTCTGTCTGC ACACCTTGAA 3600
    TCTGCTGCT GGCTCCCTTA CTTTACCTCT CTGTCAATGT CAGATGAAG CACGGGTG 3660
80  TAGAGGATTA GTTCTAAAGA CAGGAGAGAT TATTTACAAG AAGAAGCTCAC 3720
    CAGGGTTTAG TTTGCATTAA AGAATTGCCA GTCTTTTGTG CTGCATCATC TTGAACATTA 3780
    ATCCACATGT TTCAGAGCTC ACCAGGCAGT ACCAATGTCT TTTTCAAGC TATGAAGAGC 3840
    TAGAGAAAT CTGTGATG TAGAAAAATT TCACGGTTCA TTTTGAAGC TGCAATTGTG 3900
    CGTATGCAGT GTAGATTTTA TAGTGTGTG TGCTTCAAG ATCTAAATCA TATATAATAA 3960

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5 ATTAAGGGAC AATGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020  
 TCTGTGAAAT ATCATCACGT ATGTTATACA ACCTTCATTT AAAAAGGTTT AAAACTAGTT 4080  
 AGATTCACIT TGACACTTIT CATATCATT CTTAACCCAA GTGACGAAAA CATTGTCCCC 4140  
 AATGAATATA CTCATTAGAA TTACCATTGG TTAATATCAC TCATTAATTA ACCCCATAAT 4200  
 TAGATCCATT AATTAAATG ATTTAAATTT AAGTAAGTTT TATAAGGTCT GACATCAGAG 4260  
 GTATCTTACT TTCTCTGAG GATGATGTAC TTGCCCTGAC CATGCAITTT ACCATCACAC 4320  
 ATGTTAGAAA AGGGCCAAAT TCCCAACCTG CTCATTTTTT TTTTATCAG AGTCATGATG 4380  
 AATCAGTCTT AGAATGTTT ATTTGCACAA GTAGGGCTGC CTCCAAGAGG AACCTCTGAT 4440  
 10 TTATTTTGTG TGAATATAT GTGAAAGGAT ATGAATCTGA GAGATGCTGT AGACATCTGT 4500  
 CCTACACTTG AGATGATTTT CAAGCCTCTC TGGCAGTTTG AGTTAAGTCT ATCTGGTATT 4560  
 AAAATGCCAAG GACCTTTTGC TGCCTAAATC CACTCTGCAG GAAATAGGCC CAACCAACAG 4620  
 ATGAGAATTA GGCCTGGAT GAGTAGCGCT ATAGTTACTG TCCTGTGAT TAATTTCTGC 4680  
 CATTTCACTG CCATAAAGA GACCAACCAT ATCATGCACA CAATTAGATT TCTCACACTC 4740  
 15 TAACTGTATA TTTGTATGAT ATTTTAAAT CTCCTAAATG CTGGGCAATG GCTATTAAAC 4800  
 ATTAATGTCT TTGCACTGGC CTTCTGATGA AATGTTAAAC ATGCTTATG TAATATAGAA 4860  
 AAAAACATTG TTTGCTACTG TTTGGGCTGA ATGATGTAA ATAGGTTTCT AAAAAGTCAG 4920  
 ATGTTTGAAG AGTGGCTTAC AAATCAGTAA TTTTCGGGTG GGAGAGTTTC TTTACATTGC 4980  
 CGTGGCATCT TAAAGCTAT CTTTATGTA ATGACTGTA CTAGGCCTAC TGGGGATCAG 5040  
 20 AGTTCCCAAG AAAGGAAACC TTTTCTGTA TCTGGATTCA AATTTATTTT CAATGTTTCA 5100  
 AGCGGGAAAC ATGACTCTTT ATTTCTGTA AATCTAACAT TATTACTTTT CCTCTTAGAA 5160  
 GAATATTGTA TTTGTAGAT TTTGTGAGC TGGTAACATC GTTGCAACCA CTGCAATATC 5220  
 TTCGTAGTA ATCTGATAA TACTTTGAT ACAAGTACTG GTAAGATTGT TATTAAATGT 5280  
 AGCTTCAGTC ATTAATATG TATAGCAAG TAGTACTTCT TCTGTAATAT TTACAATGTA 5340  
 25 TTAAGCCAC AGTATATTTT ATTTCAATGT AATTAACTG TTAACCTTAT CAAAGAGAAA 5400  
 ACATCTCATC ATGCTTATTG TCCAAAGTTA CCTGGAATCA AATAAAAAAT CTAGATTACC 5460  
 ATGAAGAACA TA

Seq ID NO: 238 Protein sequence  
 Protein Accession #: NP\_057167.1

30 1 11 21 31 41 51  
 MKSILDGLAD TTFRTITDLD LYVGSNDIQY EDIKGDMASK LGYFPQKFPPL TSFRGSPFQE 60  
 35 KMTAGDNQPL VPADQVNITE FYNKSLSSEK ENEENIQCGE NFMIDIECFMV LNPSQQLAIA 120  
 VLSLTGTFV VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF YSFIDFHFV 180  
 HRKDSRNVL FKLGGVTASL TASVGSFLPL AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240  
 WTIAIAIAVL PLLGWNCEKL QVSCDIFPH IDETYLMFWI GVTSVLLLFV VYAYMYILWK 300  
 AHSVAVRMIQ RGTKQSIHHT TSEDGKVQVT RPDQARMDIR LAKTLVLILV LLIICWGPPL 360  
 40 AIMVYDVFGK MNLIKTVFAP FCSMLCLLNS TVNPIIYALR SKDLRHAFRS MPSPCEGTAQ 420  
 PLDMSMGDS DCLHGHANNA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL

Seq ID NO: 239 DNA sequence  
 Nucleic Acid Accession #: NM\_033181.1  
 Coding sequence: 17..1252

45 1 11 21 31 41 51  
 ATGAAGTCGA TCCTAGATGG CCTTGCAGAT ACCACCTTCC GCACCATCAC CACTGACCTC 60  
 50 CTGTACGTGG GCTCAATGA CATTAGTAC GAAGACATCA AAGGAGAATG AGGAGAACAT 120  
 CCAGTGTGGG GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCGTAACC CCAGCCAGCA 180  
 GCTGGCCATT GCACTCTCTG CCTCAGCT GGGCACTTCC ACGGTCTCTG AGAACCTCCT 240  
 GGTGCTGTGC GTCATCTCC ACTCCGCGAG CCTCCGCTGC AGGCCCTCCT ACCACTTCAT 300  
 CGGCAGCTG GCGGTGGCAG ACCTCCTGGG GAGTGTCAIT TTTGCTTACA GCTTCATTGA 360  
 55 CTTCACGTG TTCCACGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT 420  
 CACGGCTCC TTCACTGCTT CGTGGGCGAG CCGTGTCTC ACAGCCATCG ACAGGTACAT 480  
 ATCCATTAC AGGCCCTGCG CCTATAAGAG GATTGTCAAC AGGCCCAAG CCGTGGTGGC 540  
 GTTTTGCCCT ATGTGGACCA TAGCCATTGT GATCGCGTGC CTGCCCTCC TGGGCTGGAA 600  
 CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT 660  
 60 GATGTTCTGG ATCGGGGTCA CCAGCGTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA 720  
 TATTCTCTGG AAGGCTCACA GCCAAGCGGT CGCATGATT CAGCGTGCCA CCCAGAAGAG 780  
 CATCATCATC CACACGCTG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG 840  
 CATGATCATC AGGTTAGCCA AGACCTGGGT CCTGATCCTG GTGGTGTGTA TCATCTGCTG 900  
 GGGCCCTCTG CTTGCAATCA TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTAA 960  
 65 GACGGTGTGT GCATTCTGCA GTATGCTCTG CCGTCTGAAC TCCACCGTGA ACCCATCAT 1020  
 CTATGCTCTG AGGAGTAAGG ACCTGCGACA CGCTTTCGGG AGCATGTGTT CCTTCTGTGA 1080  
 AGGCACTGCG CAGCCTCTGT ATAACAGCAT GGGGGACTCG GACTGCTGTC ACAAACACGC 1140  
 AAACAATGCA GCCAGTGTTC ACAGGGCCGC AGAAAGCTGC ATCAAGAGCA CGGTCAAGAT 1200  
 TGCCAAGGTA ACCATGCTCTG TGTCCACAGA CAGTCTGCTC GAGGCTCTGT GA

Seq ID NO: 240 Protein sequence  
 Protein Accession #: NP\_149421.1

75 1 11 21 31 41 51  
 MALQIPSPAP SPLTSTWAO MTFSTKTSKE NEENIQCGEN FMDIECFMVL NPSQQLAIAV 60  
 LSLTLGTFV LLENLLVLCV LHSRSLRCRP SYHFIGSLAV ADLLGSVIFV YSFIDFHFV 120  
 RDSNRNVL FKLGGVTASL ASVGSFLFLTA IDRYVSIHRP LAYKRIVTRP KAVVAFCLMW 180  
 TTAIVAVLP LLGWNCEKLQ SVCSDFPHI DETYLMFWIG VTSVLLLFV YAYMYILWKA 240  
 80 HSHAVRMIQR GTQKSIHHT SEDGKVQVTR RPDQARMDIR AKTLVLILV LLIICWGPPLA 300  
 IMVYDVFGKM NLIKTVFAP CSMCLLNLST VNPPIIYALRS KDLRHAFRSM PPSCEGTAQ 360  
 LDNSMGDSDC LHHGHANNA SVHRAESCIK STVKIAKVTM SVSTDTSAEA L

Seq ID NO: 241 DNA sequence  
 Nucleic Acid Accession #: NM\_003596.1

Coding sequence: 82..1194

1	11	21	31	41	51	
5	GTAGACTGTC	CATGGCCTGA	ACATTTTCGG	AAAATCATTT	TGAGCAAAAT	ATCTGTTTAA 60
	TAACAAGATA	ACCACATCAA	GATGGTTGGA	AAGCTGAAGC	AGAAGTACT	ATTGGCATGT 120
	CTGGTGATTA	GTCTGTGAC	TGTGTTTAC	CTGGGCCAGC	ATGCCATGGA	ATGCCATCAC 180
	CGGATAGAGG	AACGTAGCCA	GCCAGTCAA	TTGGAGAGCA	CAAGGACCAC	TGTGAGAACT 240
10	GGCCTGGACC	TCAAAGCCAA	CAAAACCTTT	GCCTATCACA	AAGATATGCC	TTTAATATTT 300
	ATTGGRGGTG	TGCCTCGGAG	TGGAACCACA	CTCATGAGGG	CCATGCTGGA	CGCACATCCT 360
	GACATTGCGT	GTGGAGAGGA	AACCAGGGTC	ATTCCCCGAA	TCCTGGCCCT	GAAGCAGATG 420
	TGGTCACGGT	CAAGTAAAGA	GAAGATCCGC	CTGGATGAGG	CTGGTGTAC	TGATGAAGTG 480
	CTGGATTCTG	CCATGCAAGC	CTTCTTACTA	GAAATTATCG	TTAAGCATGG	GGAGCCAGCC 540
15	CCTTATTAT	GTAATAAAGA	TCCTTTTGCC	CTGAAATCTT	TAACTTACCT	TTCTAGGTTA 600
	TTCCCCAATG	CCAAATTTCT	CCTGATGGTC	CGAGATGGCC	GGGCATCAGT	ACATTCAATG 660
	ATTCTCTGAA	AAGTTACTAT	AGCTGGATT	GATCTGAACA	GCTATAGGGA	CTGTTTGACA 720
	AAGTGGATTC	GTGCTATAGA	GACCATGTAT	AACCACTGTA	TGGAGGTGG	TTATAAAAAG 780
	TGCATGTTGG	TTCACTATGA	ACAACCTGTC	TTACATCCTG	AACGGTGGAT	GAGAACACTC 840
20	TTAAAGTTCC	TCCAGATTCC	ATGGAACCA	TCAGTATTGC	ACCATGAAGA	GATGATTGGG 900
	AAAGCTGGGG	GAGTGTCTCT	GTCAAAAGTG	GAGAGATCTA	CAGACCAAGT	AATCAAGCCA 960
	GTCAATGTAG	GAGCTCTATC	AAAATGGGTT	GGGAAGATAC	CGCCAGATGT	TTTACAAGAC 1020
	ATGGCAGTGA	TTGCTCCTAT	GCTTGCCAG	CTTGATATG	ACCCATATGC	CAACCCACCT 1080
	AACCTACGAA	CACTGATGCC	CAAAATTATT	GAAACACTC	GAAGGGTCTA	TAAAGGAGAA 1140
25	TTCCAACTAC	CTGACTTTCT	TAAAGAAAA	CCACAGACTG	AGCAAGTGGG	GTAGCAGAAC 1200
	CAGGAGCTCT	TTCCATACAT	GAGGAAAGAT	TGCTGCCTTT	TCAGCAGAAG	GGAAATTCCT 1260
	AGGATTGGCT	GTCCCTGCC	AAGCTTGGTG	GAGCGTCTGC	ACCTTGGCTG	CGCGCCTCTG 1320
	GCATTTGCGA	GTCTCTCCC	ACTGAGAGGA	TGGAGGTGTC	CGCACAGCTT	TGGGCCTCGT 1380
	GAGGATCTG	CTCTCTGAGC	AAAGAGCTCT	TGATCCCGAT	TTCACTGACA	GCCCTGCAGT 1440
30	AAGGAGCCCA	GAAGGAACT	GTGTTTCTG	TTAAACTCC	TCCTGTCTC	TTTTCTTACA 1500
	TTATGACGTT	TGTTTCAAG	GAGAGGTTT	AAAAATGGGA	TCCTGTAAAG	AGACTTGGGC 1560
	AGTCTCCTTT	TGAAATAGGT	TGCTGTACA	TGTTCTAATG	TTTTGTAGAA	CACGTGTGCC 1620
	TGTTTAAAGT	TATTGATGTG	AATAATATTA	AATATCCTAA	TTATTTAATT	CATTGTATTG 1680
	TTCTGAGAA	GTTGGGAAAT	TACCATTATA	CATTTACAAC	CTAATGACTT	TGTTATTTTA 1740
35	TTTTTCAAAA	TAAAGCTTT	CAATGTGA			

Seq ID NO: 242 Protein sequence  
Protein Accession #: NP\_003587.1

1	11	21	31	41	51	
40	MVGLKQNL	LACLVISSVT	VFYLGQHAME	CHHRIERSQ	PVKLESTRIT	VRTGLDLKAN 60
	KTFAYHKDMP	LIFIGVPRPS	GTILMRAML	AHPDIRGEE	TRVIRILAL	KQMWSSRSKE 120
	KRLDEAGVT	DEVLDSAMQA	FLLEIIVKHG	EPAPYLCNKD	PFALKSLTYL	SRLFPNAKFL 180
45	LMVRDGRASV	HSMSIRKVTI	AGFDLNSYRD	CLTKWNRAIE	TMYNQCMVEG	YKCMVLVHVE 240
	QLVLHFERWM	RTLLKFLQIP	WNHSLVHHEE	MIGKAGGVSL	SKVERSTDQV	IKPFVNVGALS 300
	KWVGKIPPDV	LQDMAVIAFM	LAKLGYDPYA	NPPNYGKPDF	KIIENTRRVY	KGEFQLPDFL 360
	KEKPQTEQVE					

Seq ID NO: 243 DNA sequence  
Nucleic Acid Accession #: NM\_001492.3  
Coding sequence: 1395..2513

1	11	21	31	41	51	
55	ACGCGGGGGG	CGCGGCTCGG	TGGGCTACCG	CGGGCGGGCG	CAGGCGACGG	GCAAGCGGGG 60
	CGAGCGGGGG	GTATGGCGGC	GGCGGGGGCC	CGGCGGGGGC	CGAGCGGGCC	CGAGCCCATG 120
	CCGAGCTACG	CGCAGCTAGT	GCAGCGCGGC	TGGGGCAGCG	CGCTGGCGGC	GGCGCGGGGC 180
	TGCAACGAGT	CGCGCTGGGG	GCTGGCGCGT	CGCGGCTTGG	CTGAGCACGG	GCACCTGGCG 240
60	CGGCGCGAGC	TGCTGTCTGT	GGCGCTCGGC	CGCGTGGGCT	GGACCGCGCT	GCGCTCCGCG 300
	GCCACTGGCG	GCCTCTTTGG	GCCCTGGCG	AAGCGGTGCT	GCTTCCAGCC	CAGAGATGCC 360
	GCCAGATGCG	CGAGAGCGCG	TTGGAAGTTT	CTCTTCTACC	TGGGCGAGCT	GAGCTACAGT 420
	GCCTACCTGC	TGTTTGGCAC	CGACTACCCC	TTCTTCCATG	ACCCACCATC	TGTCTTCTAC 480
	GACTGGACGC	CGGGCATGGC	AGTGCCACGG	GACATTGCAG	CGGCTACCT	GCTCCAGGGA 540
65	AGCTTCTATG	GCCACTCCAT	CTACGCTACG	CTATACATGG	ACACCTGGCG	CAAGGACTCG 600
	TGGGTCTATG	TGCTCCACCA	CGTGGTCACT	CTCATCTCTA	TGCTCTCTCT	CTACGCTCTC 660
	CGGTACCACA	ATGTGGGCAT	CCTTGTGCTC	TTCTGTCAAG	ATATCAGTGA	CGTGCAGCTT 720
	GAGTTACCCA	AGCTCAACAT	TTACTTCAAG	TCCCGCGGGG	GCTCTTACCA	TGGCTGTGAT 780
	GCCTTGGCAG	CAGACTTGGG	CTGCCTCAGC	TTGGGCTTCA	GCTGGTTCTG	GTTCGCGCTC 840
70	TACTGTGTTCC	CGCTCAAGGT	CCTGTATGCC	ACCACTCACT	GCAGTCTGGG	CAAGGTGCTC 900
	GACATCCCCT	TCTACTTCTT	CTTCAATGGG	CTCCTGCTGC	TGCTCACCTC	TATGAACCTC 960
	TACTGTGTTCC	TGTACATCGT	GGCGTTTGCA	GCCAAAGTGT	TGACAGGCCA	GGTGACAGAG 1020
	CTGAAGGACC	TGCGGGAGTA	TGACACAGCC	GAGGCGCCAGA	GCTTGAAGCC	CAGCAAGGCC 1080
	GAGAAGCCAC	TAGGAACCGG	CCTGGTGAAG	GACAAAGCGT	TCTGAACCCC	TGGGCCCCGC 1140
75	CCCGCTGGAC	CGGCGCCAC	CCCGAATACC	CGGCGCACGC	TCCCGTCTCT	TGGCGCCCCC 1200
	TCCACCCCTC	CCAACTCTGC	TCCTCTAGGG	CGCGCGCCAC	CTCCCTTGGG	ACCCCGCCCC 1260
	CTCATCTGCG	CTCATTTTCC	CGGCCACGCC	CCCGAGGACC	CCTGCCCTCT	CGGGACACCC 1320
	GGCCCCCGCC	TCAGCCCATC	GGTCCCGGGC	CGCGCGGAGC	CCTGCGCACT	CTCTGGTCAT 1380
	GGCTTGGGAG	GAAGATGCCA	CGCGCGCAGC	AAGGTCCCTG	CGGCGACACC	CTCTCTCTCC 1440
80	TCTTGGCCCT	GCTGCTGCC	TGCGTGGCCC	TGACCCGCGC	CCCGTGGCCC	CCAGGCCCCC 1500
	CGCGCGCCCT	GCTCCAGGCT	CTAGGACTGC	GCGATGAGCC	CCAGGGTGGC	CCCAAGCTCC 1560
	GGCGGTTTCC	CCCGGTCATG	TGGCGCCTGT	TTGACGCGCG	GGACCCCGAG	GAGACAGAGT 1620
	CTGGCTCGCG	CGCGACGTCC	CCAGGGGTCA	CCCTGCAACC	GTGCCACGTG	GAGGAGCTGG 1680
	GGGTGCGCGG	AAACATATCC	CGCCACATCC	CGGACCGCGG	TGCGCCACCC	CGGGCTCGCG 1740
	AGCTGTCTCT	GGCGCGGGG	CATTGCCCTG	AGTGACAGCT	CGTCTTGGAC	CTGTGGGCTG 1800

5 TGAACCCGCG TGAGCGCCCG AGCCGGGGCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860  
 CGGCAGCCCC GGAGGGGCGG TGGGAGCTGA GCGTGGGCGA AGCGGGCCAG GCGCGGGGCG 1920  
 CGGACCCCGG GCGGGTGTCT CTCGCCAGT TGGTGCCGCG CTGGGGGCGG CCAGTGCGCG 1980  
 CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG GCGCGGCAGC CTCGCGCTGG 2040  
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGCG CTGCGCGCGG CTGGGCGGAG GCCTCGCTGC 2100  
 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTGGC CGGCGCGCGG CGGACGCGCG 2160  
 AACCCGTGTT GGGCGGGCGG CCGGGGGCGG CTGTGCGCGG GCGGCGGCTG TACGTGAGCT 2220  
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGCCTTCCTG GCCAACTACT 2280  
 10 GCCAGGTCA GTGCGCGCTG CCGGTGCGCG TGTGCGGGTC CGGGGGGCGG CCGGCGCTCA 2340  
 ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCGCGCCC GGGAGCGGCC GACCTGCCCT 2400  
 GCTGCGTGCC CGCGCGCTG TCGCCCATCT CGTGCTCTT CTTTGACAA AGCGACAAAG 2460  
 TGGTGCTGCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG 2520  
 CGGCGAGGA CGCGGGCCCA ACAATAAATG CCGGTGGTGC TGCTC

15 Seq ID NO: 244 Protein sequence  
 Protein Accession #: NP\_001483.2

20 1 11 21 31 41 51  
 | | | | | |  
 MPPPPQGGPCG HLLLLLLL LPSLPLTRAP VPPGPAAALL QALGLRDEPQ GAPRLRPVPP 60  
 VMWRLFRRRD PQETRSRR TSPGVTLQPC HVEELGVAGN IVRHIFDRGA PTRASEPVSA 120  
 AGHCPEWTVV FDLASAVEPAE RPSRARLELR FAAAAAAAE GWEELSVQA QGAGADPGP 180  
 VLLRQLVPAL GPPVRAELLG AAWARNASWP RSLRLALALR PRAPACARL AEASLLLVTL 240  
 25 DPLRLCHPLAR PRRDAEPVLG GPGGACRAR RLYVSFREVW WHRWIAPRG FLANYCQGGC 300  
 ALPVALSGSG GPPALNHAUL RALMHAAAPG AADLPCCVPA RLSPISVLFF DNSDNVVLRLQ 360  
 YEDMVVDECG CR

30 Seq ID NO: 245 DNA sequence  
 Nucleic Acid Accession #: NM\_021267.1  
 Coding sequence: 17..1125

35 1 11 21 31 41 51  
 | | | | | |  
 ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCACGGCGGG 60  
 CGAGCGGGCG GTATGGCGCG GCGGGGGCCC GCGGCGGGCG CGACGGGGCG CGAGCCCATG 120  
 CGGAGCTACG CGCAGCTAGT GCAGCGCGCG TGGGCGAGCG CGCTGGCGCG GCGCGGGGCG 180  
 TGCAAGGACT GCGGCTGGGG GCTGGCGGCT GCGGCGCTGG CTGAGCAGCG GCACCTGGCG 240  
 CGCGCGAGC TGTCTGCTGT GCGCTCGCG CGCTGGGCT GGACCGCGCT GCGCTCGCG 300  
 40 GCGACTGCGC GCTCTTTTCG GCCCTGCGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360  
 GCCAAGATGC CCGAGAGCGG TTGGAAGTTT CTCTTCTACC TGGGCGAGTG GAGCTACAGT 420  
 GCTACCTGCG TGTGGGCGAC GACTACCCG TTCTTCCATG ACCCACCATC TGTCTTCTAC 480  
 GACTGGAGCG CGGCGATGGC AGTGCCACGG GACATTGCG CCGCTACCT GCTCCAGGGA 540  
 AGCTTCTATG GCGACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600  
 45 GTGTCATGCG TGCTCCACCA CGTGGTCACT CTCATCTCA TCGTCTCCTC CTACGCTTTC 660  
 CGGTACCACA ATGTGGGCGT CTTGTGTCTC TTCTTCCAGC ATATCAGTGA CGTGACAGCT 720  
 GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCCGGGGCG GCTCTTACCA TCGGCTGCAT 780  
 GCCTTGGGAG CAGACTTGGG CTGCTCAGC TTGGGCTTCA GCTGGTCTG GTTCCGCTTC 840  
 TACTGTTTCC GCTCAAGGT CCGTATGCG ACCAGTCACT GCAGTCTGCG CACGGTGCTC 900  
 50 GACATCCCTT TCTACTTCTT CTTCATGCG CTCTGCTGCG TGCTCACCTT TATGAACCTC 960  
 TACTGTTTCC TGTACATCGT GCGGTTTGCA GCCAAGGTGT TGACAGGCCA GGTGCAGGAG 1020  
 CTGAAGGACC TGCGGGAGTA TGACACAGCC GAGGCCAGCA GCCTGAAGCC CAGCAAGGCC 1080  
 GAGAGCCAC TGAGGAACCG CCGGTGTAAG GACAAGCGCT TCTGAACCCC TCGGCGGCGC 1140  
 CCGCGTGGAC CCGGCCCCAC CCGGAATACC CCGGCCAAGC TCCCGTCTT TGGCGGCGCC 1200  
 55 TCCACCCCTT CCAACTCTGC TCCTCTAGGG CCGCGGCCAC CTCCTCTGGG ACCCGCGCCC 1260  
 CTCACTCTGC CTCATTCTC CGGCCAGGCC CCGCAGGACC CCGTCCCTCT CCGGGACACC 1320  
 GCGCGCGGCC CTAGCCCATC GGTCCCGGGC CGCGCGGAGC CCGTCCGACT CTCTGGTCACT 1380  
 CGCGTGGGAG GAGATGCGCA CCGCGCGAGC AAGGTCCCTG CGGCCACCAT CTCCTCTCTC 1440  
 TCTGCTGCTC GCTGCTGCCC TCGCTGCCCC TGACCGCGCG CCGGTGCCCC CAGGCGCCAG 1500  
 60 CCGCGCCCTT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CAGGGTGCC CCGAGGCTCC 1560  
 GCGCGGTTCC CCGGCTCATG TGGGCGCTGT TTCGACGCGG GAGCCCCAG GAGACAGGCT 1620  
 CTGCTCGCGG GCGGACGTCC CCAGGGGTCA CCTTGCAACC GTGCCAGTG GAGGAGCTGG 1680  
 GGGTGGCGCG AAACATCGTG CGCCACATCC CGGACCGCG TCGCGCCACC CCGGCTCTCG 1740  
 AGCTGTCTC GCGCGCGGGG CATTGCGCTG AGTGGACAGT GGTCTTGGAC CTGTGCGCTG 1800  
 65 TGGAAACCGC TGAGCGCCCG AGCGGGGCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860  
 CGGCAGCCCC GGAGGGGCGG TGGGAGCTGA GCGTGGGCGA AGCGGGCCAG GCGCGGGGCG 1920  
 CGGACCCCGG GCGGTGTCTG CTCGCCAGT TGGTGCCGCG CTGGGGGCGG CCAGTGCGCG 1980  
 CGGAGCTGCT GGGCGCGGCT TGGGCTCGCA ACGCCTCATG GCGCGCGAGC CTCGCGCTGG 2040  
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGCG CTGCGCGCGG CTGGGCGGAG GCCTGCTGCG 2100  
 70 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTGGC CGGCGCGCGG CGGACGCGCG 2160  
 AACCCGTGTT GGGCGGGCGG CCGGGGGGCG CTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220  
 TCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGGCGCGCG CGCTTCTCTG GCCAACTACT 2280  
 GCCAGGTGTA GTGCGCGCTG CCGGTGCGCG TGTGCGGGTC CGGGGGGCGG CCGGCGCTCA 2340  
 ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCGCGCCC GGGAGCGGCC GACCTGCCCT 2400  
 75 GCTGCGTGCC CGCGCGCTG TCGCCCATCT CGTGCTCTT CTTTGACAA AGCGACAAAG 2460  
 TGGTGCTGCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG

80 Seq ID NO: 246 Protein sequence  
 Protein Accession #: NP\_067090.1

1 11 21 31 41 51  
 | | | | | |  
 MAAAGPAAGP TGPEMPPSYA QLVQRWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60  
 LLLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAAKMP ESANKFLFYL GSWSYSAYLL 120  
 FGTDYPPFHD PPSVFYDWTG GMAVPRDIAA AYLLQGSFYG HSIATLYMD TWRKDSVVML 180

LHHVTLILI VSSYAFRYHN VGILVLFLHD ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240  
DLGCLSPFGS WFWFLRYWFP LKVLVATSHC SLRTVPDIPF YFFFNALLLL LTLNLYWFL 300  
YIVAFAAKVL TQGVHELKDL REYDTAEAS LKPSKAEKPL RNGLVKDKRF

5

Seq ID NO: 247 DNA sequence  
Nucleic Acid Accession #: NM\_002081.1  
Coding sequence: 222..1898

10 1 11 21 31 41 51  
GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCGCGCGCC CGCCGCGCGC 60  
GGCTTTTGTT GTCTCCGCCT CCTCGGCGCG CGCGCGCTCT GGACCGGAG CCGCGCGCGC 120  
CGGACCTTGT GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCCGCC AGGATCCGAG 180  
AGAGGCGCGG GCGGGTGGCC GGGGGCGCGG CCGGCCCGCC CATGGAGTCT CGGGCCCGAG 240  
15 CTTGGTGGCT GCTATGTGCG GCCGACGCGC TGGTCCGCTG CGCCCGCGGG GACCCGCGCA 300  
GCAAGAGCGG CAGAGAGCTG GAGGTCCGCC AGATCTACGG AGCCCAAGGGC TTCAGGCTGA 360  
GCCACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420  
CCTGTCTGAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480  
CCGCGCTCCG GGACAGCAGC CGGCTCTGCG AGGCCATGCT TGGCAACCG CTGCGCAGCT 540  
20 TCGATGACCA CTTCACGAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC 600  
CCGCGCGCTG CAGAGAGCTG TACACGCGAG ACGCGAGGGC CTTCGCGGAC CTGTACTCAG 660  
AGCTGCGCCT TACTACCGCG GGTGCCAACC TGCACCTGGA GGAGACGCTG GCGGAGTTCT 720  
GGGCGCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CAGCTGTCTG CTGCTGTATG 780  
25 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGGCGCTGCG GCCCTTCGGG GAGGCGCGCA 840  
GAGAGCTGGC CCGTGGGGCC ACCCGTGCCT TCGTGGCTGC TCGTCTCTTT GTGCAAGGCC 900  
TGGCGTGGG CAGCAGGCTG GTCCGGAAG TGGCTCAGGT CCGCTTGGGC CCGGAGTGTCT 960  
CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTACTGCTCT GGGAGTCCCC GCGCGCAGGC 1020  
CCTGCCCTGA CTATTGCGCA AATGTGCTCA AGGCTGTCTG TGGCAACCG GCGGACCTGG 1080  
30 ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140  
CATCGGCTGT GGAGAGTGTG ATCGGCGAGG TGACACAGTG GCTGGCGGAG GCCATCAACG 1200  
CCCTCCAGTA CAACAGGGAC ACGCTCACGG CCAAGGTCTAT CAGGGGCTGC GGGAAACCCA 1260  
AGGTCAACCC CCAGGGCCCT GGGCTGAGG AGAAGCGCGC CCGGGGCAAG CTGGCCCGCG 1320  
GGGAGAGGCC ACCTTCAGGC ACGCTGAGGA AGCTGGTCTC TGAAGCCAAG GCCAGCTGCC 1380  
35 GCGACGTCCA GGACTTCTGG ATCAGGCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC 1440  
TGAGCACTGC CAGTGATGAC CGCTGTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG 1500  
AGGTCAATGG TGAGGGCTGT GCCAACGAGA TCAACAACCC CGAGGTGGAG GTGGACATCA 1560  
CCAAGCCGGA CATGACATC CGGACGAGA TCATGACGCT GAGATCATG ACCAACCGGC 1620  
TGCGCAGCGC CTACAACGCG AACGACGTGG ACTTCCAGGA CGCAGTGAC GACGCGACGG 1680  
40 GCTCGGGCAG CGGTGATGGC TGTCTGGATG ACCTCTGGCG CCGGAAGGTC AGCAGGAAGA 1740  
GCTCCAGCTC CCGGACGCCC TTGACCCATG CCGTCCGAGG CCGTGTGAGG CAGGAAGGAC 1800  
AGAAGACCTC GAGCGGCGAG TGCCCCCAGC CCGCGACCTT CCGTGTGCCC CTCTCTCTCT 1860  
TCCTGGCCCT TACAGTAGCC AGGCCCCGGT GCGGTGAATC GCGCAAGGCG CCGAGGGAGA 1920  
GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGAG ATATTTAATT CACCTCAGCC 1980  
45 TGGAGAGGCC TGGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040  
GTCCACGCCC CAGGCTGGC CTGCGCTGCC TTCTGCGCTT TTAATTTTGT ATGAGGTCTT 2100  
CAGGTGAGTG GAGGAGCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGACCC 2160  
TCGGCTGCC TAGCCCTCCC CCGAGCTCCC TGACCCGCGG CAGAAGCAGC CCGTGGAGGC 2220  
CTACAGAGGA GGCTTCAAG CAACCCGCTG GAGCCACAG CGAGCCTGTG CCGTCTCTCC 2280  
50 CGCTCTCTCC CACTGGGACT CCGAGCAGAG CCCACGAGCC AGCCCTGGCC CACCCCCAG 2340  
CCTCCAGAGA AGCCCGGAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400  
TCTGAGATGA GCTGATGAGC CCTCCCTCA CGCGAGGCTG CAGAGCCCGG CCGCACTCTC 2460  
CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGTGAGCGCC TGAGACAGCA CCACTGCTGA 2520  
GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCAGTGAGG GGCCCTCCAT GCGCAGATGA 2580  
55 GGGGCCACTG ACCCACTGCT GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAG 2640  
GGAGGACAGG TGGGCTGTGC CAATGTGGGC TGCCCCGCG ACACAGGGCT CAGAGGGCAG 2700  
CGCTTGTGG GGTGAGGGGC TGTGGAGGA CCGCGAGGCG TGAGGAGCAG CCAGGACCGG 2760  
CCTGTCTCCA TCTTCAACCA GATCAGGAAC CAGGGCTCTC CTGTTACAGG TGACACAGGT 2820  
CAGGGCTCAG AGTGACCTCT GGCTGTACCC TGCTACAGG GATGCTGGTG GCTGTGAGA 2880  
60 CCGCGCAGTG CACACGGGAA TGCTAGGTTC CCTTCCGAC CAGCCAGCT GCACTGCAGG 2940  
GCACGGGAGC CTGGATAGTT AAGGGCTTTT CCAACATGC ATCCATTAC TGACACTTCC 3000  
TGTCCTTGT CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTGCGAGGC CCGCAGGGCC 3060  
CAGCTTGGAC CTTGCTGACC TCTGTCTACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120  
CTGAGCGGGC CTTCTTCCC TCTGTGCCC CAGCTGCCAG GTGGCCCTGG GAGGGGGTGG 3180  
65 TGTGTGTGT GGAAGGGGTC CTGAGGGGG AGGAGGACTT GGAGGTCTG GGGGCGAGTG 3240  
TCTGAACCG ACTGACCTTG AGGAGGCGCG TTAGTGTCTG TTTGCTTTT ATCACCCTCC 3300  
CGCAGAGTGG ACGGAGGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360  
CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCAACACAG CCAAGTCCAC CCCATAATAA 3420  
CCCTGCCAGT CCGAGGGTGG GCTGGGAGCT CTGGCACAGT GATGCGGGGC GCCAGGACAG 3480  
70 CAGCACTCCC GCTGCACACA GACGGCTTAG GGGTGGGCT CAGACCCAC CCTACGCTCA 3540  
TCTCTGGAAG GGGCAGCCCT GAGTGGTCTG TGGTCAGGGC AGTGGCCAG CCTGCTGTGT 3600  
CCTTCTCCA CAAGGTCCCC CCAACGCTCA GTGTACAGGG GTGACGTGTG TCTTTTGGAG 3660  
TCCTGTATG AATAAAGGC TGGAAACCTA AA

75

Seq ID NO: 248 Protein sequence  
Protein Accession #: NP\_002072.1

80

1 11 21 31 41 51  
MELRARGWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSQVP QAEISGEHLR 60  
ICPQGYTCT SEMEENLANR SHALELTALR DSSRVIAQML ATQLRSFDDH FQHLNDSDR 120  
TLQATPPGAF GELYTNARA FRDLYSELRL YRGRANLHLE ETLAEFWARL LERLFQQLHP 180  
QLLLPDDYLD CLGQAEALR PFGEAPRELRL LRATRAVFAA RSFVQGLGVA SDVVRKVAQV 240  
LPGECRAV MKLVYCAHCL GVPGARPCPD YCRNVKGLCL ANQADLDAEW RNLLDSMVLII 300  
TDFKFWGTSGV ESVGSVHTW LAEAINALQD NRDTLTAKVI QCGGNPKVNP QGPGPEEKRR 360

RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA 420  
RGRYLPVEMG DGLANQINNP EVEVDITKPD MTIRQIMQL KIMTNRLRSA YNGNDVDFQD 480  
ASDDGSGSGS

5 Seq ID NO: 249 DNA sequence  
Nucleic Acid Accession #: NM\_001492.3  
Coding sequence: 8..1864

10 1 11 21 31 41 51  
GAAGGCCATG GTCTCCCCAC GGATGTCCGG GCTCCTCTCC CAGACTGTGA TCCTAGCGCT 60  
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GCGGGGTCCA GGCCTTGGGG CCCCOCGGTC CCCCTGCAGC GCGCGGCTCC CTGCGCGCT 180  
CTTCTTCAGA GTCTGCCTGA AGCCTGGGCT CTGAGAGGAG GCCGCGAGT CCCCGTGCSC 240  
15 CCTGGGCGCG GCGCTGAGTG CCGCGGAGCC GGTCTACACC GAGCAGCCCG GAGCGCCCGC 300  
GCCTGATCTC CCACGTGCCC ACGGGCTCTT GCAGGTGCCC TTCCGGGACG CCTGGCCTGG 360  
CACCTTCTCT TTCATCATCG AAACCTGGAG AGAGGAGTTA GGAGACCAGA TTGGAGGGCC 420  
CGCCTGGAGC CTGCTGGCGC GCGTGGCTGG CAGGCGGCGC TTGGCAGCCG GAGGCCCGTG 480  
GGCCCGGGAC ATTGAGCGCG CAGGCGCCTG GGAGCTGCGC TTCTCGTACC GCGCGCGCTG 540  
20 CGAGCGGCTT GCCGTGCGGA CCGCTGTCAC GCGCTCTGCG CGTCCGCGCA GCGCCCGCTC 600  
GCGGTGCGGT CCGGGAAGTC GCGCTGCGC ACCGCTCGAG GACGAATGTG AGGCGCGCTG 660  
GGTGTGCGGA GCAGGCTGCA GCCCTGAGCA TGGCTTCTGT GAACAGCCCG GTGAATGCGG 720  
ATGCTAGAGC GCGTGGACTG GACCCCTCTG CACGTCCTCT GTCTCCACCA GCAGCTGCTT 780  
25 CAGCCCGCAG GGCCTGCTCT CTGCTACAC CCGATGCTTT GTCCCTGGGC CTGGGCGCTG 840  
TGACGGGAAC CCGTGTGCCA ATGGAGGCGAG CTGTAGTGAG ACACCCAGGT CCTTTGAATG 900  
CACCTGCGCG CGTGGGTTCT ACGGGCTGCG GTGTGAGGTG AGCGGGGTGA CATGTGCAGA 960  
TGACCCCTGC TTCAACGCGG GCTTGTGTGT CCGGGGTGCA GACCCCTGCT CTGCTACAT 1020  
CTGCTACGCG CCACCTGCTT TCCAAGGCTC CACTGTGAG AAGAGGGTGG ACCGTGCGAG 1080  
30 CCTGCAGCCA TGCCGAATG GCGGACTCTG CTTGAGCTG GGCACGSCC TGCGCTGCGG 1140  
CTGCGCGGCC GGCCTGCGGG GTCCCTGCTG CGAGCACGAC CTGGAGACTG GCGCGGGCGG 1200  
CGCCTGCGCT GCGCGGCGCA CGTGTGTGGA GCGCGCGCGC GCGCACGCTG GTCCTGCGCG 1260  
GCTGGGCTTC GCGCGGCGCG ACTGCCGCGA GCGCGCGGAC CCGTGCAGCG CCGCGCCCTG 1320  
TGCTACGCGC GCGCGCTGCT ACGCCACTT CTCCGCGCTC GTCTGCGCTT GCGCTCCCGG 1380  
35 CTACATGGGA GCGCGGTGTG AGTTCCAGT GCACCCCGAC GCGCGAAGCG CCTTGCCTGC 1440  
GGCCCGCGCG GGCCTCAGGC CCGGGGACCC TCAGCGCTAC CTTTTCCTC CGGCTCTGGG 1500  
ACTGCTCGTG GCGCGGGCGG TGGCGGCGCG TGCGCTCTTG CTGGTCCACG TGCGCGCGCG 1560  
TGGCCACTCC CAGGATGCTG GGTCTGCTT GCTGGCTGGG ACCCCGAGC CGTCAGTCCA 1620  
CGCATCCCG GATGCACCTA ACAACCTAAG GACGAGGAG GGTTCGGGG ATGCTCOGAG 1680  
40 CTCGTCGCTA GATTGGAATC GGCCTGAAGA TGTAGACCCT CAAGGGATT ATGTATATC 1740  
TGCTCTTCC ATCTACGCTC GGGAGGTAGC GACGCCCTT TTCCCGCGC TACACACTGG 1800  
GCGCGCTGG CAGAGGCGAG ACCTGCTTTT TCCTTACCTT TCCTGATTG TGTCGCTGAA 1860  
ATGAATTGG TAGAGTCTCT GGAAGGTTT AAGCCCATTT TCAGTCTAA CTTACTTTCA

45 Seq ID NO: 250 Protein sequence  
Protein Accession #: NP\_058637.1

1 11 21 31 41 51  
MVSPRMSGLL SQTIVILALIP LPQTRPAGVF ELQIHSFPGP PGPGAPRSPC SARLPCRLFF 60  
50 RVCLKPGLSE EAAESPCLAL AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAMPWTF 120  
SFIIETWREE LGQIGGPAW SLLARVAGRR RLAAAGFWAR DIQRAGAWEL RFSYRACEP 180  
PAVGTACTRL CRPSRAPSRC GPGLRPAAPL EDECEAPLVC RAGCSPENGF CEQPGCECRL 240  
EGWTGELCTV PVTSSCLSP RGPSSATTGC LVPGPGPCDG NPCANGGSCS ETPRSFECTC 300  
55 PRGFYGLRCE VSGVTCADGP CFNGSLCVGG ADPDSAYICH CPPGFQGSNC EKRVDRCSLQ 360  
PCNRGSLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGTCVEGG GAHRCSCALG 420  
FGRGRDCRERA DPCAARPCAH GGRCYAHFSG LVCACAPGYM GARCEFPVHP DGASALPAAP 480  
PGLRPGDPQR YLLFPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTPPEFVHAL 540  
60 PDALNNLRTO EGGSGGPPSS VDWNRPEVDV PQGIYVISAP SIYAREVATP LFPPPLHTGRA 600  
GQRQHLLFPY PSSILSVK

Seq ID NO: 251 DNA sequence  
Nucleic Acid Accession #: CAT cluster

65 1 11 21 31 41 51  
GAAATATAAC CATGCAATT AGAAAATATC CAAAATAGCC TGTATCTTC CACGTGGCCT 60  
AGATTATGTA CAATCCCAAA TATACAATTT TTCCTTAAA GTAGTACAA TTCCTTTGTA 120  
GCTTCAATTC CTTATATGAC TTCAGACTGG AGAAGCCTGT TAAACCACTG TTAGTTTCAG 180  
70 TTAGAAAGTC TGAGAGACTT TATACATAAA TTCTCAATTT GGCTGCTGTA CACGTGCCAG 240  
AGTTTACTA CTGTAGTGAC CGTTGAGAAG ACCCTTGTTT ATTTACATTT GAAGCACTGT 300  
TTGTGCAAA CACCTTTTCT TGTAAAGTGC CTGTATTCCT TTCATTACT TCATGTCCAG 360  
GGGTGCTATT TACCTAGAAC CATTGTCTAC TACAATTAAC ATTTACATTA CAAAGTGTGT 420  
GGTTTCTCTT TCAAGGAGG TTCAATTAAG GCAATAAGAT GTTTGCTGGA GAAACCTATT 480  
75 GTTTACTGAA AGCACTCAAT GAAGTCAAT TACTGAAGCT TTTGCTACA TCTTGTCTT 540  
TTATGTAAT ATGTTAATA TAACATCTAA GGAATAATA CAATATTATA ATTATGTGTT 600  
TGCCATTGTC ATATCAAACT TGCTTTGTAT CATACTAATG TTACTAATCT TATCATCAAA 660  
TAAATATACA TTCAATGTT AAAAAAATA AAAAAAATA

80 Seq ID NO: 252 DNA sequence  
Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51  
AGGTACTGCC AGAAAGGATC AGGACCTGGA GTCTGGCAAG AGGAAGACAG AGGCCTGTGT 60

5 GGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC 120  
 TAGATAACCG AAAGTAAAAA CTCTTCAAG ATCGCCGGGG AGCGTGTGAG AATGAAAGAC 180  
 TACAGCCGAG AGACAGTAAA AACCAGAAAAG GTCAGGAATA CTTATTGAAT CTAACCTTGT 240  
 TTTTGTGTTG TTTTCTTCTT TATGATTAAG GGTGGGATGA GAGAAAATTA AATGACACAC 300  
 ACATGCTAAA ATATCAAGGT TCCAGATATG TCTTGAGAGG GGTGTGTGCA GCTGCAARGG 360  
 AGAAGTGTAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTTCTATT TTAAGGCAAA 420  
 AGTTATATCA GGGATTTTTT TCTTAGAAAG GTGTTGCAGA GATGCTGGT ACCTAGTTTA 480  
 AAAATGATTC CATAATATGT AGACTTGGGC AGTTCCTTTG GGAGGCACCT CCCTCTCAAA 540  
 ATTTGAAGAT TGTGCTTGGG AATTACTTTA CATGTATTGT GGCTGTATGT CAATTGTGAC 600  
 10 GAAATTAGAC TTTCAGAAAA GTTTATACTG GAAGGTTAAT AATTGTATAT TACTGAGGAC 660  
 TTAGAGCTAG CAGGCAGAAA GAAAAAARAA AAAAAAARG CAAGGGCTGA TTTTATTCT 720  
 TCTATTCAAA ATACAAGGAC AGATGCTTCT CTGTTCCTAG AGGGTTTCTT TGAGGAAGCT 780  
 ACTGAAGCAG AAAGACATGA TGGAGACGAG ATCGCCTCCC CTCTTGTCAG AGTGTAAAAA 840  
 AAATGTTCTG TCTTACTCTG CGCCTAGCAT TGGAAATGAA AGTGACATTT ACGCCACAAC 900  
 15 CCACGTGTGC GCCTCCTCTC TTTTGTGTTA AGGATGATCA GGTCTATCCA GGAAACAGCT 960  
 CTGGCATCCC AAACGTAAAT AATTAGGACG TATATAGACC TGACAAAAAT GGAAAGGGGG 1020  
 TGGGGAATCT GAGGGTCTGT CTGCTCTAAT TGATTCCTCT AAACGGAAATG CAGGAGATGT 1080  
 GAACGGCAGG ACGCTCCGAT TCCCACGCTC GGGGGCAAGT GATAAAGCGG GCGCGGGCAG 1140  
 CCTATGACAG ACAGCCCTGT TGGGGGTGGG GGGTATGAAA AAAACATCAA GTGCACACAC 1200  
 20 CATACTCATC TCCATCGCTT AAGAAAGTAA AGGCATTTC CACCCACAGC CATCTGCAGC 1260  
 TTCCCAATTT GCAGCACCAA CTGGTCTGTA GCTGCTACAT AGTCTGCTTC TGTTAATTTT 1320  
 TTAACCACTG TTAAATCTGG CCATAATTA GTTTGGCTTT CTTCGTGTTT TGAGATTTTC 1380  
 AGAATTTCAAG CAAAGCTAGT AGAAAGCAAT TCCAAGAAAG TCCCATGACT GCCTGCCCT 1440  
 25 AATGTCAAAA TCTCAGTCCA TGAGATTATG GCCTGTGAC CACATTTTGT CTTTGTGTTT 1500  
 GGGTGGGCAA ATGTGTATAG AGATAAAATA CATATCTCTA TATAACAGTC GTTATTATAA 1560  
 TTTTCATGAG CTTTCTTACT CTTAACATGA TACATCTAGG AACTTGGTCT AATGTGTCTA 1620  
 GTAGATATAC ACTAGAATAA AAATATAAAA GTCAATAGCC TGTAAGAAAT TGATTATGAT 1680  
 AACAAATAGA TAAAGAGTTT GTTTTGAAT AGTCTCAGCT AGATGGGTCT AAATAGCCAT 1740  
 30 TTTAATGTAA TCTAAAAATA AACTATGCC TAGCAGAAAC TTTGGCGCTT TGGAGGTCCC 1800  
 CATTGTGCCC TTTTCATAAA AGTCCTTAAG TTTTCCATAT GTCACCAAGC AAACATTTGT 1860  
 ATAGGCATTG ACACAGAAAT ATAACCATG CAATTAGAAA ATATCCAAAA TAGCCTGTGA 1920  
 TCTTCCAGCT GGCCTAGATT ATTGCAATC CCAATATATC AATTTTCTT TAAAGTAGT 1980  
 ACAATTTCTT TGTAGCTTTC AATTCTTAT ATGACTTCAG ACTGGAGAAG CCTGTAAAC 2040  
 35 CACTGTTAGT TCCAGTTAGA AAGTCTGAGA GACTTTATAC ATAAATTTCT AATTGTGCTG 2100  
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 CATTGGAAGC ACTGTTTGTG CAAACAACCT TTTATTGTTA AGTGCCTGTA TTCCTTTTAT 2220  
 TTAATTCATG TCCAGGGGTG CTATTACCT AGAACCATTG TCTACTACAA TTAACATTTA 2280  
 CATTACAAAG TGTGTGTTT TCTTTTCAA GGAGGTTCAA TTAAGGCAAT AAGATGTTG 2340  
 40 CTGGAGAAAC CTATTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC 2400  
 TACATCTTGT GTCTTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA 2460  
 TTATAATTAT GTGTTTGCCA TTGTATATC AAACCTGCTT TGTATCATAC TAATGTTACA 2520  
 TAACTTATCG ATCAATAAAA ATACATTCA ATGTT

Seq ID NO: 253 DNA sequence

Nucleic Acid Accession #: NM\_001650.2

Coding sequence: 40.1011

1 11 21 31 41 51  
 50 GGGGCGAGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCACAGCA 60  
 AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCCTTCAAA 120  
 GGGGTCTGGA CTCAGCTTCT CTGGAAGGCA GTCACAGCGG AATTCTTGCC CATGCTTATT 180  
 TTTGTTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240  
 55 GTCGACATGG TTCTATCTC CTTTGTCTTT GGACTCAGCA TTGCAACCAT GGTGTCAGTGC 300  
 TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CRTGTGCCAT GGTGTGCCAC 360  
 AGGAAGGATG GCATGCGCAA GTCTGTCTTC TACATCGCAG CCCAGTGCGT GGGGGCCATC 420  
 ATTGGAGCAG GAATCCTCTA TCTGGTCACA CTCCCAAGTG TGGTGGGAGG CTTGGGAGTC 480  
 ACCATGGTTC ATGGAATATC TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540  
 60 TTTCAATTGG TGTTACTAT CTTTGCAGC TGTGATTCCA AACGGACTGA TGTACTGGC 600  
 TCAATAGCTT TAGCAATTGG ATTTCTGTGT GCAATTGGAC ATTTATTGTC AATCAATTAT 660  
 ACTGGTGCCA GCATGAATCC CGCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720  
 GAAACCAATT GGATATATTG GGTGGGCCC ATCATAGGAG CTGCTCTGCG TGGTGGCCTT 780  
 TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840  
 65 AAAGCTGCCC AGCAACAAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900  
 GAGACGAGTG ACCTGATTCT AAAACCTGGA GTGGTGATG TGATTGACGT TGACCGGGGA 960  
 GAGGAGAAGA AGGGGAAGA CCAATCTGGA GAGGTATTGT CTTAGTATG ACTAGAAGAT 1020  
 CGCACTGAAA GCAGACAGA CTCCTTAGAA CTGTCTCAG ATTTCTTCC ACCCATTAAG 1080  
 GAAACAGATT TGTATAAAT TAGAAATGTG CAGGTTTGTG GTTTCATGTC ATATTACTCA 1140  
 70 GTCTAAACAA TAAATATTTT ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200  
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 TCTAGTTACC TTTCAATTAAC AACCAATTTT AACCGTGTGT CAAGATTGGG TTAAGTCTTG 1320  
 CCTGACAGAA CTCRAAGACA CGTCTATCAG CTTATTCTCT CTCTACTGGA ATATTGGTAT 1380  
 AGTCAATTCT TATTGAATA TTTATTCTAT TAAACTGAGT TTAACAATGG C

Seq ID NO: 254 Protein sequence

Protein Accession #: NP\_001641.1

1 11 21 31 41 51  
 80 MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG 60  
 GTEKPLPVDV VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120  
 AQCLGAIIGA GLYLVTTPPS VVGLGVMTVM HGNLTAGHGL LVELIITPQL VFTIFASCD 180  
 KRTDVTGSIA LAIGFSVAIG HLFAINYTG A SMNPARSFGP AVIMGNWENH WIYWGPIIG 240  
 AVLAGGLLEY VFCPDVEFKR RFKEAFSKAA QQTGSGYMEV EDNRSQVETD DLILKPGVVH 300

VIDVDRGEEK KGDQSGEVL SSV

Seq ID NO: 255 DNA sequence  
Nucleic Acid Accession #: U26742.1  
Coding sequence: 325..1449

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GGCAGCGGAC	CCGGCACTTC	CAACATTATT	AAATAATAAG	AAAGCGGCTC	CTACTCCAGG	120
CTCAAACCTC	CCTGCAGACC	AATGGACACC	TTCTAAGAGT	TGGCCGAGTC	AGTGACTGAA	180
GGCCCGCTCC	ATTCCAAGAT	AAATAGGATT	TACCAATCCT	TGGATGAAGT	GCTTGGGAAG	240
TCITTAAGTG	CCATAATCAA	CTGCCATTTC	AAAGAATATA	GATGGTTTGT	AAAAGTTCAT	300
GCTGTCCCTT	CATTGAATTT	TAGAATGATT	GAAGATAGTG	GGAAAAGAGG	AAATACCATG	360
GCAGAAAGAA	GACAGCTGTT	TGCAGAGATG	AGGGCTCAAG	ATCTGGATCG	CATCCGACTC	420
TTCCACTACA	TAGCCAGCATG	CAAGCTTAGG	TTTGTTCAGA	AGAAATGCAA	TTTGACCTTG	480
GTGGACATAT	GGAATGTCTAT	AGAAGCATTG	CGGGAAAATG	CTCTGAACAA	CCTGGACCCA	540
AACACTGAAC	TCAACGTGTC	CCGCTTAGAG	GCTGTGCTCT	CCACTATTTT	TTACCAGCTC	600
AACAAACGGA	TGCCAACCAC	TCACCAAAATC	CATGTGGAGC	AGTCCATCAG	CCTCCTCCTT	660
AACTTCTCTG	TTGAGCGGTT	TGATCCGGAA	GGCCATGGTA	AAATTTTCAGT	ATTGTCTGTC	720
AAAATGGCTT	TAGCCACATT	GTGTGGAGGG	AAGATCATGG	ACAAATTAAG	ATATATTTTC	780
TCATGATTTT	CTGACTCCAG	TGGGGTGTATG	GTATTATGAC	GATATGACCA	ATTCCTTCGG	840
GAAGTTCTCA	AACTACCCAC	GSCAGTTTT	GAAGTCTCCT	CATTGTGTTA	CACAGAACAG	900
TCAGCCAGAT	CTGTCTTCTC	CCAACAGAAA	AAAGTCAAGT	TAAATGGTTT	CTTGGACACG	960
CTATGTGAG	ATCCTCCCCC	GCAGTGTCTG	GTCTGGTTGC	CTCTTCTGCA	TCGACTAGCA	1020
AAATGGGAAA	ATGTCTTCCA	TCCGGTTGAG	TGTTCTCTACT	GCCACAGTGA	GAGTATGATG	1080
GGATTTCGCT	ACCGATGCCA	ACAGTGTAC	AATTACCAGC	TCTGTCAAGG	CTGCTTCTGG	1140
AGGGGACATG	CCGGTGGTTC	TCATAGCAAC	CAGCACCAAA	TGAAAGAGTA	CACGTCATGG	1200
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CGTGAACCTT	TGCACCCCAT	GTCTCCAGAT	CAGCCTGAGA	AGCCACTCAA	CTTGGCTCAC	1320
ATCGTTGATA	CTTGGCTTCC	CAGACCTGTA	ACCAGCATGA	ACGACACCTT	GTCTCTCCAC	1380
TCGTTCCTCT	CCTCAGGAAG	TCCTTTTATT	ACCAGGAGCT	CGGACGGTGC	TTTGGTGGGA	1440
TGCGTCTAGA	TGGATAACAT	GACTTCTTCT	ACCCTAAAT	ATTCTATATA	TACTTTGAGC	1500
TGTTCTGGTT	CCTCCAGGGT	GCATGGTACC	CATTAAACCA	AAATATGATT	ATTTCCCTTT	1560
TTTCCCATTT	TCAGTCATTT	TGGAATGTTT	TCTGTGAACC	ACAGTTGGGT	TGTTTAAAGC	1620
TCACATTCTT	TTCTGTCAAC	ACAGAGATTG	GCCTACGGTT	TCTGTTTGA	GGGTGCTGTT	1680
CAATAAGCT	GTGTACACTA	AATGTCC				

Seq ID NO: 256 Protein sequence  
Protein Accession #: AAC50424.1

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MIEDSGKRG	N TMAERRQLF	A EMRAQDLDR	I RLSTYRTACK	L LRFVQKKCNL	L HLVDIWNVIE	60
ALRENALN	L DPNTLNVSR	L LEAVLSTIFY	L QLNKRMPPTH	L QIHVEQSISL	L LNFLLAAFD	120
PEGHGKIS	V AVKMALATLC	L GKKIMDKLRY	L IFSMISDSSG	L VMVYGRYDQF	L LREVLKLPAT	180
VPEGPSFG	V YEQSARSCFS	Q QKKVTLNGFL	D DTLMSDPPPO	C CLVWLPLLHR	L LANVENVFHP	240
VECSYCHS	E MMGFRYRCQ	Q CHNYQLQDC	F FWRGHAGGSH	S SNQHQMKKEYT	S SWKSPAKKLT	300
NALSKSL	S SCASSREPLHP	M PDQPEKPLNL	L AHIVDTWPPR	F PVTSMNDILF	S SHSVSPSSGSP	360
FITRSSD	G GAFGGCV					

Seq ID NO: 257 DNA sequence  
Nucleic Acid Accession #: NM\_004172.1  
Coding sequence: 179..1807

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CACCCCTTAC	AAAATCAGAA	AAGTTGTGTT	TTCTAATACC	AAAGAGGAGG	TTTGGCTTTC	120
TGTGGGTGAT	TCCCAGACAC	TGAAGTGCAA	AGAAGAGACC	CTCCTAGAAA	AGTAAATAT	180
GACTAAAGC	AAVKGAGAA	AGCCCAAGAT	GGGGGSCAGG	ATGGAGAGAT	TCCAGCAGGG	240
AGTCCGTAAA	CGCACACTTT	TGGCCAAGAA	GAAGTGCAG	AACATTACAA	AGGAGGATGT	300
TAAAGTTAC	CTGTTTCGGA	ATGCTTTTGT	GCTGCTCACA	GTCAACGCTG	TCATTGTGGG	360
TACAATCCTT	GGATTATACC	TCCGACCATA	CAGAATGAGC	TACCGGGAAG	TCAAGTACTT	420
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CTCCAGTCTT	GTACAGAGAA	TGGCGGCGCT	AGATAGTAAG	GCATCAGGGA	AGATGGGAAT	540
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 Protein Accession #: NP\_004163.1

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	AGCTCAGCAG	CCCGGGCCCT	GAGGCTCTCT	TCCCCACTGA	GCCAGCAGCC	CAGGAGGAGT	1560
	CACTCTCCCA	GGCGCCAGCA	AGGGCAGTCC	TGCAGCCTGG	TGCATCACCA	CTTCTGTATG	1620
	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
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	CCGCATCAGG	TGACTGTGTC	CCCAGCCCTT	GCCACAATGG	TGGGACATGC	TTGGAGGAGG	2040
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15	GCATCAGCCA	ACCAGAGGAA	CAGGACTTCA	TCAACAACCG	GTACCGGGAG	TACCAGTGGG	2280
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Seq ID NO: 260 Protein sequence  
Protein Accession #: NF\_068767.1

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35	SLALSELRFN	DSGIYRCEVQ	HGIDSSDAV	EVKVKGVVFL	YREGSARYAF	SFSGAQEACA	180
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	DPDDLVDVYC	YADDLNGLF	LGDPPKILTL	EEARAYCQER	GAEIATTGQL	YAAWDGGLDH	300
	CSPGWLADGS	VRYPIVTPSQ	RCGGGLPGVK	TLFLFPNQTG	FPNKHRSFNV	YCFRDSAQPS	360
	AIPEASNPAAS	NPASDGLLEAI	VTVTETLEEL	QLPQEATESE	SRGAIYSIPI	MEDGGGSSST	420
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	GENCVGMPVH	DQQWSDVPC	NYHLSYTKM	GLVSCGPPE	LPLAQVFGRG	RLRYEVDTVL	840
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Nucleic Acid Accession #: NM\_004386.1  
Coding sequence: 2..3967

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Protein Accession #: Eos sequence

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ATTGTGACTT TATAGCTTAA ACTGGAGCTG TCTGAACCTG TGGTCAAGCT CAAGAGCCAG 2400
CAGGGGGAGC AGCAAACTC

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Seq ID NO: 268 Protein sequence  
Protein Accession #: AAC50426.1

1 11 21 31 41 51  
| | | | |

MIEDSGKRGN TMAERQFLFA EMRAQDLDR IRLSTYRTACK LRFVQKKCNL HLVDIWNVIE 60  
 ALRENALNNL DPNTLNVSRL LEAVLSTIFY QLNKRMPTTH QHVEQSISL LNFLLAALPD 120  
 PEGHGKISVF AVKMALATLC GGKIMDKLRY IFSMISDSSG VMVGRYDQF LREVLKLPTE 180  
 VLEGPSFGYT EQSARSCFSQ QKVKTLNGFL DTLMSDPPPQ CLVWLPLLHR LANVENVFHP 240  
 VECYSCHSES MMGFYRCQQ CHNYQLCQDC FWRGHAGGSH SNQHQKEYT SWKSPAKKLT 300  
 NALSKSLSCA SSREPLHPMF PDQPEKPLNL AHIVDTWPPR PVTSMNDTLF SHSVPSGSSP 360  
 FITRSMLESS NRDDEEHLRI ARYAARLAAE SSSSQPPQQR SAPDISFTID ANKQQRQLIA 420  
 ELENKNREIL QEIQRLRLEH EQASOPTFEK AQQNPTLLAE LRLLRQRKDE LEQRMSALQE 480  
 SRRELMVQLE GLMKLLKEEE LKQGVSVVPY CRS

Seq ID NO: 269 DNA sequence  
 Nucleic Acid Accession #: NM\_001276.1  
 Coding sequence: 127..1278

1 11 21 31 41 51  
 AGTGGAGTGG GACAGGTATA TAAAGGAAGT ACAGGGCCTG GGAAGAGGC CTGTCTAGG 60  
 TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCCTGCCCTG CTCTGCTGCA 120  
 GCCAGAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGTG GCTCCAGTGC 180  
 TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240  
 GGGAGCTGCT TCCAGATGTC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300  
 GCCAATATAA GCAACGATCA CATGACACCC TGGGAGTGGG ATGATGTGAC GCTCTACGGC 360  
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTGC TGTGGGAGGA 420  
 TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480  
 TTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540  
 TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCTAATCAA GGAATGAAG 600  
 GCGCAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGTCTAG CGCAGCACTG 660  
 TCTGCGGGGA AGGTCAACAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG 720  
 GATTTCAATTA GCATCATGAC CTACGATTTT CATGGAGCCT GGCCTGGGAC CACAGGCCAT 780  
 CACAGTCCCC TGTTCCGAGG TCAGGAGGAT GCAAGTCTCT ACAGATTCAG CAACACTGAC 840  
 TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC 900  
 CCCACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGCTGTGAG AGCCCCAATC 960  
 TCAGGACCGG GAATTCACAG CCGGTTCAAC AAGGAGGCAG GGACCCCTGC CTACTATGAG 1020  
 ATCTGTGACT TCCTCCGCGG AGCCACAGTC CATAGAACC TCAGCCAGCA GGTCCCCCTAT 1080  
 GCCACCAAGG GCAACCAAGT GGTAGGATAC GACGACCAGG AAAGCCTCAA AAGCAAGGTG 1140  
 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200  
 TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260  
 GCACTCGCTG CAACGTAGCC CTCTGTTCTG CACACAGCAC GGGGGCCCAAG GATGCCCGCT 1320  
 CCCCCTCTGG CTCACGCTGG CCGGGAGCCT GATCACTGCG CCTGCTGAGT CCCAGGCTGA 1380  
 GCCTCAGTCT CCTCCCTCTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA 1440  
 GCCTCTGGTG GCAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500  
 GACTCGGGAT TAGTACACAC TTGTTGATGA TTAATGGAAA TGTTTACAGA TCCCAAGGCC 1560  
 TGGCAAGGTC AATTCTTCAA CTCCTGCCCC CTTAGCCCTC CTTATCAAAG GACACCAATT 1620  
 TGGCAAGCTC TATCACCAGG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680  
 TACCCCTGCG AAAGCCAGCT TGAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCTC 1740  
 ACTTCCCTTT CCTAATTTCA CAGCTGCTCA ATAAAGTACA AGAGTTTAAAC AGTGTGTTGG 1800  
 CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCTCCATC 1860  
 TCTTCTGGGT TCCTTCTCT GAGCCTTGGG ACCCCTGAGC TTGCAGAGAT GAAGGCCGCG 1920  
 ATGTT

Seq ID NO: 270 Protein sequence  
 Protein Accession #: NP\_001267.1

1 11 21 31 41 51  
 MGVKASQTGF VVLVLLQCCS AYKLVCIYTS WSQYREGDGS CFPDALDRFL CTHIYSPAN 60  
 ISNDHIDTWE WNDVTLYGML NTLKNRNPNI KTLLSVGGWN FGSQRFKSLA SNTQSRRTPI 120  
 KSVPPFLRTH YPGGLDLAWL YPGRDRKQHF TTLIKEMKAE FIKERQPGKK QLLLSAALSA 180  
 GIVTIDSSVD IAKISQHLDF ISIMTYDFHG AWRGTTGHHH PLFRGQEDAS PDRFSNTDYA 240  
 VGYMLRLGAP ASKLVMGIPT PGRSPTLASS ETGVGAPISG PGIPGRFTKE AGTLAYEYC 300  
 DFLRGATVHR TLGQQVPIYAT KGNQWVGYYD QESVSKVQY LKDRQLAGAM VWALDLDDFQ 360  
 GSFCQDLRF PLTNAIKDAL AAT

Seq ID NO: 271 DNA sequence  
 Nucleic Acid Accession #: NM\_006474.1  
 Coding sequence: 181..669

1 11 21 31 41 51  
 GCTGCCTAGG GTCTGGAAG CTCGGGCACC CTCCTCTCC GGGGCTCCTG CTCACCCOC 60  
 TCGGCCCCCC CCACCGTCGC GCTCCTCCAG GCTGGGCTCG TGGCCGCGST GCTTTTAAT 120  
 TTCCCCCAAG TCAGAACTCT GCTGCTCGGC CCCAGGAGA GCAACAACTC AACGGGAACG 180  
 ATGTGGAAGG TGTCTAGCTC GTCTTCTGTT TTGGGAAGCG CGTCTGCTCG GGTCTGCGCA 240  
 GAAGGAGCCA GCACAGGCCA GCCAAGAT GACACTGAGA CTACAGTTT GGAAGGCGGC 300  
 GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAAGGA AGACCGCTAT 360  
 AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTCGCTAC 420  
 GAGGATCTGC CAATCTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480  
 GCCTCAAAGC TGGCCACCCG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540  
 GTTGAGAAAG ATGTTTGTCT AACAGTGACC CTGTTTGGAA TCATAGTTGG GGTCTTACTA 600  
 GCCATCGGTT TCATTGGTGG AATCATCGTT GTGTTATGCG GAAAAATGTC GGGAGGTGAC 660  
 TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720  
 TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCTG GGAACATTG 780  
 CGGGCCCAAT CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGGA GAAAGACCTT 840

TCACCAGATT TGGTTCTTAA ACTTT

Seq ID NO: 272 Protein sequence  
Protein Accession #: NP\_006465.1

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1      11      21      31      41      51
|      |      |      |      |      |
MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDY 60
KSLTLTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVDGDTQTT 120
VEKDLSTVT LVGIIVGVLL AIGFIGGIIV VVMRKMSGRY SP

```

Seq ID NO: 273 DNA sequence  
Nucleic Acid Accession #: CAT cluster

```

1      11      21      31      41      51
|      |      |      |      |      |
GCGGCCGCCA GCTTGCAAAG CCGAAGTCTG GCCGCGCTCT TCGACTCGCT GCGCCACGTC 60
CCCGGGGGTG CCGAGCGCGC GGGGGGTGAG GTGGCTGCGC CGCGCGCCGG GCTAGGAGGT 120
GCGGCCACTG GGGCGCGCGG AGGGGACGTG GCAGGCCCGC CGGGGGCCAC GCGGATCCCA 180
GGGGCCAGGA AGGTCCCGCT GCGGGCACGC AATCTGCCTC CGTCCTTCTT CACGGAGCCG 240
TCCCGGGCAG GCGCGCGCGG GTGTGGCCCG TCGGGGCGGG ACCTGAGCTT GGGGACCTG 300
GAGAAGGGCG CGGAGGCCGT GAGTTCTTT GAGCTGTGCG GCGCCGACTA CGGCGCCGCG 360
ACGGAGGCGG CAGTCTTTCG TGCCGCGGAG CCTCTCGACG TGTTCGCCCG CGGAGCCTCC 420
GTACTGCGGG GACCCCGGGA GCTGGAGCCC GGCCTCTTTG AGCCGCGGCC GGCAGTGGTG 480
GGAAACCTAC TGTATCCCGA GCCCTGGAGC GTCCCGGGCT GCTCCCGGAC CAAAAGAGC 540
CCCTGACTG CCCTCCGCGG CGGGTTGACC TTGAACGAGC CCTTGAGCCC CCTGTACCCC 600
GCGCTGCGGA ATTTCTCCCG GCGGGGAGGA CGGGCGGGCG CATTGGCTT CTTTCGCCCC 660
CTTCTTCCA GACTGCGCTT TGC

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Seq ID NO: 274 DNA sequence  
Nucleic Acid Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
CAAAGAGGCC GGGCTCCAGC TCCGGGGGTC CCCGCAGTAC GGAGGCTCCG GCGGGGAACA 60
CGTCGAGAGG CTCGGCGGCA AGCAAGACTG CCGCTCCGTG CGCGCGCCGG TAGTCGGGCC 120
CCAGCAGCTC AAAGAACTCC ACGGCTCCCG CGCCCTCTCT CAGGTGCGCC AAGCTCAGCT 180
CGGGCCCGGA CGGGCCACAC CCGCGCGCGC CTGCCCGGGA CGGCTCCGTG AAGAAGGAGC 240
GAGGCAGATT GGTGCGCCGC AGCGGACCTT TCCTGGCCCC TGGGATCGCC GTGGCCCCCG 300
CGGGGCTGCG CAGCTCCCTT CCCGCGCCCC CAGTGCCCGC ACCTCCTAGC CGGCGCGCGC 360
GCGCAGCCAC CTCACCCCCC GCGGCTCGG CACCCCGGGG GACGTGGCGC AGCGAGTCGA 420
AGAGCGCGGC CAGACTTCGG CTTTCAAGC TGGCGCGCCG

```

Seq ID NO: 275 DNA sequence  
Nucleic Acid Accession #: NM\_001118.1  
Coding sequence: 74..1651

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1      11      21      31      41      51
|      |      |      |      |      |
AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTCTG 60
GCCAAGAAGT GTCATGGCTG GTGTCTGTGA CGTTTCCCTG GCTGCTCACT GCGGGGCTG 120
TCCTGGGGGC CGGGGCGAGC TCCGCAAGAG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGTCT GGCCAAGAAG 240
TGTCATGCTC GTGTGCTGTC ACGTTTCCCT GGCTGCTCTC TCCTGCTGTC CTATGGCCCC 300
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCTCTG AGAAGATCCA 360
GAGGGCCAAAT GAGCTGATGG GCTTCAATGA TTCTCTTCCA GGCTGTCTCT GGATGTGGGA 420
CAACATCAGC TGTGTGAAGC CCGCCCATGT GGGTGAGATG GTCTCTGTCA GCTGCCCTGA 480
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCAATT GAGAGTCTGA 540
TTTGTGTGAC AGTAACCTCT TAGATCTCTC AGACATGGGA GTGGTGAAGC GGAAGTGCAC 600
GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTACTTTGAT GCCTGTGGGT TTGATGAATA 660
TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACAGGCT 720
TGCTACAGC ACATCCCTCG TCACCTCTAC CACTGCCATG GTCTCTCTT GTGCTTCCG 780
GAAGCTGCAC TGCACAGCA ACTTCATCCA CATGAACCTG TTTGTGTGCT TCACTGTGAG 840
GCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900
CTTCACTCC ACTGTGGAAT GTAAGGCGGT CATGGTTTTC TTCCACTACT GTGTGTGTCT 960
CACTACTTC TGGCTGTTC TCGAGGGCCT GTACCTCTTC ACTCTGTCTG TGGAGACCTT 1020
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGA CCCCACCTGT 1080
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140
GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT 1200
TAACCTTGTG CTTTTTATTG GCATTATCGT CATCCTGTGT CAGAACTTCT AGTCTCCAGA 1260
CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT 1320
CCCACTATTG GGAATCCACT ACACAGTATT TGCCCTCTCC CCAGAGAATG TCAGCAAAAG 1380
GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCCTTTGTG TGGCTGTTCT 1440
CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAATATGG GAAGCTGGAA 1500
GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACCGACAC CGCTCTCTGG CCAGCAGTGG 1560
GGTGAATGGG GGCACCCAGC TCTCATCTCT GAGCAAGAGC AGCTCCCAA TCCGATGTCT 1620
TGGCTCCCT GCTGACAATC TGGCAACTG AGCCATGCTC CCTT

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Seq ID NO: 276 Protein sequence  
Protein Accession #: NP\_001109.1

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1      11      21      31      41      51
|      |      |      |      |      |
MAGVVHVSLSA AHCACAPWGR GRLRKGRAAC KSAAQRHIGA DLPLLSVGQG WCNPRSVMAG 60

```



5 VVHVSALALL LLPAPAMHS DCIFKKEQAM CLEKIQRANE LMGFNDSSPG CPGMMDNITC 120  
 WKPAHVGMF LVSCPELPRI FNPDQVWETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180  
 SEPPFHYEDV CGFDYESEET GDQDYIYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC 240  
 TRNFHIMNLF VSMFLRAISV PIKDILYAE QDSNHCFIST VECKAVMVVF HYCVVSNYFW 300  
 LFIEGLYLFET LLVETFFPER RYFYWYTIIG WGTPTVCVTV WATLRLYFDD TGCWMDNDST 360  
 ALWWVIKGFV VGSIMVNEVL FIGIIVILVQ KLQSPDMGNG ESSYILRLAR STLLLIPLFG 420  
 IHYTVFAFSP ENVSKRERLV FELGLGSPQG FVAVLYCFL NGEVQAEIKR KWRSMKVNRY 480  
 FAVDFKRRHP SLASSGVNG TQLSILSKSS SQIRMSGLPA DNLAT

10 Seq ID NO: 277 DNA sequence  
 Nucleic Acid Accession #: NM\_004000.1  
 Coding sequence: 36..1193

15 1 11 21 31 41 51  
 AGAAGAAGCT GGCCAAGGAT ATGGGAGCAA CCACCATGGA CCAGAAGTCT CTCTGGGCAG 60  
 GTGTAGTGGT CTGTGCTGCT CTCAGGGGAG GATCTGCCTA CAAACTGGTT TGCTACTTTA 120  
 CCAACTGTGTC CAGGACCGG CAGGAACCGA GAAAATTCAC CCCTGAGAAT ATTGACCCCT 180  
 20 TCCTATGCTC TCATCTCATC TATTTCATCG CCAGCATCGA AAACAACAAG GTTATCATCA 240  
 AGGACAAGAG TGAAGTGATG CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA 300  
 AACTGAAAAT TCTCTGTGCC ATTGGAGGGT ACCTGTTTGG TTCCAAAGGG TTCCACCCTA 360  
 TGGTGGATTG TTCTACATCA CGCTTGAAT TCATTAACTC CATAATCCTG TTTCTGAGGA 420  
 ACCATAACTT TGATGGACTG GATGTAAGCT GGATCTACCC AGATCAGAAA GAAAACACTC 480  
 25 ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTCA GAAGGACTTC ACAAATCCA 540  
 CCAAGGAAG GCTTCTCTTG ACTGCGGGCG TATCTGCAGG GAGGCAATG ATTGATAACA 600  
 GCTATCAAGT TGAGAAACTG GCAAAAGATC TGGATTTCAT CAACCTCCTG TCCTTTGACT 660  
 TCCATGGGTC TTGGGAAAAG CCCCTTATCA CTGGCCACAA CAGCCCTCTG AGCAAGGGGT 720  
 GGCAAGCAGC AGGGCCAAAG TCCTACTACA ATGTGGAATA TGCTGTGGGG TACTGGATAC 780  
 30 ATAAGGGAAT GCCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA 840  
 CACTGGCCTC TGCAGAAACC ACCGTGGGGG CCCCTGCCTC TGGCCCTGGA GCTGCTGGAC 900  
 CCATCACAGA GTCTTCAGGC TTCCTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG 960  
 CCAAGATCAC GCGCCTCCAG GATCAGCAGG TTCCTACGCG AGTCAAGGGG AACCAGTGGG 1020  
 TGGGCTATGA TGATGTGAAG AGTATGGAGA CCAAGGTTCA GTTCTTAAAG AATTATAACC 1080  
 TGGGAGGAGC CATGATCTGG TCTATTGACA TGGATGACTT CACTGGCAAA TCCTGCAACC 1140  
 35 AGGGCCCTTA CCTCTTGTG CAAGCAGTCA AGAGAAGCCT TGGCTCCTTG TGAAGGATTA 1200  
 ACTTACAGAG AAGCAGGCAA GATGACCTTG CTGCTGGGG CCGCTCTCTT CCCAGGAATT 1260  
 CTCATGTGGG ATTCGCCCTG CCAGGCTGGC CTTTGGATCT CTCTTCCAAG CCTTTCCTGA 1320  
 CTTCTCTTGA GATCATAGAT TGGACCTGGT TTTGTTTTC TGCAGCTGTT GACTTGTGTC 1380  
 40 CCTGAAGTAC AATAAAAAAA ATTCATTTTG CTCCAGTA

Seq ID NO: 278 Protein sequence  
 Protein Accession #: NP\_003991.1

45 1 11 21 31 41 51  
 MDQKSLWAGV VVLLLIQGGG AYKLVCFYTN WSQDRQEPGK FTPENIDPFL CSHLIYSFAS 60  
 IENNKVIKD KSEVMLYQTI NSLKTNPXL KILLSIGGYL PGSKGFHFMV DSSTSRLEFI 120  
 NSIILFLRNH NFDGLDVSNI YPDQKENTHF TVLIHELAEA FQKDFTKSTK ERLLLTAGVS 180  
 50 AGRQMIDNSY QVEKLAKDLF FINLLSFDHF GSWEKPLITG HNSPLSKGWQ DRGPSSSYNV 240  
 EYAVGYWIHK GMPSEKVVMG IPTYGHSEFTL ASAETTVGAP ASGPGAAGPI TESSGFLAYY 300  
 EICQFLKGAH ITRLDQQVVP YAVKGNQWVG YDDVKSMTK VQFLKXNLNLG GAMINSIDMD 360  
 DFTGKSCNQG PYPYLVQAVKR SLGSL

55 Seq ID NO: 279 DNA sequence  
 Nucleic Acid Accession #: NM\_015166.1  
 Coding sequence: 116..1249

60 1 11 21 31 41 51  
 TGCTGGAAGT CCTCACCCA GAGACCAAGT CTCCCAACGG CAGAGCAGCG GGGGAGATAA 60  
 AGAACTGGTG ACAGTGGCT GTACATTGAG CACAGCTGTG GTGTCCCAA GTGCCATGAC 120  
 CCAGGAGCCA TTCAGAGAGG AGCTGGCCTA TGACCGGATG CCCAGCTGG AGCGGGGCGG 180  
 GCAAGACCCC GCCAGCTATG CCCAGACGCG GAAGCCGAGC GACCTGCAGC TGTGAAGAG 240  
 65 ACTGCCCCCC TGCTTCAGCC ACAAGACGTG GGTCTTCTCT GTGCTGATGG GGAGCTGCCT 300  
 CTGGGTGACC TCGGGGTTTT CGCTGTACCT GGGGAACGTG TTCCCGGCTG AGATGGGATTA 360  
 CTTGCGCTGT GCTGCAGGCT CTGTCATCCC CTGGCAATT GTGAGCTTCA CGGTCTCCAG 420  
 GAGGAACGCC AATGTGATTC CCAACTTCA GATATGTTT GTTCCAGCT TTGCTGTGAC 480  
 CACTACGTGT TTAATTTGGT TTGGATGCAA ACTAGTCTGT AACCCATCAG CAATAAACAT 540  
 CAACCTCAAC CTCATCTGCG TGCTCCTGCT GGAGCTGTCT ATGGCGGCCA CGGTGATCAT 600  
 70 CGCTGCACGG TCCAGCGAGG AGGACTGCAA GAAAAAGAG GGCTCCATGT CTGACAGCGC 660  
 CAACATTCGT GACGAAGTGC CATTTCTGCG TCGGTCCTGT AAATCTTACT CAGTGTGCGA 720  
 GGTAAATCCA GGCACTCTCG CGGTCTCGG GGGGATCATT GCCTGAACG TGGATGACTC 780  
 AGTTTCAGGC CCACACCTCT CAGTGACGTT CTTTGTGATC CTAGTGGCCT GCTTTCACAG 840  
 TGCCATTGCC AGTCACTGTT CAGCAGAGTG TCCAGCAAG TGCTTGGTGG AGGTCTTGAT 900  
 75 TGCCATAAGC AGCCTCAGT CTCCGCTGCT GTTCAACGCC TCTGGATATC TGTCATTGAG 960  
 CATCATGAGA ATCGTGGAGA TGTTAAAGGA TTACCGGCCA GCCATAAAC CATCTACGGA 1020  
 TGTGCTGCTG CTGCTGCTGC TGCTAGTGCT CCGCTGCGAG GCGGCTCA ACACGGGCAC 1080  
 CGCCATCCAG TCGGTGCGCT TCAAGGTCAG TGCAAGGCTG CAGGTCATCT CCTGGGACAC 1140  
 CCAGAACCGC CCGAGGAGC GCCTGGCTGG GGAGGTGGCC AGGAGCCCCC TGAAGGAGTT 1200  
 80 CGACAAGAGC AAGACCTGGA GAGCCGCTGT GGTGCAATG GCCCAGTGAC CCCAGACGCG 1260  
 GGAAACCGGG TGCAGCGGCC CAGCTGGGCC CCAAGCATGG AAACGACCAA CCCCTAATCG 1320  
 CCTGAGCTA CTGCTCTTAA CACCTCTTTT CCTTGTGTG AGGGCAAAAC AGGCTGCAGG 1380  
 TGGGGTTTTT ACTTCTTAGG GTAGTTTAAT TTTAAATAG GCCAATGTTG GCTAGTCTGT 1440  
 GCCTCAGTGA GATCAGTCAG CTCGAGTGG CTCCGCTGTC GTACAGCAG GAGCATGGCC 1500

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GCAACTTCCC AGGCGGAGGA AGGGCCCCCG GCTCGGCTTC TTGAGAGCCC CACCCCTGAA 1560  
 CTGGCCCCAG CTCCTCTTCC TGCCCTCTCTC ATGGCTTGGG CTGGAGTGGG CTCTCTGGAC 1620  
 CTGACACAGC TGTGGGTCCC TGCGTCTCCT GCCACTCTG ACCGGGCTTC CTCCTCCAC 1680  
 GCTTAGGGTC TGTCCGGGT ACTCAGTCAG CCCAGTGGGA TCTTACCAC TTCCTGCAA 1740  
 GTTGCACTGC CCCAGGCTC AGGCTGCCCA GCGGCTCTTC CTGGACAGTG AGAGCAGGGC 1800  
 TTGGGCGCTC TGTCTTGCC CGGGAGCCGC AGGGGCCCCCT CCTCCAGAGC CTGGGCGCAA 1860  
 GCGACACAGG CTGCGCTGC TCTCCAGGT GAAATCCCA CCAGTCCAGC CCGGGTCGCC 1920  
 TGCCCTGTCT CCTACTTAG ACCCAGTCAT TCTAGAGGGA TCCACCGCCA CACTGGCCGG 1980  
 CCCAGTCCT GGTGTCTGT ATGCCAGCT TGGAGTGCCA CGTGGCCGCT GCCACGTCC 2040  
 CGGCACTGT CATGCCAGC TTGGAGTGCC ACATGGCCGC TGCCACGTC CCGGGCACTG 2100  
 TCATGCCAG CTGGAGTGC CAGTGGCCG CTGCTGTGAC AGGCAGTGT CTGGGGGTG 2160  
 GGCTGTCAT CAAGGCTTTG TAAACCGGCT GGACCACTG TCCCTGGCCC CAGTGACCGG 2220  
 GGAAGCTGA GCCCTCCCT CTGTGTTTG CTCCATTAC TCAAAATGCA GGACAGATCA 2280  
 GGTACAGACC CAGGAATTC CACAGTTCA CCCAGGCCC TCTACCTCT AGCAAGTACT 2340  
 TTGTCTTAG CCTCACTAG AAGGCCCCAG GGCAGCGTC TTCTCATCT CCGCTGTTTT 2400  
 GGGTCTTAG GTTACAGCCC AGGCGGTAC TGCCCACTG CCAGGTGCA GGGACAGTTG 2460  
 GGTGTGAGAA TAACATGCG TTTGGGTAG GCCATGCCA GGAGTGGGT TCCCTGCGTC 2520  
 TCCCTGCTCC GCGGGGCGCT GGTCTCTCC AGCTGACGC AGTAAATCCA CAGTGAGTTG 2580  
 GGGCACTGT GAACTGGA TGTGTACT TTGATAATTA CTTTCCAGCA GGTGTTTTCC 2640  
 TTCACATGG TTTTGTCTT TTCTTCTGA TCTGAGAAGA CATGAACGT TTCTCTTAC 2700  
 CGCGGTGGG TGTATTGACT GGTCCCAT GGGCTGCTGG AAAGGCCCG AGATGCATCT 2760  
 GTGGCTGGG GCCATCAAGA TCAAGAAC AGGAGGCTG GGAGATGCAG CTGGATGGG 2820  
 CGGCTGCGG GCGGCTCCAG GGGGTTTGG GACCTCCCA GGTTCCTCC TGCGGAACAG 2880  
 GAGTACTCT GGTGCGAAT ATACCTTCAT GGTGTTTATG ACAAGTGGAA TCATTATTTT 2940  
 CAACATTGA AGGGGATGC AGGCAAGACA CCTTCCAGC TGCTCTAGA GGGGACAAAG 3000  
 CAGGCCCTCT CTGCACTCT CGGCAGTCC GGAAGGAC AGTCAGGGG CGGGCAAAACA 3060  
 CTTTGCCAC AGCCCCAAC AAGCGCCACC GTGGGAGAG AGAGGCTGCT GTCACTGGTA 3120  
 CGGATGCAG ACCCCACCT GTCTGAGGC CACCCCACT TCCCTGACG TTTGAGGCTG 3180  
 GCGGGGTCTG CTCTGGGAA TGGGGTGGG GCCACAGGA CGACCCGGG CGGGCTGATG 3240  
 TCTTCTTGG GGCAGACCAG AGAGCTCAAG TTTGAGTCA AGAATTAGG ACTTGAACG 3300  
 TTTTGTCTG CTGCACTTT CTTATTTCT TATTTTAGAG CGCTTAAAA ATCCGAAAA 3360  
 ATGGGTTTA AAGAACTGT CTCCTTCAGT CTACATTTT GTTTAATACG CTGAGCAAT 3420  
 AAGCGTGC TGCAGACGT G

Seq ID NO: 280 Protein sequence  
 Protein Accession #: NP\_055981.1

40  
45

1 11 21 31 41 51  
 MTQEPFREEL AYDRMPTLER GRQDPASYAP DAKPSDLQLS KRLPPCFSHK TWVPSVLMGS 60  
 CLLVTSQFSL YLGNVFPALM DYLRCAAGSC IPSAIVSFTV SRRNANVIPN FQILFVSTFA 120  
 VTTTCLIWFG CKLVLPNSAI NINFMILL LLELLMAATV IIAARSEED CKKKKGSMSD 180  
 SANILDEVFP PARVLKSYSV VEVIAGISAV LGGILALNVD DSVSGPHLSV TFFWILVACF 240  
 PSAIASHVAA ECPFKCLVEV LIAISSLTSP LLFTASGYLS PSIMRIVEMP KDYPPIAKPS 300  
 YDVLILLILL VLLQLAGLNT GTAIQCVRFK VSARIQGAWS DTQNGPQERL AGEVARSPK 360  
 EFDKEKAWRA VVVQMAQ

Seq ID NO: 281 DNA sequence  
 Nucleic Acid Accession #: NM\_004518.1  
 Coding sequence: 43..2577

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60  
65  
70  
75  
80

1 11 21 31 41 51  
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	TGGCAGCCAT	CACAGGAGGG	GGCTCTACCA	GATGCCAAGG	TGCCCCGGTG	TCTGTATGGG	4620
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	GAGGGCTTCT	CAGAGGGGAC	ACCCCTTGAG	CTGTGGGTCT	GATCACCCCA	AGTCCCGCAC	5040
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	CTCAGTGTCT	CTAGATTCCA	GACCTTGTCT	CCAGAGAGAC	CTGCTGCCGG	AGAGAAGGGG	5160
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Protein Accession #: NP\_004509.1

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Protein Accession #: AAD43757.1

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 ACGGGGATCG CACCAACATT GCGCGAGTGG CAGCGGTGG TCTGGGCACC GGTGCCATCG 2220  
 TGGCATCTCT CATCTGCATC CTATCTCTGC TGACCATGGT CCGTGTCTTT GTCATGTGGA 2280  
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 65 ACCCCAGGCC ACCCCCTAT GACTCCCTGC TGGTCTTCCA CTACGAGGG AGCGGCTCCA 2640  
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 70 GGAGGCCCCC CAATCCACAC GTTGAAGTGT CTAGCATGAG CACCCACCCC CACAGCGCCC 2940  
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Seq ID NO: 286 Protein sequence  
 Protein Accession #: NP\_001785.2

80 1 11 21 31 41 51  
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 VAQTSPPHSG HKPQKGGKVV ALDPSPPPKD TLLPWPQHQH ANGLRRKRK WVIPPINVE 180  
 NSRGPPFQQL VRIRSDKND IPIRYSITGV GADQPPMEVF SIDSMGRMY VTRPMDREEH 240  
 ASYHLRAHAV DMNGKVENP IDLYIYVIDM NDNRPFINQ VYNGSVDEGS KPGTYVMVT 300  
 ANDADDSTTA NGMVRYRIVT QTPQSPSQNM FTINSETGDI VTVAGLDRE KVQYTVIVQ 360

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ATDMEGNLNY GLSNTATAII TVTDVNDNPP EFTASTFAGE VPENRVETVV ANLTVMDRDQ 420  
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AVRYSKLSDP ASWLHINATN GOITTAVALD RESLYTKNNV YEATFLAADN GIPPASGTGT 600  
LQIYLIDIND NAPELLPKEA QICEKPNLNA INITAADADV DENIGPYVFE LPFVPAVRK 660  
NWTITRLNGD YAQLSLRILY LEAGMYDVPI IVTDSGNPPI SNTSIIKVKV CPCDDNGDCT 720  
TIGAVAAAGL GTGAIVAILI CILILLTMVL LPVMMMKRRE KERHTKQLLI DPEDDVRDNI 780  
LKYDEEGGGE EDQDYDLSQL QQPEAMGHVP SKAPGVRRVD ERFPVGAEPQY PIRPMVPHPG 840  
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Seq ID NO: 287 DNA sequence  
Nucleic Acid Accession #: AF152495.1  
Coding sequence: 1..2397

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1 11 21 31 41 51  
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GCGAGCTAC GGAATAGGGA GATAATGAT CATTCCCGAG TTTCTCTAGA CAAAGAAATA 420  
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GACTTGGATG TAGGAACCAA CAGTCTCCAA AATTACAAA TCAGTCCCAA TTTCACATT 540  
CATCTTAAT TACAGACAG TCTCGATGGC ATAATATTAC CACAGCTGGT GCTGAACAGA 600  
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TTGCTCCGGG AGAACAACAG CCGGCGCTG CACATCGGCA GCGTCAGCGC CACAGACAGA 1440  
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COGGGTTGA GCAGCGAGG GCTGGTGGC GTGCTGCTG TGGACGCCAA CGACAACCTG 1680  
CCCTTCGTGC TGTACCCGCT GCAGAACGGC TCCGCGCCCT GCACCGAGCT GGTGCCCGG 1740  
GCGGCGAGC CGGGCTACT GGTGACCAAG GTGGTGGCGG TGGACGGCGA CTCGGGCGAG 1800  
AAGCGCTGC CTCTGTACCA GCTGCTCAAG GCCACGGAGC CGGCGCTGT CCGGCTGTG 1860  
GCGCAATATG GCGAGGTGCG CACCGCCAGG CTGCTGAGG AGCGGAGCG TGCCAAGCAG 1920  
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CACGTGCTCC TGGTGGAGCG CTCTCCAG CCGTACCTGC TGCTCCCGGA GCGGCGACCG 2040  
GCCAGGCCC AGGCGGACT GCTCACGCTG TACCTGTTGG TGGCGTTGCG CTCGGTGTCT 2100  
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Seq ID NO: 288 Protein sequence  
Protein Accession #: AAD43756.1

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LAVRGARVVS KGXQHLQPD RQTGDLLENE KLDREELCGP TEPCVLPPQV LLENPLQFFQ 120  
AELRIRDVND HSPVFLDKEL LLKIPESITP GTTFLIERAQ DLDVGTNSLQ NYTISPNFHF 180  
HLNLQDSLGG IILPQLVLNR ALDREEQPEI RLTLTALDGG SPFRSGTALV RIEVVINDIN 240  
VPEFAKLLYE VQIPEDSPVG SQVAIVSARD LDIGTNGEIS YAFSQASEDI RKTFRLSAKS 300  
GELLRLQKLD FESIQTITVN IQATDGGGLS GTCVVFQVM DLNDNPPELT MSTLINQIPE 360  
NLQDTLIAVF SVSDPDSDGN GRMVCISQDD LPFFLKPSVE NFYTIVISTA LDRETRSEYN 420  
ITITVDFGT PRLKTEHNT VLVSDVNDNA PAFTQTSYTL FVRENNSPAL HIGSVSATDR 480  
DSGTNAQVTV SLLPPQDPHL PLASLVSINA DNHGLFALQS LDYEALQAFE FRVGAADRGS 540  
PALSSEALVR VLVLDANDNS PFVLYPLQNG SAPCTELVPR AAEPGYLVTK VVAVDGDSGQ 600  
NAWLSYQLLK ATEPGLFGVW AHNGEVRTAR LLRERDAAKQ RLNVLVKDNQ EPPRSATATL 660  
HVLLVDGFSQ FYLLLPAPAP AQAQADLLTV YLVVALASVS SLFLPSVLLF VAVRLCRRSR 720  
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Seq ID NO: 289 DNA sequence  
Nucleic Acid Accession #: NM\_018674.1  
Coding sequence: 390..2009

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	GCCCCAACC TGTCCTGTGC CTCTCCCGC TTGCCCTGAG TTTAGAAGAG CAGCCGCTGC 300
	CACCACTGCC ACTCGGGAGG GCACCAGGGC TGCTGGCTAG GGAGGGACAG GGCAGGGAGG 360
	CTCTGGCCAG TCCGAGCAGC CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT 420
	TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTCG 480
10	GGGCTGTGTC CCCTGGAGCA GCGCCCGAG ACCTGGCCAC CTTTGCCAGC ACCAGCAGCC 540
	TGATGGGTGC GGGCCGGGCC TGTGGCCAG GCGCCACGG ACTGCGCAGA ACCCTGTGGG 600
	CACCTGGCCCT ACTCACCTCG CTGGCTGCCT TCCTGTACCA GCGGCTGCGC CTGGCCCGGG 660
	GCTACCTGAC CCGGCTCTAC CTGGTGGCAA TGGACCCCGC TGCCCCAGCC CCAGTGGCGG 720
	GCCTCCGGC TGTCAACCTC TGCAATATCA ACCGCTTCGG GCATTCCGCA CTCAGCGATG 780
15	CCGACATCTT CCACCTGGCC AATCTGACAG GGCTGCCGCC CAAAGACCGG GATGGGCACC 840
	GTGCGGTGCT AGACCGCTAC CCAGAGCCTG ACATGCTAGA CATCTCAAC CGCACTGGCC 900
	ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTGC TCCGCCAGCA 960
	ACTTCTCTGT GGTCTATATC CGCTATGGGA AGTGTACAC CTTCACCGG GACCCGCGGA 1020
	GCTCGCTGCC CAGCCGGGCA GGGGGCATGG GCAGTGGCCT GGAGATCATG CTGGACATCC 1080
20	AGCAGAGGGA GTACCTGCCC ATCTGGAGGG AGACAAATGA GACGTCGTTT GAGGCAGGTA 1140
	TTGCGGTGCA CAGCCACAGC CAGGAGGAGC GCGCTACAT CCACCACTG GGGTTGCGGG 1200
	TGTCCCGAGG CTTCCAGACC TTTGTGTCTT GCCAGGAACA GCGGCTGACC TACCTGCCCC 1260
	AGCCCTGGGG CAACTGCGCG GCAGAGAGTG AGCTCAGGGA GCCTGAGCTT CAGGGCTACT 1320
	CGGCTACAGG TGTGTCTGCG TGCCGGCTGC GCTGTGAAAA GGAGGCCGTG CTTGAGCGCT 1380
25	GCCACTGCCG GATGGTGCAC ATGCCAGGCA ATGAGACCAT CTGCCCAACA AATATCTACA 1440
	TCGAGTGTGC AGACCAACA CTGGAATCCC TGGGTGGGG CCGTGGGGC CCGTGTCTCT 1500
	GCCCCACCCC CTGCAACCTG ACACGCTATG GGAAGAGAT CTCCATGGTC AGGATCCCCA 1560
	ACAGGGGCTC AGCCCGGTAC CTGGGAGGGA AGTACAACCG CAACGAGACC TACATACGGG 1620
	AGAATCTCTT GGTCTAGAT GTCTTCTTTG AGGCCCTGAC CTCTGAAGCC ATGAGAGCAG 1680
30	GAGCAGCCTA TGGCTGTGCA GCGCTGTGCG GAGACCTCGG GGGACAGATG GGCCTGTCCA 1740
	TTGGGGCCAG CATCTCAGC TTGCTGGAGA TCTCGACTA CATCTATGAG GTGTCTGGG 1800
	ATCGACTGAA GCGGGTATGG AGCGTCCCA AGACCCCTCC GCGGACCTCC ACTGGGGGCA 1860
	TCTCCACTTT GGGGCTTCAG GAGCTGAAGG AACAGAGTCC CTGCCGAGC CTGGGCGGAG 1920
	CGGAGGGTGG GGGGCTCAGC AGTCTGCTCC CCAATCACCA CCACCCACAC GGTCCCGGAG 1980
35	GAGGTCTCTT TGAAGATTTT GCTTGTCTAG ACGGTGCTGT GACTGAAAGG ACCCAGGAGT 2040
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	GCTGCTTTGC ACAAGGTGCC TTCTTGTCCA CACCCCTTAT CCCCAGGCTG GTGCCCGGGG 2220
	AGGGCTGGAG ACCAGGCCAT GGGCCCTCAC GGAGAGGAAG GGAAGGAAGG AGAGGGGAGG 2280
40	GGAGGATAGA GCCATCCCA GCGGGGAGG GGGAGCCCTC GTTACATTTG TAAATATTTA 2340
	GGGAAGCCG GGTGGGGGGA GGGGATACAG ATGTAGAAGG TGGGTAGGGC TACAGGGGTG 2400
	GGTGATTAGG GGACAGCCAG GGTCCAGGCC CCAATGTCTC CAGGATAGGG AGAGCCCCAG 2460
	GACTCAGGAG TGCTGGGCTG GTCTACTTTC CTGCCCTCT CCAGGCCCAG CTCCCCCTCT 2520
	GGCAGGGGGA GAGGATGGCC CAGCAGGCTT GCGCCAGCTC CAGTTCCTCC CAGCACCAGC 2580
45	CCACCCCTTA GAGTCCCTTC TATAGGAGG GGCAGGAGA CCTTCAGAC TTCGGCTGAG 2640
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Seq ID NO: 290 Protein sequence  
Protein Accession #: NP\_061144.1

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55	NFRHRSALSD ADIFHLANIT GLPPKDRDGH RAAGLRYPEP DMVDILNRTG HQLADMLKSC 180
	NFGSHHCAS NFSVVYTRYG KCYTFNADPR SSLPSRAGGM GSGLEIMLDI QOEYLPINR 240
	ETNETSFEAG IRVQIHSQEE PPYIHLQGFV VSPGFQTFVS QOEQLTYLP QPWGNCRAS 300
	ELREPELQV SAYSVSACRL RCEKEAVLQR CCRMVHMPG NETICPPNIY IECADHTLDS 360
60	LGGPELQPCF CPTPCNLTRY GKEISMVRIP NRGSARYLAR KYNRNETYIR ENPLVLVDFP 420
	EALTSEAMEQ RAYGLSALL GDLGGQMLF IGASILTLE ILDYIYEVSW DRLLKRVWRRP 480
	KTPLRTSTCG ISTLGLQELK EQSPCPSLGR AEGGVSSLL PNHHHPGPP GGLFEDFAC

Seq ID NO: 291 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 62..895

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70	CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACACAG 180
	AGAAGCACGG TCTGGCAAT ACAAAGCTCAC CTACGCAGAA GCTAAGCGCG TGTGTGAATT 240
	TGAAGCGCGC CATCTGCCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAA TTGGATTCTA 300
	TGTCTGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATG TGAAGCCAGG 360
75	GCCCACTGT GGAATTGGAA AAAGTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
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80	TGATGTCCAT GGTCTTGTGG GAAGATACTG TGGAGATGAG CTTCCAGATG ACATCATCAG 720
	TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
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	TACTACTTCT ACTGGAATA AAAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAA 900
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Seq ID NO: 292 Protein sequence  
Protein Accession #: Eos sequence

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DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKLFL SDASVTAGGF 240  
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Seq ID NO: 293 DNA sequence  
Nucleic Acid Accession #: NM\_007115.1  
Coding sequence: 69..902

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TTGTATTTGT GGTATGTGA TATATGTACC TATATGTATT TGCATTGAA ATTTTGGAA 1200  
CCTGCTCTAT GATACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260  
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Seq ID NO: 294 Protein sequence  
Protein Accession #: NP\_009046.1

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DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKLFL SDASVTAGGF 240  
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Seq ID NO: 295 DNA sequence  
Nucleic Acid Accession #: NM\_001218.2  
Coding sequence: 116..1180

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CAGCCCGGCC CCAGTGAACG GTTCCAAGTG GACTTATTTT GGTCTTGATG GGGAGAAATG 240  
CTGCTCCAGG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCCATAG ACCTGCACAG 300  
TGACATCCTC CAGTATGACG CCGAGCTCAC GCCCTCGAG TTCCAAGGCT ACAATCTGTC 360  
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GGGCATCATC CTCTCACTGG CCTGGGCTGG CATTCTTGGC ATCTGTATTG TGGTGGTGGT 1080
GTCCATTGCG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA 1140
CAAGCCAGCC ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCCGGA GCTCCCGGGC 1200
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AAAAACATTT CATCCGGGGC TTTGCCAGAG CGTGCTTTCA AGTGTCTTGG AAAGTCTGCT 1560
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CTTTAATCTG CACCTTACAA CTCGGGGACA AATGGGGACA GGAAGGATCA AGTTGTAGAG 1740
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CACTTCTGCA GGATCCCTAC TGCCAACCTG GAATGGAGAC TTTTATCTAC TTCTCTCTCT 2280
CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTC AACTATAAAA GCAGGAGGTT 2340
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CCCTCTGACT CTAAAGATTCT TCTCTCTGG AATCGCTTGA ACCCAGGAGG CGGAGGTTGC 2700
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AAAAAATAAA AAAAA

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Seq ID NO: 296 Protein sequence  
Protein Accession #: NP\_001209.1

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1 11 21 31 41 51
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HWGNPNPDHG SEHTVSGQHF AAEHLIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSFN 180
PSYDKIFSHL QHVRYKQGEA FVPGFNIEEL LPRTAEYR YRGLSTTPPC NPTVLWTVFR 240
NPVQISQEL LALLETALYCT HMDDPSPREM INNFRQVQKF DERLVYTSFS QVQVCTAAGL 300
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Seq ID NO: 297 DNA sequence  
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Coding sequence: 377..1582

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1 11 21 31 41 51
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GACAAGAAGA CCGGCATCAT CTGCGCCAC CTGTAGCTGG CCATTGCGAA CGGCGAGGAG 180
CTTAACAAAG TGCTGGGCGA AGTCACCATC GCGCAGGGGG GTGTCTCTGC CAACATTTCAG 240
GGCGTGTCTC TGCCCCAGAA GACCAAGAGC CACCACAAGG CCAAGGGTGA AAACCATTTCA 300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAGC CAAGGGAGAG 360
CAAGAAGCCA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT 420
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CCCAAGAGCT CTTCTGCGAA AGTCCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA 660
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GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCAATTAG TAAACCCCTG GGTGGCCCTT 780
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Seq ID NO: 298 Protein sequence  
Protein Accession #: NP\_006623.1

1 11 21 31 41 51  
5 MQVDETLIPR KGPSLCSARY GIALVLHFCN FTIAQNVIM NITMVAMVNS TSPQSQLNDS 60  
SEVLVDSFSG GLSKAPKSLP AKSSILGGQF AIWEKWPPO ERSRLCSIAL SGMLLGCTA 120  
ILIGGFISET LGWPFVFIYF GVGVCVCLL WFWVIYDDPF SYPWISTSEK EYIISLKKQ 180  
VGSSKQPLPI KAMLRSLPIW SICLCGFSHQ WLVTMVVYI PTYISSVYHV NIRDNGLLSA 240  
LPFIWVWIG MVGGYLADFL LTKKFLRLITV RKIATILGSL PSSALIVSLP YLNSGYITAT 300  
10 ALLTLSCGLS TLQSGSIYIN VLDIAPRYSS FLMGASRGFS SIAPVIVPTV SGFLLSQDPE 360  
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Seq ID NO: 299 DNA sequence

Nucleic Acid Accession #: NM\_003058.1

Coding sequence: 145..1812

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20 TCGGGCCCTC CTGCCCTGCG GATCATGCC ACCACCGTGG ACGATGTCCT GGAGCATGGA 180  
GGGAGTTTC ACTTTTCCA GAAGCAAATG TTTTCTCTT TGGCTCTGCT CTCGGCTACC 240  
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25 TACACGGTGC CGGCGCCAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420  
GAGTGGACT GGAACCAAG CACCTTTGAC TCGTGGACC CCTGGCCAG CCTGGACACC 480  
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TCGTCCATG TCAACGAGTT TAACCTGGTA TGTGCCAACT CCTGGATGTT GGACCTATTC 600  
CAGTCATCAG TGAATGTAGG ATTCTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660  
AGGTTTGGCC GTAAGCTCTG CCTCTAACT ACAGTCTCCA TAAATGCTGC AGCTGGAGTT 720  
30 CTCATGGCCA TTTCCCAAC CTATACGTGG ATGTTAATTT TTCGCTTAAT CCAAGGACTG 780  
GTCAGCAAAG CAGCTGGTT AATAGGTAC ATCCTGATTA CAGAAATTTGT TGGGCGGAGA 840  
TATCGGAGAA CAGTGGGGAT TTTTACCAA GTTGCCATA CAGTTGGGCT CTTGGTGCTA 900  
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35 AACTTCTCT TCTGCTCTA TTAAGTGGT ATACCTGAGT CTCCAGGTG GCTGATCTCC 1020  
CAGAATAAGA ATGCTGAAG CATGAGAATC ATTAAGCACA TCGCAAAGAA AAATGGAAAA 1080  
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CCTTCACTT TGAAGTGGT CAGAAGTCT CAGATAAGGA AACATACTAT GATATTGATG 1200  
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50 ACCAAAGTA GAAATCCCTG CACTCATCAC AAAGCCCAT AACTCAACC AAATCTACCC 1920  
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CATTGGACAT TGGTTTTCTG GAGGGTTTTT TTTCCGATCT TTGTATTTT TTAATTTGA 2100  
TTCTTTTCTT TGCAATGCTA GCAACCAGAA TACATAGGGG AACTGTGGGC TAGGCAANA 2160  
55 AAATAGAAAA AGTGTGAAAA ACAGTAAAGT TGGGAGAGGA GCATCTATTT TCTTAAAGAA 2220  
ATAAACACCC NAAACAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 300 Protein sequence

Protein Accession #: NP\_003049.1

1 11 21 31 41 51  
60 MPTTVDDVLE HGGEFHFQK QMFLLALLS ATFAPYVGI VFLGFTPDHR CRSPGVAELS 60  
LRGWSPAEE LNYTVPGPGP AGEASPRQR RYVDWNQST FDCVDPLASL DTNRSRLPLG 120  
65 PCRDGWVYET PGSSIVTEFN LVCAANSWMLD LQSSVNVGF FIGSMSIGYI ADRFRKRLCL 180  
LTTVLNAAA GVLMAISPTY TWMLIFRLIQ GLVSKAGWLI GYILITEFVG RRYRRTVGIF 240  
YQVAYTVGLL VLAGVAYALP HWRNLQFTVA LPNFFFLYY WCIPESPRWL ISQNKNAEAM 300  
RIIKHIAKQI GKSLPASLQR LRLEESTGKX LNPSFLDLVR TPQIRKHTMI LMYNWTSSV 360  
LYQGLIMHMG LAGDNIYLDY FYALVEFPA AFMIILTIDR IGRYPWAAS NMVAGAACLA 420  
70 SVFIPGDLQW LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480  
TPFLVYRLTN INLELPLMVF GVLGLVAGGL VLLLPETKPK ALPETIEEAE NMQRPRNKKE 540  
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Seq ID NO: 301 DNA sequence

Nucleic Acid Accession #: NM\_012206.1

Coding sequence: 52..1131

1 11 21 31 41 51  
75 GTTACCACAG ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT 60  
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80 GTTGGTGGAG AGGCAGGTCC ATCTGTGACA CTACCCCTGCC ACTACAGTGG AGCTGTGACA 180  
TCAATGTGCT GGAATAGAGG CTCATGTTCT CTATTCACAT GCCAAAATGG CATGTCTGG 240  
ACCAATGGAA CCCACGTGAC CTATCGGAAG GACACAGCTC ATAAGCTATT GGGGGACCTT 300  
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5 TGTGCGGTG TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCATTGGAG 420  
 ATTGTGCCAC CCAAGGTCCAC GACTACTCCA ATTGTACAAA CTGTTCCAAC CGTCACGACT 480  
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 AGCGTTCCAA CGACAACGAG CATTCCAACA ACAACAAGTG TTCCAGTGAC AACAAACGGTC 660  
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 10 ACGGCCAATA CCACTAAAGG AATCTATGCT GGAGTCTGTA TTTCTGTCTT GGTGCTTCTT 960  
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 AGTGTTCAT TTAGCAGCCT TCAAAATAAA GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080  
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 15 ATGTCTTTTA GACTCCAAGA CAATTTTCTT GTTTCAGTTT CATCTGGCAT TCCAACATGT 1260  
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20 Seq ID NO: 302 Protein sequence  
 Protein Accession #: NP\_036338.1

25 1 11 21 31 41 51  
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 SLEIVPKVT TPIVITVPT VTTVTRSTTV PTTTIVPTT VPTTMSIPTT TTVPTTMTVS 180  
 TTSVPTTTS IPTTTSVPVT TTVSTFVPPM PLPRQNHPEV ATSPSPQPA ETHPTTLQGA 240  
 30 IRREPTSSPL YSYITDNDT VTESSDGLWN NNQTLFLEH SLLTANTTKG IYAGVCISVL 300  
 VLLALLGVII AKKYFFKKEV QQLSVSFSSL QIKALQNAVE KEVQEDNIY IENSLYATD

35 Seq ID NO: 303 DNA sequence  
 Nucleic Acid Accession #: NM\_001044.1  
 Coding sequence: 129..1991

35 1 11 21 31 41 51  
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 40 AAAGCCACAG CCCGGGCGGC CAGACCAAGA GGAAGAAGC ACAGAATTCC TCAACTCCCA 120  
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 AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTCTCTCT GTCCGTGATT GGTCTTGTCT 360  
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 70 ACGGCTGGG CTGGGTGATC GCCACATCCT CCATGGCCAT GGTGCCCATC TATGGGCGCT 1860  
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Seq ID NO: 304 Protein sequence  
Protein Accession #: NP\_001035.1

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1 11 21 31 41 51
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GQFNREGAAG VKIKICPILKG VGFTVILISL YVGFFYNVII AWALHYLFSS FTTELPHIHC 180
NNSWNSPNCB DAHPGDSGSD SGLNDTFTGT TPAEYFERG VLHLHQSHGI DDLPGRWQL 240
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DSAMGGMESV ITGLIDEFQL LHRHRELFLL FIVLATFLLS LFCVTNGGIY VFTLLDHFAA 480
GTSILEFVLI EAIGVAFWPG VQGFSDDIQO MTGQRPSLYW RLCWKLVSVC PLLFVVVSI 540
VTFRPHYGA YIFPDWAL GWVIATSSMA MVPIYAYKF CSLPGSFREK LAYAIPEKD 600
RELVDGRGEVR QFTLRHLKV

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Seq ID NO: 305 DNA sequence  
Nucleic Acid Accession #: NM\_001216.1  
Coding sequence: 43..1422

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70

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1 11 21 31 41 51
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CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCACAGAGT TGCCCGCGAT GCAGGAGGAT 180
TCCCTCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGCGCAGGA GSATCTGCCC 240
AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGAGGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGATGCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAAGCCGAG 420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
CGCCCTTGCC CCGCGGTGTC CCCAGCCTGC GCGGGCGGCT TCCAGTCCCC GGTGGATATC 540
CGCCCTCAGC GAGGCGCTTC CTGCCCAGGC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG 600
CTCCCGCCGC TCCAGAACT GCGCCTGCGC AACATGGGCC ACAGTGTGCA ACTGACCCCTG 660
CCTCTGGGCG TAGAGATGCG TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGAGCACA CTGTGGAAGG CCACCGTTTC 780
CCTGCGGAGA TCCAGCTGGT TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCGCTG 840
GGGCGCCCGG GAGGCGCTGC GGTGTTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
AGTGCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
CAGGTCCAGG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCG CTACTTCCAA 1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC 1080
CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCTT GTGGGGACCT 1140
GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGACG CTTTGAATGG GCGAGTGATT 1200
GAGGCTCTCT TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCTCCT TTTTGTCTGC 1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
GTGAGCTACC GCCCAGCAGA GSTAGCCGAG ACTGAGCGCT AGAGGCTGGA TCTTGAGAG 1440
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Seq ID NO: 306 Protein sequence  
Protein Accession #: NP\_001207.1

75  
80

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1 11 21 31 41 51
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GEEDLPSEED SPREDPPGE EDLPGBEDLP GEEDLPEVKP KSEEGSLKL EDLPTVEAPG 120
DPQEPQNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
ELLGFQLPFI PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
VEGHRFPAPL VVHLSTAFAP RVDEALGRPG GLAVLAFL EGEENSAYE QLLSRLEBIA 300
EEGSETQVPG LDISALLPSD PSRYPYEGS LITPPCAQGV IWTVPNQTM LSAQLHLTSL 360
DTLWGPDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
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Seq ID NO: 307 DNA sequence  
Nucleic Acid Accession #: NM\_003039.1  
Coding sequence: 76..1581

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GTGCTTGCCC TGGCAACCTT GATAGCTGCC TTTGGGTCAT CCTTCCAGTA TGGGTACAAC 180
10 GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAA TTTACAATGA GACTTACTAT 240
GGTAGGACCG GGAATTTCAT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAAACGTG 300
TCCATGTTTC CATTGGAGG GTTTATCGGA TCCCTCCTGG TCGGCCCTT GGTGAATAAA 360
TTTGGCAGAA AAGGGGCTT GCTGTTCAAC AACATATTTT CTATCGTGCC TGCATCTTA 420
ATGGGATGCA GCAGAGTCGC CACATCATTT GAGCTTATCA TTATTCCAG ACTTTTGGTG 480
15 GGAATATGTG CAGGTGTATC TTCCAACGTG GTCCCCATGT ACTTAGGGGA GCTGGCCCCCT 540
AAAAACGCTG CGGGGGCTCT CGGGGTGGTG CCCAGCTCT TCATCACTGT TGGCATCCTT 600
GTGGCCAGTA TCTTTGGTCT TCGGAATCTC CTTGCAAAAG TAGATGGCTG GCGCATCCTG 660
TGGGGCTGTA CCGGGGCTCC CGGGGCTG CAGCTCCTTC TGCTGCCCTT CTTCGCCGAG 720
AGCCCCAGGT ACCTGCTGAT TCAGAAGAAA GACGAAGCGG CCGCCAGAA AGCCCTACAG 780
20 ACCTGTCGGG GCTGGGACTC TGTGGACAGG GAGGTGGCGG AGATCCGGCA GGAGGATGAG 840
GCAGAGAAGG CCGCGGGCTT CATCTCGGTG CTGAAGCTGT TCCGGATGCG CTCGCTGCGC 900
TGGCAGCTGC TGTCCATCAT CGTCTCATG GCGGCCAGC AGCTGTGCGG CGTCAACGCT 960
ATCTACTACT CCGGAGACCA GATCTACCTG AGCGCGGGG TCGCGGAGGA GCACGTGCAG 1020
TAGTGACAGG CCGGCACCGG GCGCGTGAAC GTGCTCATGA CCTTCTGCGC CGTGTTCGTG 1080
25 GTGGAGCTCC TGGGTGGGAG GCTGCTGCTG CTGCTGGGCT TCTCCATCTG CCTCATAGCC 1140
TGCTGCGTGC TCACTGCAGC TCTGGCACTG CAGGACACAG TGTCTGGAT GCCATACATC 1200
AGCATCGTCT GTGTCTCTC CTACGTCTCA GGCATGCCC TCGGGCCAGG TCCCATACCC 1260
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30 GGCTCGGGC GTTACAGCTT CATTGTCTTC GCGGTGATCT GCCTCTCAC CACCATCTAC 1440
ATCTTCTTGA TTGTCCCGGA GACCAAGGCC AAGACGTTC TAGAGATCAA CCAGATTTTC 1500
ACCAAGATGA ATAAGTGTG TGAAGTGTAC CCGGAAAAGG AGGAAGTCAA AGAGCTTCCA 1560
CCTGTCACTT CGGAACAGT ACTCTGGAGA GGAAGCCAGT GGAGCTGGTC TGCCAGGGGC 1620
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35 ACTCTGATGT GGAATGCAGT CCTCATCTCC AGCCTCCCCA CCCCAGTGGG AACTGTGCAA 1740
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CCGAGTCAA TTAACAGCT GGTCTCTCC TTGTCTGGT CAGCCTTCTG GTGGCTCTG 1860
GTAACGTGGC TCAACCTTGA TGGGTCAACC TTGTGTGGC TCTGTGTAAC ATAACAACAA 1920
40 CAGTTACTAT AGTGGTGAGA TGAAGGAAT CAAATTTTGC CAGAGAACT AACTCGTGG 1980
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GATCCTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAAT GACATCCAGA 2100
AAGCTAGGA ACAGGTTCT GTGGAGACAC TGAGTCAGAA TTCTTATCC AAATTAATTT 2160
GTTAGTGGA AATGGAATTG CTTCTGTGTA GTCAATAAAA TGAACCTGAT CACTTTTC
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45 Seq ID NO: 308 Protein sequence  
Protein Accession #: NP\_003030.1

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50 1 11 21 31 41 51
| | | | |
MEQQDQSMKE GRLTLVLALA TLIAAFSSSP QYGVNVAVN SPALLMQQFY NETYYGRTGE 60
FMEDFPLTL WSVTVSMPPF GFIGSLLVG PLVNFGRKG ALLFNNIFS VPAILMGCSR 120
VATSFELIII SRLVLGICAG VSSNVVPMYL GELAPKNLRG ALGVVPLQFI TVGILVAQIF 180
GLRNLNLANVD GPILLGLTG VPAALQLLL PFPSPRYL LIQKDEAA KKAQLTLRG 240
55 DSVDRVABEI RQEDAEKAA GFISVLKLER MSLRWQLLS IIVLMGGQQL SGVNAIYYA 300
DQIYLSAGVP EEHVQYVTAG TGAVNVMTF CAVFVVELL RRLILLIGFS ICLIACCVLT 360
AALALQDTS WMPYISIVCV ISYVIGHALG PSPIPALIT EIFLQSSRPS AFMVGGSVHW 420
LSNFTVGLIF PPIQEGLPY SFIVFAVICL LTTIYIFLIV PETKAKTPIE INQIPTMMNK 480
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60 Seq ID NO: 309 DNA sequence  
Nucleic Acid Accession #: NM\_001252.1  
Coding sequence: 138..719

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65 1 11 21 31 41 51
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70 ATGGGTGCGT CTTGCGGGCT GCTTTGGTCC CATTTGGTCC GGGCTTGGTG ATCTGCTCG 240
TGGTGTGATC CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCGCTGCGG TCACTTGGGT 300
GGGACGTAGC TGAGCTGCAG CTGAATCACA CAGGACCTCA GCAGGACCCC AGGCTATACT 360
GGCAGGGGGG CCGCAGCTG GCGCGCTCCT TCCTGCTATG ACCAGAGCTG GACAAGGGGC 420
AGCTAGCTAT CATTGTGAT GGCATCTACA TGGTACACAT CCAGGTGAGC CTGGCCATCT 480
75 GCTCCTCCAC GACGCGCTCC AGGCACCACC CCACCACCT GGCCTGGGA ATCTGCTCTC 540
CCGCTTCCCG TAGCATCAGC CTGCTGGTTC TCAGCTTCCA CCAAGTTGT ACCATTGCTT 600
CCGAGCGCT GACGCGCTG GCGGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC 660
TTTTGCTTTC CCGAAACACT GATGAGACCT TCTTTGGAGT GCAGTGGGTG CGCCCTGAC 720
CACTGCTGCT GATTAGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAAA 780
80 AGGTACACCA CAGGGGCCAC CCGGGTTGG GGTGGGAGTG TGGTGGGGG TAGTGGTGGC 840
AGGACAAGAG AAGGCATTGA GCTTTTCTT TCATTTCTT ATTAATAAA
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Seq ID NO: 310 Protein sequence  
Protein Accession #: NP\_001243.1

1 11 21 31 41 51  
 MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL 60  
 5 QLNHTGPQD PRLYVQGGPA LGRSFLHGPE LDKGQLRIHR DGIYMVHIQV TLAICSSTTA 120  
 SRHHPTTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLPSRN 180  
 TDETFFGVQW VRP

Seq ID NO: 311 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..3978

1 11 21 31 41 51  
 15 ATGGTGGGTG AAGGACCCTA CCTATCTCA GATCTGGACC AGGAGGCGCG GCGGAGATCC 60  
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 20 GTAGCAAGGG TGGGTCTCTG GAAGGCCCTC CTGAGCCACG TGGTGTGGAA ATTCCAGAGG 360  
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 25 TTGGTTTTTG AAAACCTAGT GTCCTTCAAG ACATTGACCC ACATCTCTGT TGGGAGGTTG 660  
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 CCAGCCACCA TCCCGATCCT AATGGTCTTT TGTGGCGCGT ACCTCTTTTT CATTCTGGGG 780  
 CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCCGTCCA GATGTTTATG 840  
 GCCAAGCTCT ACTCAGCTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTTCA 900  
 30 ACAATGAATG AGTTTCTGAC CTGATCAGG CTGATCAAAA TGTATGCCTG GGAGAAATCT 960  
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 35 ATGGCTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAGCCCC 1260  
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 40 TTGTGGGTGA GAAAGTTATG TCGTTATCCC GAAGCCGAGC TCCTGGCTTG GAGGTGGCCA 1560  
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 45 ACTTTGGCCT ACCTTTTACA GCAGGCGATG ATCTTTTATG GAAATGTGAG AGAAAACATA 1860  
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 CTCACACAG TTCTCAACTG CGATCAGTCT CTGGTTATGG AAAATGGGAA GGTGATTGAG 3900  
 80 TTTGACAGC CTGAAGTCCT TGCAGAGAAG CCAGATTCTG CATTGCGCAT GTTACTAGCA 3960  
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Seq ID NO: 312 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
MVGEOPYLIS DLDQGRRRS FAERYDPSLK TMIPVRPCAR LAPNVDDAG LLSFATFSML 60  
5 TPVMVGYRQ RLTVDTLPPL STYDSSDTNA KRFRVLWDEE VARVGPKEAS LSHVVMKFQR 120  
TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEFTKVFFW 180  
ALAWAINYRT AIRLKVALLST LVFENLVSKF TLTHISVGEV LNLSSDSYS LFEAALFCPL 240  
PATIPILMVF CAAYAFPIIG PTALIGISVY VIFIPVQMFM AKLNSAFRRS AILVTDKRVQ 300  
TMNEFLTICR LIKMYAWEKS FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360  
10 TLSCHILLRR KLTAFVAFSV IAFNVVMKFS IAILPFSSKA MAEANVLRR MKKILIDKSP 420  
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GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSKAD 540  
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15 NLSGGQRQRI SLARAVYSR QLYLLDDPLS AVDAHVGKHF FECEIKTLR GKTVVLVTHQ 720  
LQFLESCDEV ILLEDEGEICE KGTHKELMEE RGRYAKLIHN LRGLQFKDPE HLYNAAMVEA 780  
FKESPAEREE DAGIIGYLLS LFTVFLFLM IGSAAFSNNW LGLWLDKGRS MTCGPQGNRT 840  
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20 ASLAVGFIL LRIFHRVQE LKKVENVSRS PWFTHITSSM QGLGIHAYG KESCIITYTS 1020  
SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKDW 1080  
PSCGEITFRD QMRVYRNTPT LVLDLNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140  
SGTIFIDEVD ICILSLEDLR TKLTVPQDP VLFVGTVRYN LDFPESHTDE MLWQVLERTP 1200  
MRDTIMKLPE KLQAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMSKTDTL 1260  
25 VQNTIKDAFK GCTVLTIAHR LMTVLNCDHV LVMENGKVIE FDKPEVLAEK PDSAFAMLLA 1320  
AEVRL

Seq ID NO: 313 DNA sequence  
Nucleic Acid Accession #: Z31560  
Coding sequence: 1-966

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CGCAAGATGG CCCAGGAGAA CCCAAGATG CACAACCTCG AGATCAGCAA GCGCCTGGGC 240  
GCCGAGTGGG AACTTTTGTG GGAGACGGAG AAGCGGCCGT TCATCGACGA GGCTAAGCGG 300  
CTGCAGCGC TGACATGAA GGAGCACCCG GATTATAAAT ACCGGCCCCG GCGGAAAACC 360  
40 AAGAGCTCTA TGAAGAAGGA TAAGTACACG CTGCGCGCGG GGCTGCTGGC CCGCGCGGCG 420  
AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCGCGCTGG GCGCGGCGT GAACAGGCG 480  
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45 ATGAACGGCT CGCCACCTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT 720  
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50 ATGTAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAGAAAAA ACGAGGGAAA 1020  
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AAAAA

Seq ID NO: 314 Protein sequence  
Protein Accession #: CAA83435

1 11 21 31 41 51  
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60 RKAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKHP DYKYRPRRKT 120  
KTLMKDKYT LFGGLLAPGG NSMASGVGVG AGLGAGVNR MDSYAHMNGW SNGSYMMQD 180  
QLGYPPHPL NAHGAAQMQP MHRVDVSALQ YNSMTSSQTY MNGSPYYSMS YSQQGTGMA 240  
LGSMSVVK SSSSPFPVT SSSHSRAPC AGDLRDMISM YLPGAEPPEP AAPSRLLMSQ 300  
HYQSGFPVGT AINGTLPLSH M

Seq ID NO: 315 DNA sequence  
Nucleic Acid Accession #: U91618  
Coding sequence: 29..541

1 11 21 31 41 51  
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70 CATGCTACTC CTGGCTTTCA GCTCTTGAG TCTGTGCTCA GATTGAGAAG AGGAAATGAA 120  
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TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGAGTCTT GTAAATAATT TGAACAGCCC 240  
75 AGCTGAGGAA ACAGAGAGA TTTATGAAGA GGAGCTTGT GCAAGAAGGA AACTTCTAC 300  
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TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420  
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80 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540  
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Protein Accession #: AAB50564

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 Protein Accession #: NP\_000219.1

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	CCTTCTAAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTTGGAAGA	GTGCTTCAGG	240
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	TACACAGCCA	GGGCTGTTGC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
	GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
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	GAATCTGATG	CAGCAGAGAA	CTATCTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
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Seq ID NO: 327 DNA sequence  
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	AGCCAAGGTT TTGTGGTATC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAACCAATT	2400
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	ACCCCTGGAT CCTCGAGGGG AGGACACACG GAGGTGGACA ACTGCAGATA CACTTACTCG	2520
	GAGTGGCACA GTTTTACTCA ACCCGTCTC GGTGAAAAAT TGCATCGATG TAATCAGAAT	2580
	GAAGACCGCA TGCCATCCCA AGATTATGTC CTCACITATA ACTATGAGGG AAGAGGATCT	2640
	CCAGCTGGTT CTGTGGGCTG CTGCAGTGAA AAGCAGGAAG AAGATGGCCT TGACTTTTAA	2700
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	CCAATTATA TTTTAAAGC CAGTTGTGTC TTATCTTTTC CAAAAGTGTA AAAATGTTAA	2940
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30	TCCTTTTCTT TTTTACGGAT ATTTTAGTAA TAAATATGCT GGATAAATAT TAGTCCAACA	3060
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	ATAAACCAAG AATATTGAGT ATCACTATGT GAAGAAAGTT TTGGAAGAAGA AACAATGAAG	3180
	ACTGAATTAA ATTAATAAAT TTGCAGCTCA TAAAGAATTG GGACTCACCC CTACTGCACT	3240
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	CTTTTCTCTA GGCTTGGGAC TGCTTTTCC TTTCTCAGGC CAATGGCAAC TGCCATTGTA	4440
	GTCCGGTAGG GGATCAGCCA ACCTCTTCTC TATGGCTCAC CTTATTGGA GTGAGAAATC	4500
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	GTGTGTCAGA ACAAACAAGG CATTCTAGG AATTGTGTGA TTCTTCTGCG AGCCCTCTCT	4620
	CTGGGCCTTA AGAAGGTCTA TGAATTAAAT GCCTATCTAA AATTCTGATT TATTCTTACA	4680
	TTTTCTGTTT TCTAATTGGA CCCTAAAATC TATGTGTTTT AGACTTAGAG TTTTATTGCT	4740
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	CAAGAAAAATA TATTTTAAA GCTTTCAATT TTCCCCAGT GAATGATTGA GAAATTTTAA	5640
	TGTAATAATA CAGAATGTT TTTCTTACT TTATAAGGAA CGAGCTGTCT AAAATGCAGT	5700
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	TGCTTTTAAA GAACTTGGC TGCTTAAAAA AAGCAAAAAT TGGATGCATA AAGTAATATT	5820
	TACAGATGTG GGGAGATGTA ATAAACAAAT ATTAACCTGG TTTCTGTGTT TTGCTGTATT	5880
	TAGAGATTAA ATAACTCTAA GATGATCACT TTGCAAAATT ATGCTATTGG CTGGCATGGA	5940
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	ATTATCAAA TGTGACATC ATTAATATAT ATTGTAATGT TGGGAAGAGA TCACTATTTT	6060
	GAAGCACAGC TTTACAGAT ACTATCTATG ATACATATGT ATAATAAATT TTGATCGGGT	6120
	ATTAAAGTA TTAGAAGGTG GTTATAATTG CAGAGTATTC CATGAATAGT ACAGTGACAC	6180
	AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA	6240
	GGCAATTATG CAGTCTTATG TCTGCCACTT ACAGGATAGA TAATGCTGTA ACTTTAATGA	6300
	CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCAATGCAGG	6360

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Seq ID NO: 328 Protein sequence  
Protein Accession #: NP\_001932.1

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1 11 21 31 41 51
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ADLIRSSDPD PRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS 120
KTRHRTRETVL RRAKRWAPI PCSMQENSLG PFPLFLQOVE SDAQNYTVF YSISGRGVDK 180
EPLNLFYIER DTGNLFCTRP VDREYDVDFD LIAYASTADG YSADLPPLPL IRVEDENDNH 240
PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDMHTRL KYSILQOTPR SPGLFSVHPS 300
TGVIITVSHY LDREYVDKYS LIMKVQMDG OFFGLIGTST CIITVDSND NAPTFRQNAV 360
EAFVEENAFN VEILRTPIED KDLINTANWR VNFTILKNE NGHPKISTDK ETNEGVLVSV 420
KPLNVEENRQ VNLEIGVUNE APPARDIPRV TALNRALVTV HVRDLDEGPE CTAAQYVRI 480
KENLAVGSKI NGYKAYDPEN RENGNGLYKK LHPDKGWITI DEISGSIITS KILDREVETP 540
KNELYMITVL AIDKDRSCT GTLAVNIEDV NDNPPFELQE YVVICPKMG YTDILAVDPD 600
EPVHGAPFFX SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQETIPI TVKDRAGQAA 660
TKLLRVNLCE VEILRTPIED SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATGK 720
KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTNNSS QGFCGTMSGG MKNGGQETIE 780
MMKGGNQTLE SCRAGGHHHT LDSCRGGHTE VDNCRYTYSE WHSFTQPRLG EKLHRCNQNE 840
DRMPSQYVYL TYNVEGRGSP AGSVGCCSEK QEEDGLDFIN NLEPKFITLA EACTKR

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Seq ID NO: 329 DNA sequence  
Nucleic Acid Accession #: NM\_016583.2  
Coding sequence: 72..842

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CCATGGCCCA GTTGGAGGCG CTGCCCGTGC CCTCGGACCA GACCCTGCCCT TTGAATGTGA 180
ATCCAGCCCT GCCCTTGAAT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
ATGGCCTGCT GTCTGGGGGC CTGTGGGGCA TTCTGGAAAA CCTTCGCTC CTGGACATCC 300
TGAAGCCTGG AGGAGGTACT TCTGGTGCC TCCTTGGGGG ACTGCTTGGA AAAGTGACGT 360
CAGTGATTCG TGGCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
TAAAGCTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGTGCC 600
TTGTGACTCG CACCATTCC CCTGGAAGCC TGCAAATTC TCTGCTTGAT GGACTTGGCC 660
CCTCCCATTC TCAAGGTCTT CTGGACAGCC TCACAGGAT CTTGAATAAA GTCTGCGCTG 720
AGTGTGTGTA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGC TTGGACATCA 780
CCTGTGTGTA TGACATGTGT AACATGCTGA TCCACGGACT ACAGTTGTG ATCAAGGTCT 840
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GCCCATGTGC TGAAGATGTA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCTT 960
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AAAAAAAAA AAAAAAAAAA AAAAAAAAAA

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Seq ID NO: 330 Protein sequence  
Protein Accession #: NP\_057667.1

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1 11 21 31 41 51
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VQSPDGHRLY VTPLGKIKL VNTPLVGASL LRLAVKLDIT ABILAVRDKQ ERIHLVLGDC 180
THSPGLQIS LLDGLGLPLI QGLDLSLTGI LNKVLPPLVQ GRVCPVNEV LRGLDITLVH 240
DIVNMLHLGL QFVIKV

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Seq ID NO: 331 DNA sequence  
Nucleic Acid Accession #: NM\_004363.1  
Coding sequence: 115..2223

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1 11 21 31 41 51
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TCTCCCTCGG CCCCTCCCCA CAGATGTTGC ATCCCTGGC AGAGGCTCCT GCTCAGAGCC 180
TCACCTCTAA CCTTCTGGAA CCGGCCACCC ACTGCCAAGC TCACATATGA ATCCAGCCG 240
TTCAATGTGC CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
TTTGCTTACA GCTGTATCAA AGGTGAAAGA GTGGATGGCA ACCGTCAAT TATAGGATAT 360
GTAATAGGAA CTCACAGAGC TACCCACAGG CCGCATACA GTGGTCGAGA GATAATATAC 420
CCCAATGCAT CCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCTA 480

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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540  
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 CAGAGCCTCC CCGTCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720  
 5 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAATGTG AAACCCAGAA CCCAGTGAGT 780  
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 10 GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020  
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 15 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAAT AAGTGTGTAG 1320  
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 TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440  
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 20 GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCCAAG 1620  
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 25 GACCCAGTCA CCTGTGATGT CCTCTATGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920  
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Seq ID NO: 332 Protein sequence  
 Protein Accession #: NP\_004354.1

1 11 21 31 41 51  
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 50 HLFPGYSWKY ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIONDTGEY 120  
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 NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGPDAP 240  
 TISPLNTSYR SGENLNLSYR AASNPPAQYS WFNVTGTFQS TQELFIPNIT VNNSSGYTCQ 300  
 55 AHNSTGLNLR TTVTITVYA EPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVWNN 360  
 QSLFVSPRLQ LSNDRILTL LSVTRNDVGP YEOGIQNELS VDHSDPVILN VLYGPDDEPTI 420  
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Seq ID NO: 334 Protein sequence  
 Protein Accession #: NP\_008883.1



1 11 21 31 41 51  
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 FLKQMLERYQ NNSPPNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAPRTENN 180  
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10 Seq ID NO: 335 DNA sequence  
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1 11 21 31 41 51  
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 20 TCAATGGACA AGATCCGCTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300  
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 25 CGGTCTCTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCATCTGGT CTAAGTCCC 540  
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30 Seq ID NO: 336 Protein sequence  
 Protein Accession #: NP\_002629.1

1 11 21 31 41 51  
 35 MRASSFLIVV VFLLIAGTLVL EAAVTGVVPVK GQDITVKGRVP FNGQDPVKQ VSVKQGDVKV 60  
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Seq ID NO: 337 DNA sequence  
 Nucleic Acid Accession #: NM\_001793.2  
 Coding sequence: 71..2560

1 11 21 31 41 51  
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 45 CTGGCTGCAG TGCCCGGCTT CCGAGCCGTG CCGGGCGGTC TTGAGGGAGG CTGAAGTGAC 180  
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 CTGCCCTGGG CAGAGGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300  
 TGCGGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360  
 ATCCAAAGCT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420  
 TGAATAATGC AAGGCTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480  
 50 AGACACCAAG ATTTTCTACA GCATCAGGGG GCGGGGGGCA GACAGCCCCC CTGAGGGTGT 540  
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTTGAAT AAGCCACTGG ACCGGGAGGA 600  
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGTGCTCT CAGTGGAGGA 660  
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAAATGAC CACAAGCCCC AGTTTACCCA 720  
 55 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTTCTG TGATGCAGGT 780  
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTGG CTACTCCAT 840  
 CCATAGCCAA GAACCAAGG ACCCACAGCA CCTCATGTTT ACCATTACCC GGAGCACAGG 900  
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960  
 CATCCAGGCG ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020  
 60 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTGACCCC CAGAAGTACG AGGCCCATGT 1080  
 GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140  
 CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATT 1200  
 TACCATCACC ACCCACCTGT AGAGCAACCA GGGCATCTCT ACAACCGAGA AGGTTTGGGA 1260  
 TTTTGAGGCG AAAAACCAGC ACACCTGTGA CGTTGAAAGT ACCAACGAGG CCCCCTTTGT 1320  
 65 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGTCCAC GTGGAGGATG TGAATGAGGC 1380  
 ACCTGTGTTT GTCCCACTCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440  
 GCGTGTGTGT GTCTACACTG CAGAAGACCC TGACAGGAGG AATCAAAGA TCAGCTACCG 1500  
 CATCTGAGA GACCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560  
 TGTGGGCACC CTCGACGCTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620  
 70 GGTCTTGGCC ATGGCAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680  
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC GTTCAGATCA CCATCTGCAA 1740  
 CCAAGCCCTT GTGGCCAGG TGCTGAACAT CAGGACAAG GACCTGTCTC CCCACACCTC 1800  
 CCCTTTCCAG GCGCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860  
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920  
 75 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980  
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAGGGAG GTTTCATCT 2040  
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGCTGC TTTTGTGTT 2100  
 GAGAAGAGAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGGTGACAA 2160  
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220  
 80 GCTCCACCGA GGTCTGGAGG CCAGGCGGGA GGTGGTCTC CGCAATGACG TGGCACCAAC 2280  
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGCAACTT 2340  
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCCGCCCT ACACACCTC 2400  
 CTGTGGTGTG GACTATGAGG GCAGCGGCTC CGAGCGCGCG TCCCTGAGCT CCCTCACCTC 2460  
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGGCTTCAA 2520  
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTGCCC TGCAGGGCTG 2580

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GGGACCAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640  
GACTTCGGAG CTGTGCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700  
ACGTTAGAGT GGTGCTTCCT TTAGCCTTTC AGSATGGAGG AATGTGGGCA GTTTGACTTC 2760  
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCTCAG AGCCCAAGTT TCCAGAAGCC 2820  
TCTTACCTGC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCTGCT GTGACTGACC 2880  
TACAGTGGAC TTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940  
TTTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000  
GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTCCAGAC CCAATGCCT CCCATTGCGA 3060  
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGCC CCTTATTTT TATTTTCCCT 3120  
GTTCGTGTG TATAGATGAA GGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180  
TAAAGAAAT TTTCCAGAA AAAAA

Seq ID NO: 338 Protein sequence  
Protein Accession #: NP\_001784.2

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1 11 21 31 41 51  
MGLPRGPAS LLLLQVCWLQ CAASEPCRAV PREAEVTLEA GGAEQEPGQA LGKVPMGCPG 60  
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDV VAPISVPENG 120  
KGPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLNL KPLDREEIAK 180  
YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
DEDDAIYTN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIOA 300  
TDMGDSGSTT TAVAVVEILD ANDNAPMDFP QKYEAHVPEM AVGHEVQRLT VTDLDAPNSP 360  
AWRATYLMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDK NQKISYRILR 480  
DPAGWLANDP DSGQVTAVGT LDREDBQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLD 540  
VNDHGFVEP RQITICNQSP VRQVLNITDK DLSPTSPFF AQLTDDSDIY WTAEVNEEGD 600  
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILFVL 660  
GAVLALLFL LVLLLVRRK RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720  
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 339 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..672

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1 11 21 31 41 51  
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AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180  
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240  
GCGAGACAAC GAGATCCAGA GGACTCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300  
TGTCACTGTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATGG 360  
ACAGAGCCAT ACTCGGTAT AGCGGCCGTG AAAATATTC CACGTTTTT CATGGTTGCG 420  
AAGCAGTGCT CGGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480  
CTCTGGAAG AGCCCATGCC CTCTTTTAC CTCAAGTGT GTAAAATTG CTACTGCAAT 540  
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600  
AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATGCG AGCGCGCCTC 660  
AGCCTGTCTT GA

Seq ID NO: 340 Protein sequence  
Protein Accession #: Eos sequence

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1 11 21 31 41 51  
MRLQRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRFFQ KGGEGAPRAD PPWAPLGTM 60  
LLALLLVVAL PRVWTDANLT ARQDPEDSQ RTDEGDNVW CHVCERENTF EQCNPRCKW 120  
TEPYCVIAAV KIFPRPFMVA KQCSAGCAAM ERPKPEEKRF LLEPMPPFY LKCKKIRYCN 180  
LEGPPINSSV FREYAGSMGE SCGLWLAIL LLLASIAAGL SLS

Seq ID NO: 341 DNA sequence  
Nucleic Acid Accession #: XM\_035292.2  
Coding sequence: 53..1576

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1 11 21 31 41 51  
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TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCGGCGCGCC GAGGAGAAGG AAGAGGCGCG 120  
GGAGAAGATG CTGGCGCCCA AGAGCGCGGA CGGCTCGCGC CCGGAGGCG AGGGCGAGGG 180  
CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGGCTG GCCATCATCG TGGGGACCAT 240  
TATCGGCTCG GGCATCTTCT TGACGCCACG GGGCGTCTC AAGGAGGCG GCTCGCGCGG 300  
GCTGGCGCTG GTGGTGTGGG CCGGTGCGCG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360  
CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420  
CTACGGCTCG CTGCGCGCCT TCTCTAAGCT CTGGATCGAG CTGCTCATCA TCGGCGCTTC 480  
ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAGGCGC TCTTCCCCAC 540  
CTGCGCGGTG CCGCAGGAGG CAGCCAAGCT CGTGGCTGCG CTCTGCTGTC TGCTGCTCAC 600  
GGCGGTGAAC TGTCTACAGG TGAAGGCCCG CACCGGGTCT CAGGATGCTT TGGCGCGCG 660  
CAAGCTCTGT GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720  
TGTGTCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGATG TGGGGAACAT 780  
TGTGCTGGA TTATACAGCG GCCTCTTTCG CTATGAGGGA TGAATTAAT TGAATTTCTG 840  
CAGAGGAGAA ATGATCAACG CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCTGCG 900  
CATCGTGAGC CTGGTGTAGG TGCTGACCAA CCTGGCTTAC TTCACCAACC TGTCACCGA 960  
GCAGATGCTG TCGTCCGAGG CCGTGGCGGT GCACTTGGG AACTATCACC TGGGCGTCAT 1020

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GTCCTGGATC ATCCCCGTCT TCGTGGGCTT GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTCCATATC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCG CGTGTGTGAT 1200
GACGCTGCTC TACGCTCTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TCGGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
CCTCTTCTGT ATCGCCGTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCTCT AGCGGGCTGC CGGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCAGCAC CGTCTGTGT CAGAAGCTCA TGCAGGTGCT 1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

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Seq ID NO: 342 Protein sequence

Protein Accession #: XP\_035292.2

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1 11 21 31 41 51
| | | | |
MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIGSGIFV TPTGVLKEAG SPGLALVWMA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
LEVYGSGLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLV 180
LITAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
GNIVLALYSY LPAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSSEA VAVDFGNYHL GVMSNIIIPV VGLSCFSGSVN GSLFTSSRLF FVSGREGHLP 360
SILSMIHPQL LTFVPSLVFT CVMTLIYAFS KDIFSVINFF SFFNWLCLVAL AITGMINLRLH 420
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWRN 480
KPKWLLQGIF STTVLQQLM QVVPQET

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Seq ID NO: 343 DNA sequence

Nucleic Acid Accession #: NM\_005268.1

Coding sequence: 168..989

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1 11 21 31 41 51
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TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCTCTATTGC CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGTTCTTGST CTTCATCTTC GCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCGTCT 360
TTGATGAGTT CTTCCTCTGT TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCTCTGTGA 420
CATGCCCTCT ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAG GCGAGCGGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCRAGTGCC 660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCTATCT CAAGCCCTCA GAGAAGAACA 720
TTTTACACCT CTTTCTGTGT GCCACAGCTG CCATCTGCAT CTGCTCAAC CTGCTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGACACGG TCATCACCCT CACGGTACCA CCTCTTCTGT CAAACAAGAC GACCTCTCTT 900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCGCCCTC 960
GAGACCATGT GAAGAAACCC ATCTTGTGAG GGGCTGCGCT GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACCTGGCC AGTTCCCTCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC

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Seq ID NO: 344 Protein sequence

Protein Accession #: NP\_005259.1

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1 11 21 31 41 51
| | | | |
MNWSIFEGLL SGVNYSTAF GRIWLSLVFI FRVLVYLVA ERVWSDDRKD FDCNTRQPGC 60
SNVCFDEFPF VSHVRLNALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
GKRGGLWWT YVCSLVFKAS VDIAPLYVPH SFYPKYILPP VVKHADPCP NIVDCPIKRP 180
SEKNIFLPM VATAAICILL NLVELIYLV KRCHECLAAR KQAMCTGHH PHGTTSSCRQ 240
DBLLSGDLIF LGSDSHPLLL PDRPRDHVK TIL

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Seq ID NO: 345 DNA sequence

Nucleic Acid Accession #: NM\_002391.1

Coding sequence: 26..457

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1 11 21 31 41 51
| | | | |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACTCTCTC 60
CGCCCTGCTG GCGCTCAACT CCGCGSTGCG CAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGGCTGT AGTGGGCTGT GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
CGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCCAAGCC CAGCGCATCC GGTGAGGGT 240
GCCCTGCAAC TGAAGAAGG AGTTTGAGC GACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGCGTGTGAT GGGGGCAGC GCACCAAGT CCGCCAAGC ACCCTGAAGA AGGCGCGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAG GACTAGACG CCAAGCTTGG ATGCCAAGGA 480
GCCCTGGTGT TCACATGGGG CTGGCCACG CCTCTCTCT CCCAGGCCCG AGATGTGAAC 540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCTT TGTCTCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGCCCAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCTCCCC CCAAAGCAAT GTGAGTCCA GAGCCCGCTT TTGTTCTTCC CCACAAATTC 720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780

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TAATAT

Seq ID NO: 346 Protein sequence  
Protein Accession #: NP\_002382.1

1 11 21 31 41 51  
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPTPSSK DGVGFREGT 60  
CGAQTQIRIC RVPCNWKKEF GADCKYKPEF WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120  
RVTKPCTPKT KAKAKAKGK GKD

Seq ID NO: 347 DNA sequence  
Nucleic Acid Accession #: NM\_006783.1  
Coding sequence: 1..786

1 11 21 31 41 51  
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTACT CACCAGCATC 60  
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120  
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTGCTCTGCA ACACACTGCA ACCGGGATGC 180  
AAAAATGTGT GCTATGACCA CTTTTCCCG GTGTCCACA TCCGGCTGTG GGCCTCCAG 240  
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300  
GAAACCACTC GCAAGTTTCA GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360  
ATTAAAAAGC ACAAGTTTCG GATAGAGGGG TCGCTGTGGT GGAAGTACAC CAGCAGCATC 420  
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480  
TACCACCTGC CTGGGTGTTT GAAATGTGGG ATTGACCCCT GCCCAACCTT TGTGACTGC 540  
TTTATTTCTG GGCCACACGA GAAGACCGTG TTTACCATTT TTATGATTTT TGCCTCTGTG 600  
ATTTGCATGC TCGTTAAAGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTAGG 660  
AGATCAAAGA GAGCAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720  
CAGATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780  
AGCTAA

Seq ID NO: 348 Protein sequence  
Protein Accession #: NP\_006774.1

1 11 21 31 41 51  
MDWGLTHTFI GGVNKHSTSI GKVVITVIFI FRVMILVVA QEVWGDEQED FVCNTLQPGC 60  
KNVCYDHPFF VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKPRRGE KRNDFKDIED 120  
IKKHVRIEG SLWYTTSSI FFRIFEEAF MYVFYFLYNG YHLPWLKCG IDPCPNLVDC 180  
FISRPTKTV FTIFMISASV ICMILNVDEL CYLLKVCFR RSKRAQTQKN HPNHALKESK 240  
QNEANLISD SQQNAITGFP S

Seq ID NO: 349 DNA sequence  
Nucleic Acid Accession #: NM\_002571.1  
Coding sequence: 99..587

1 11 21 31 41 51  
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60  
TCACCCCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120  
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180  
ACATCTCCCT CTGCGCAGA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240  
CCACCCCGGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTG 300  
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360  
TGGCGAAGCA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCTGTTT CTCTGCCTAC 420  
AGGACACCCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CTGGCCAGA GTCTGTGTG 480  
AGGACGATGA GATCATGCAG GGATTTCATCA GGGCTTTCAG GCCCTGCCCC AGGCACCTAT 540  
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCT 600  
CCAGGAAGAC CAGACTCCCA CCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCC 660  
TTTCAAAGAA TAAACACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT 720  
TCCTGCTGCA CACTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780  
GCAGAGGTTA TTAATAAACC CTGGAGCAT G

Seq ID NO: 350 Protein sequence  
Protein Accession #: NP\_002562.1

1 11 21 31 41 51  
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR 60  
WENNSCVEKK VLGEKTKGNPK KFKINYTVAN EATLLDIDYD NFLFLCLQDT TPIQSMHCQ 120  
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPK RF

Seq ID NO: 351 DNA sequence  
Nucleic Acid Accession #: NM\_006500.1  
Coding sequence: 27..1967

1 11 21 31 41 51  
ACTTGGCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60  
TCGCGCGCTG CTGCTGCTGT CCTCGGTGCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120  
CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180  
AGTCCCAAG CAACTCAGC CATGTGACT GGTTCCTGT CCACAAGGAG AAGCGGACGC 240  
TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGAGTAC GAGCAGCGGC 300

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TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC 360  
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TCTACAAAGC TCCGAGGAG CCAAAACATCC AGGTCAACCC CTTGGGCATC CTTGTGAACA 480  
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCAAG 540  
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAGT 600  
CGTCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660  
TGGTTAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAATACCCGG CTGCCAGTG 720  
GGAACCATAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG 780  
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGGTG GAAATCAGGT 840  
GTTTGCTGTA TGGCAACCTT CCACCACT TCAGCATCAG CAAGCAGAAC CCCAGACCA 900  
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CTTGCCCGGA 960  
AGGAACACAG TGGGCGCTAT GAATGTGAGG CTTGGAACCT GGACACCATG ATATCGCTGC 1020  
TGAGTGAACC ACAGGAACCTA CTGGTGAAC TGTGTCTGA CTTGCGAGTG AGTCCCGCAG 1080  
CCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140  
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAAGT GCTGGAAGG GGGCCTGTGC 1200  
TTCACTTGA CAGAGGAGAT ACCAGGAGC GAGGCGGCTA TCGCTGCGTG CGCTCTGTGC 1260  
CCAGCATACC CGGCTGAAC CGCACACAG TGGTCAAGCT GGCCATTTTT GGGCCCCCTT 1320  
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAGAGAA TATGGTGTG AATCTGTCTT 1380  
GTGAAGCGTC AGGGCACCCC CGGCCACCA TCTCTGGAA CGTCAACGGC ACGGCAAGTG 1440  
AACAGACCA AGATCCACAG CGAGTCTCTG GCACCTGAA TGTCTCTGT ACCCCGAGGC 1500  
TGTGAGGAC AGTGTGTGAA TGCACGGCCT CCAACGACCT GGGCAAAAC ACCAGCATCC 1560  
TCTTCTGGA GCTGGTCAAT TTAACACCCC TCACACAGA CTCCACACA ACCACTGGCC 1620  
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CAGCTCCCTT CCTGCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG 2040  
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Seq ID NO: 352 Protein sequence  
Protein Accession #: NP\_006491.1

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1 11 21 31 41 51  
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RSQYRIQLR VYKAPPEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIQP VIWYKNGRPL 180  
KEEKNRVHIQ SSQTVESSGL YTLQSLKAQ LVKEDKDAQF YCELNYRLPS GNMHKSREV 240  
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NGVLVLEPAR KEHSGRYEQ AwnLDMISL LSEPOELLVN YVSDVRVSPA APERQEGSSL 360  
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Coding sequence: 165..2639

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TATTCCTGAC CAGCGTGGT CTTTCTGTGC TGGCGCGCG ACCTCCGAT GACCGGGGCT 240  
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 CGCCACTACA CTCCAGCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 354 Protein sequence  
 Protein Accession #: NP\_003174.2

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 GEPDSRLVAH IRDDVVIIRI NTDGAENIE PLWRVNDTK DKRMLVYKSE DIKNVSLRQS 180  
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 Nucleic Acid Accession #: NM\_021832.1  
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Seq ID NO: 356 Protein sequence  
 Protein Accession #: NP\_068604.1

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 65 PKVCGYLKVD NEELLPGKLV DREPEELVH RVKRRADPDF MKNTCKLLV ADHRFYRYMG 240  
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 KVCCRDLGR CVPYVDAEQK NLFLRKGRPC TVGFCDMNGK CEKRVQDVIE RFWDPIDQLS 660  
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Seq ID NO: 357 DNA sequence  
 Nucleic Acid Accession #: NM\_004994.1  
 Coding sequence: 20..2143

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5	CGAGAAGCAA	CTGTCCCTGC	CCGAGACCGG	TGAGCTGGAT	AGCGCCACGC	TGAAGGCCAT	300
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	CACCTTCACT	CGCGTGTACA	GCCGGGACGC	AGACATCGTC	ATCCAGTTTG	GTGTGCGGGA	540
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15	GGGTAAAGGAG	TACTCGACCT	GTACCAGCGA	GGGCGCGGGA	GATGGGCGCC	TCTGGTGGCG	1140
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20	AACCACCACC	ACACCGCAGC	CCACGGCTCC	CCGACGGTTC	TGCCCCACCG	GACCCCCCAC	1440
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	TGCTGTGAGC	TCGACGGCAT	CGCGGAGATT	GGGAACACAG	TGTATTGTGT		1620
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25	CCTTATCGCC	GACAGTGGC	CCGCGCTGCC	CCGCAAGCTG	GACTCGGTCT	TTGAGGAGCC	1740
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	GGTGTCTGGC	CGGAGCGGTC	TGGACAAGCT	GGGCGTGGGA	GCCGACGTGG	CCGAGGTGAC	1860
	CGGGGCCCTC	GAGAGTGGCA	GGGGGAAGAT	GCTGCTGTTC	AGCGGGCGCG	GCCTCTGGAG	1920
	GTTCGACCTG	AAGGCGCAGA	TGGTGGATCC	CCGAGCGGCC	AGCGAGGTGG	ACCGGATGTT	1980
30	CCCCGGGGTG	CCTTTGGACA	CGCACGACGT	CTTCCAGTAC	CGAGAGAAAG	CCTATTCTCT	2040
	CCAGGACCGC	TTCTACTGGC	GCGTGAGTTC	CCGAGTGTAG	TTGAACAGG	TGACCAAGT	2100
	GGGCTACGTG	ACCTATGACA	TCCTGCAGTG	CCCTGAGGAC	TAGGGCTCCC	GTCTCTGCTT	2160
	GCACTGCCAT	GTAATATCCC	ACTGGGACCA	ACCGTGGGGA	AGGAGCCAGT	TTGCCGGATA	2220
35	CAAACTGGTA	TTCTGTCTTG	GAGGAAAGGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC	2280
	TCACCTTTGT	TTTTTGTGG	AGTGTCTTCA	ATAAACTTGG	ATTCTCTAAC	CTTT	

Seq ID NO: 358 Protein sequence  
Protein Accession #: NP\_004985.1

40	1	11	21	31	41	51	
	MSLWQPLVLV	LLVLGCCFAA	PRQRQSTLVL	PPGDLRLNLT	DRQLAEELY	RYGYTRVAEM	60
	RGESKSLGPA	LLLLQKQLSL	PETGELDSAT	LKAMRTPRCG	VPDLGRFQTF	EGDLKWHHHN	120
	ITYWIQNYSE	DLPRAVIDDA	FARAFALWSA	VTPLFTFRVY	SRDADIVIQF	GVAEHGDSYF	180
45	PDGKDLLLAH	AFPPGPGIQG	DAHFDDELW	SLKGVVVVPT	RFGNADGAAC	HFPFIPEGRS	240
	YSACTTDRSR	DGLPWCSTTA	NYDDDRFPG	CPSERLYTRD	GNADGKPCQF	PFIFQGSYS	300
	ACTTDRSRDR	YRWCAATTANY	DRDKLFGFCP	TRADSTVMGG	NSAGELCVFP	FTFLGKEYST	360
	CTSEGRGDRG	LWCATTNFD	SDKKGWFCPD	QGYSLFLVAA	HEFGHALGLD	HSSVPEALMY	420
	PMYRFTGPPF	LHKDDVNGIR	HLKGRPEPE	PREPTTTTPQ	PTAPPTVCPT	GPPTVHPSE	480
50	PTAGTGPPTS	AGPTGPPTAG	PSTATTVPLS	FVDDACNVNI	FDALAEIGNQ	LVLFDGKYW	540
	RFSEGRGSRP	QGFLIADKW	PALPRKLDV	FEEPLSKLFL	FFSGRQVWVY	TGASVLGPRR	600
	LDKLGGLADV	AQVTGALRS	RGMMLFSGR	RLWRFDVKAQ	MVDPRSASEV	DRMFPGVPLD	660
	THDVQYREK	AYFQDRFYW	RVSSRSELNQ	VDQVGYVTD	ILQCPED		

Seq ID NO: 359 DNA sequence  
Nucleic Acid Accession #: NM\_000213.1  
Coding sequence: 127..5385

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	AAGAGGATGG	CAGGGCCACG	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
	AGCGTCAGCC	TCTCTGGGAC	CTTGGCAAAC	CGCTGCAGAA	AGGCCCCAGT	GAAGAGCTGC	240
65	ACGGAGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTCAGGGAC	300
	CGGCGCTGCA	ACACCCAGGC	GGAGCTGCTG	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
	GTCTAGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TGACACCAC	CCTGCGGCGC	420
	AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGCTGAGGA	GCGGCATTTT	480
	GAGCTGAGGG	TGTTTGAGCC	ACTGGAGAGC	CCGCTGGACC	TGTACATCCT	CATGGACTTC	540
70	TCCAACCTCA	TGTCGATGA	TCTGGACAAC	CTCAAGAAGA	TGGGGCAGAA	CCTGGCTCGG	600
	GTCTTGAGCC	AGCTCACCA	CGACTACACT	ATTGGATTTC	GCAAGTTTGT	GGACAAAGTC	660
	AGCGTCCCGC	AGACCGACAT	GAGGCGCTAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
	CCCCCTTCT	CCTTCAAGAA	GCTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCCGGAAT	780
	AACTGCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATGCC	840
75	ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGCTGGC	GCCGCGACAG	CACCCACCTG	900
	CTGGTCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCAA	CGTGTGGCT	960
	GGCATCATGA	GCCGCAACGA	TGAACGCTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
	TACAGGACAC	GAGCACTACC	GTCGGTGGCC	ACCCTGGTGC	GCCTGCTCGC	CAAGCACAAC	1080
80	ATCATCCCCA	TCTTGTCTGT	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCACACC	1140
	TATTTCCCTG	TCTCTCACT	GGGGGTGCTG	CAGGAGGACT	CGTCCAACAT	CGTGGAGCTG	1200
	CTGGAGGAGG	CCTTCAATCG	GATCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCT	1260
	CGAGGCTTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCTTTT	1320
	CACATCGCGC	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
	GATGGGACGC	ACGTGTGCCA	GCTGCCGGAG	GACCAAGAAG	GCAACATCCA	TCTGAAACCT	1440



5	TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
	CTGCAAAAAG	AGGTGCGGTC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
	TGTGTGTGCA	GCGAGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
	GACATTCAGC	CCTGCCTGGG	GGAGGGCGAG	GACAAAGCGT	GCTCCGGCGG	TGGGGAGTGC	1680
	CAGTGGCGGC	ACTGTGTGTG	CTACGGCGAA	GGCGGCTAOG	AGGGTCAGTT	CTGCGAGTAT	1740
	GACAACTTCC	AGTGTCCCGG	CACCTCCGGG	TTCCTCTGCA	ATGACCGAGG	ACGCTGTCTCC	1800
	ATGGGCGAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTTCAGC	1860
	AATGCCACCT	GCAATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
10	GGCGCTGCC	ACTGCCACCA	GCAATCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
	TGCGGATCC	ACCGGGGCTT	CTGCGAGGAC	CTACGCTCCT	GCGTGCAGTG	CCAGGCGTGG	2040
	GGCACCGCG	AGAAGAAGGG	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
	GACGAGCTTA	AGAGAGCCGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
	GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
15	CTGGTGACA	AGAAGAAGGA	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
	CTCCTCTTCC	TGCCGCTCCT	GGCCCTGCTA	CTGCTGTCTAT	GCTGGAAGTA	CTGTGCTGTC	2340
	TGCAAGGCTC	GCCTGGCACT	TCTCCCGTGC	TGCAACCGAG	GTCCATAGGT	GGGCTTTAAG	2400
	GAAGACCACT	ACATGCTGGG	GGAGAACCTG	ATGGCCTCTG	ACCCTTGGGA	CACGCCCATG	2460
	CTGCGCAGCG	GGAACCTGAA	GGGCGGTGAC	GTGGTCGCT	GGAAGGTGAC	CAACAACATG	2520
20	CAGCGGCTG	GCTTTGCCAC	TCATGCCGCC	AGCATCAACC	CCACAGAGCT	GGTGCCTTAC	2580
	GGGCTGTCTT	TGCGGCTGGC	CCGCTTTTGC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
	GAGTGGCGCC	AGCTGGCCCA	GGAGGTGGAG	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
	TCCGGTGTAC	ACAAGCTCCA	GCAACCAAG	TTCGGGACGC	AGCCCAATGC	CGGGAAGGAG	2760
	CAAGACACCA	GCATGCTGCA	CACAGTGTCT	ATGGGCGCCC	GCTCGGCCAA	GCCGGCCCTG	2820
25	CTGAAGCTTA	CAGAGAAGCA	GGTGGAAACG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
	GGCTACTACA	CCCTCACTGC	AGACCAAGAC	GCCCCGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
	GTGGAGCTGG	TGGAGCTACG	GGTGCCCTCT	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
	CAGCTGTCTG	TGGAGGCTCA	CGACGTGCCC	CGAGGCACTG	CCACCTCTGG	CGCGCGCTGG	3060
	GTAAACCTCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGCTCTTTGA	GCAGCCTGAG	3120
30	TTCTCGGTCA	GCCGCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGGG	TGCTCTGGAC	3180
	GGCGGGAGT	CCGAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
	TACATCCCCG	TGGAGGTGTA	GCTGTGTTTC	CAGCCTGGGG	AGGCTTGGAA	AGAGCTGCAG	3300
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	TTCCAGSTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
35	ACCATCATCA	TCAGGGACCC	AGATGAACTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCTCCAGCG	CGACCTGGGC	GCCCCGCGCA	ACCCCAATGC	TAAGGCGGCT	3540
	GGGTCCAGGA	AGATCCATT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
	GTAAAGTACT	GGATTCAAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGTCTGA	CAGCAAGGTG	3660
	CCCTCAGTGG	AGCTCAGCAA	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
40	TACGGGGCTC	AGGGGAGGGG	ACCTTACAGC	TCCCTGTGTG	CCTGCGGCAC	CCACAGGAA	3780
	GTGCCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTGCTCT	CCTCCACGGT	GACCCAGCTG	3840
	AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
	CTGGTCAAGG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGTCTGT	TGACAACCTT	3960
	AAGAACCAGG	TGCTGCTTAT	TGAGAACCTT	CGGAGTCCCT	AGCCCTACCG	CTACACGGTG	4020
45	AAGGCGGCA	ACGGGGCCGG	CTGGGGGCTT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
	CAGCCCAAGA	GGCCCATGTC	CATCCCATC	ATCCCTGACA	TCCCTATCGT	GGAAGCCGAG	4140
	AGCGGGGAGG	ACTACGACAG	CTTCTTATG	TACAGGATG	ACGTTCTACG	CTCTCCATCG	4200
	GGCAGCCAGA	GGCCGAGCGT	CTCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGATGGGAC	4260
	TTTGCTTCC	CGGGCAGCAG	CAACTCCCTG	CACAGGATGA	CCACGACAGG	TGCTGTCTGC	4320
50	TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGGTGCG	TAAGCACATC	CTCCACCTTC	4380
	ACACGGGACT	ACAACCTCACT	GACCGGCTCA	GAACACTCAC	ACTCGACACC	ACTGCGGAGG	4440
	GACTACTCCA	CCCTCACTTC	CGTCTCCTCC	CACGACTCTC	GCCTGACTGC	TGGTGTGCCC	4500
	GACACGCCCA	CCCGGCTGGT	GTCTCTGCCC	CTGGGGCCCA	CATCTCTCAG	AGTGAAGCTG	4560
	CAGGAGCCCG	GGTGGGAGCG	GCCGCTGCG	GGCTACAGTG	TGGAGTACCA	CTGCTGAAC	4620
55	GGCGGTGAGC	TGCATCGGCT	CAACATCCCC	AACCTGCCCC	AGACCTCGGT	GGTGGTGGAA	4680
	GACCTCTGCG	CCAACCACTC	CTACGTGTTT	CGCGTGGGG	CCCAGAGCCA	GGAAGGCTGG	4740
	GGCGGAGAGC	GTGAGGGTGT	CATCAACATT	GAATCCAGG	TGCAACCGCA	GAGCCCACTG	4800
	TGTCCCTGCG	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCGCTGGTGG	4860
	TTCACTGCGC	TGAGCTGCGC	CTGCTGCG	CTGAGCTGGG	AGCGGCCACG	GAGGCCCAAT	4920
60	GGGATATCG	TCGGCTACCT	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCGGAG	AGCCGCTGTA	CGTGGCGGG	CCTCAGCGAG	5040
	AACGTGCCCT	ACAAGTTCAA	GGTGAGGGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGGCG	5100
	GAGGGGATCA	TCACCATAGA	GTCCAGGAT	GGAGGACCTT	TCCCGCAGCT	GGGCGAGCGT	5160
	GCCGGGCTCT	TCCAGCACCC	GCTGCAAGC	GAGTACAGCA	GCATCACACC	CACCCACACC	5220
65	AGCGCCACCG	AGCCCTTCTT	AGTGGATGGG	CCGACCTGG	GGGCCACGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TCACCGGCGA	TGTGACCCAG	GAGTTTGTGA	GCGGACACT	GACCAACGAG	5340
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	CCCCCGCCAT	GTCCCACTAG	GCGTCTCTCC	GACTCTCTCT	CCGAGGCTCT	CTCAGTACT	5460
	CCATCTCTGC	ACCCCTGGGG	GCCAGGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
70	TCCTGGGAGG	CATGAAGGGG	GCAAGGTCCG	TCCTCTGTGG	GCCCAACCTT	ATTGTGAACC	5580
	AAAGAGCTGG	GAGCAGCACA	AGGACCCAGC	CTTTGTCTCT	CACCTAATAA	ATGTTTGTGC	5640
	TACTG						

Seq ID NO: 360 Protein sequence  
 Protein Accession #: NP\_000204.1

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1	11	21	31	41	51	
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CNTQAEALLA	GCQRESIVVM	ESSPQITEET	QIDTTLRSQ	MSPOGLRVRL	RPGEERHFEL	120
EVFPELESPL	DLYILMDFSN	SMSDDLNLK	KMGQNLARVL	SQLTSDYTIG	FGKPFVDKVSU	180
PQIDMRPEKL	KEPWFNSDPP	FSFRNVISLT	EDVDFRNKL	QGERISGNLD	APEGGFDAIL	240
QTAVCTRDIG	WRPDSHTLLV	FSIESAFHYE	ADGANVLAGI	MSRNDERCHL	DTTGTYYQYR	300
TQDYPSPTLL	VRLLAKHNI	PIFAVTNYSY	SYEKLHTYF	PVSSGLVQLE	DSSNIVELLE	360
EAFNRIRSNL	DIRALDSPRG	LREVTSTSMF	QKTRTGSFHI	RRGEVGIVQV	QLRALEHVDG	420

5 THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480  
 CSBGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEQFCEYDN 540  
 FQCPRTSGFL CNDGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNNGIC NGRGHCECGR 600  
 CHCHQQLSYT DTICEINISA IHPGLCEDLR SCVQCQANGT GEKKGRTCEE CNFKVKMVD 660  
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDDG AEPNSTVLV HKKDCPPGS FWWLIPLLLL 720  
 LLPLALLLLL LCWKYCACCK ACLALLPCCN RGHMVGPKED HYMLRENLMA SDHLDTPMLR 780  
 SGNLKGKRDVW RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840  
 AQLRQVEVEN LNEVYRQISG VHKLQOTKFR QQPNAKQKD HTIVDTVLM PRSAKPALLK 900  
 LTERQVEQRA PHDLKVAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDEKQL 960  
 10 LVEAIDVPAG TATLGRRLVN ITIIKEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020  
 KSQVSYRTQD GTAQGNRDYI PVEGELLEFP GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080  
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDGLAP QNPNAKAAGS 1140  
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 15 AQGEGPVSSYL VSCRTHQEVV SEPGRFAFNV VSSVTQLSW AEPATNGEI TAYEVCYGLV 1260  
 NDDNRPIGPM KKVLDVNPKN RMLLIENLRE SQPYRYTVKA RNGAGWGP ER EAINLATOP 1320  
 KRPMSPPIIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSDDTE HLVNGRMDFA 1380  
 PFGSTNLHR MTTTSAAYG THLSPHVPHR VLSTSSLTTR DYNLSRSEH SHSTTLPRDY 1440  
 20 SLTTSVSSHD SRLTAGVPTD PTRLVPSALG PTLRLVSWQE PRCEPLQGY SVEYQLNGG 1500  
 ELHRLNIPNP AQTSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSPCLP 1560  
 LPGAFTLST PSAPGPLVFT ALSPDSLQLS WERPRPENG DVGLVTCM AQGGGPATAF 1620  
 RVDGDSPEER LTVPLSENVP PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG 1680  
 LFQHPQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHTQEP VSRLLTTSGT 1740  
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25 Seq ID NO: 361 DNA sequence  
 Nucleic Acid Accession #: NM\_013332.1  
 Coding sequence: 1..63

30 1 11 21 31 41 51  
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 CGGCTGTTC CCGGAGGGT CCAGAGGCTT TCCAGAGGA GAAGGCAGCT CTGTTTCTCT 180  
 35 GCAGAGGAGT AGGTCCTTT CAGCCATGAA GCATGTGTG AACCTCTACC TGTTAGGTGT 240  
 GGTACTGACC CTACTCTCCA TCTTCGTTAG AGTGATGGAG TCCCTAGAAG GCTTACTAGA 300  
 GAGCCCATCG CCTGGGACCT CCTGGACCAC CAGAAGCCAA CTAGCCACA CAGAGCCAC 360  
 CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATA GACCTCCTC CATACTGGCC 420  
 40 ATATTTTGA ACACCTGACCT AGACATGTCC AGATGGGAGT CCCATTCTA GCAGACAAGC 480  
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 CTCATTGCCT GGGCAAGGCC TGTTTAGGCC GGTGCGGTG GCTCATGCT GTAATCCTAG 600  
 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTGCG 660  
 CAACATGGCG AAACCCCATC TCTACTAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720  
 GGCTGTGAAT CCCAGTTCTT TGGGAGGCTG AGGCGGGAGA ATTGCTTGA CCCGGGGACG 780  
 45 GAGGTGCGAG TGAACCGAGA TGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840  
 CATCTCAAAA AAAAAAAGAA AAAAAAAGC CTGTTAATG CACAGGTGTG AGTGGATTGC 900  
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 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020  
 TGATATTTC AACCTACTT CCTAAACATC TGTCTGGGTG TCCTTTAGTC TTGAATGTCT 1080  
 50 TATGCTCAAT TATTGTGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140  
 CAGTTGAGA GGTGTGTGTG GTGGGCTGTT GGGAGTGGG ATGGAGTGT CAGTGCCCAT 1200  
 TTCTCATTTT ACATTTTAAA GTCGTTCTCT CAACATAGTG TGTATTGCTG TGAAGGGGGT 1260  
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55 Seq ID NO: 362 Protein sequence  
 Protein Accession #: NP\_037464.1

60 1 11 21 31 41 51  
 MKHVLNLYLL GVVLTLISIF VRVMESLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60  
 RSM

65 Seq ID NO: 363 DNA sequence  
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 Coding sequence: 250..1326

70 1 11 21 31 41 51  
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 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAC CAGGAATAAC CTATGCTGAA 180  
 CCCACGCCCT AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGATCATC 240  
 AACTGAAGAA TGGGGTTTCA CTTGACGCTT GCAAAATTAC CAATAACGA GCTGCACGGC 300  
 75 CAAGAGAGTC ACAATTGAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360  
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 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480  
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 ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320  
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 TTCATTATCC TTAAAAAAA AA

Seq ID NO: 364 Protein sequence  
 Protein Accession #: NP\_076404

1 11 21 31 41 51  
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 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTITPKV LSVCVWVIMA VLSLPNIILT 180  
 NGQPTEDNIH DCSKLSKPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240  
 ISQSSRRKKH NQSIKVVAV FFTCFLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300  
 FLSACNVCLD PIIFYFMCRS PSRRLFKSN IRTSRSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 365 DNA sequence  
 Nucleic Acid Accession #: NM\_005365.1  
 Coding sequence: 1..948

1 11 21 31 41 51  
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 TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAGAGT 180  
 CCTCAGGGAG CGCTTCCTCT CTCCATTTCG GTCTACTACA CTTTATGGAG CCAATTGAT 240  
 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGACCC AGCTCAGCTG 300  
 GAGTTTATGT TCCAAGAAGC ACTGAAATG AAGGTGGCTG AGTTGGTTCA TTCTCTGCTC 360  
 CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420  
 AATTACAGC GCTACTTTCC TGTGATCTTC GGCAGAGCCT CCGAGTTTCA GCAGGTGATC 480  
 TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGCCACT CCTACATCCT TGTCACTGCT 540  
 CTGGCCCTCT CGTGCATAG CATGCTGGGT GATGTCATA GCATGCCCAA GGCCGCCCTC 600  
 CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAACT GCGCCCTGA AGAGGTTATC 660  
 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAG AGCAGATGTT CTACGGGGAG 720  
 CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAACT ACCTGGAGTA CCGGCAGGTG 780  
 CCGGCAGTGT ATCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840  
 AGCTATGAGA AGGTCAATAA TTATTGCTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900  
 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 366 Protein sequence  
 Protein Accession #: NP\_005356.1

1 11 21 31 41 51  
 MSLEQRSPHC KPDEDLEAQQ EDLGLMGAQE PTGEEETTS SSDSKEEVS AAGSSSPFQS 60  
 PQGASSSSIS VYITLWSQFD EGSSSQESEE PSSSVDPAQL EFMFOEALKL KVAELVHPLL 120  
 HKYRVKEPVT KAEMLSEVIK NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180  
 LGLSCDSMLG DGHSMFKAAL LIIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMPYGE 240  
 PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LMWSKAHAET SYEKVINYL VMLNAREPICY 300  
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Seq ID NO: 367 DNA sequence  
 Nucleic Acid Accession #: NM\_014400  
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1 11 21 31 41 51  
 GGTACTCAT CCTGGGCTCA GGTAAGAGGG CCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60  
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 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180  
 GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CGAACAAGA TGAAGACAGT 240  
 GAAGTGCAGC CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300  
 CGGACAAATC TGCGTGGCAG TGCSGGGTG CGGTTGCGGA CTCGCCGCA AGAATGACCG 360  
 CGGCCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420  
 CTGCAACGCC AAGCTCAACC TCACTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480  
 ATACCCGCC AACCGCGTGG AGTGTACAG CTGTGTGGGC CTGAGCCGG AGGCGTGCCA 540  
 GGGTACATCG CCGCGGTGCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600  
 CTTGACCGGC AACGTCACT TGACGGCAGC TAATGTGACT GTGTCTTTCG CTGTCCGGGG 660  
 CTGTGCTCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCCGAGGT TCACGCTCAG 720  
 TGGCTCCTAT TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780  
 CCTCGAATC CCACCCCTTG TCCGCTGCC CCTCCAGAG CCAACGAGT TGGCCTCAAC 840  
 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAACCCAT 900  
 GCCAGCGCCA ACCAGTCAGA CTCGAGACA GGGAGTAGAA CAGAGGCCCT CCGGGGATGA 960  
 GGAGCCGAGG TTGACTGGAG GCGCGCTGG CCAACAGGAC CGCAGCAATT CAGGGCAGTA 1020  
 TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080  
 ATTGGCAGCC CTCTGTGTGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCCACCTGG 1140  
 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTGTGT 1200  
 CCCACCACTG GACTGGGCTG GCCCAGCCCC TGTTTTCCA ACATTCCCCA GTATCCCCAG 1260  
 CTCTGCTGCG GCTGTTTTCG GGCTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320

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 TCCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440  
 AGGATGCTAA GCTTCTTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500  
 GGTGGGACAA TGGCTCCCA CTCTAAGCAC TGCCTCCCT ACTCCCGCA TCTTTGGGGA 1560  
 ATCGGTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGCA GGGACCGTGC 1620  
 CTTATGTCTG TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680  
 TTGTATAGTG AAAAAAAA

Seq ID NO: 368 Protein sequence  
 Protein Accession #: NP\_055215

1 11 21 31 41 51  
 MDPARKAQAQ AMIWTAGWLL LLLLRRGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGV DV 60  
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 SRALDPAGNE SAYPENGVEV YSCVGLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVTLT 180  
 AANVTSLPLV RGCVDDEFT RDGVTGPFT LSGSCCQGSR CNSDLRNTY FSPRIPLVR 240  
 LPPPEPTTVA STTSVTTSTS APVPTSTTK PMPAPTSQTP RQGEHEASR DEEPRLTGGA 300  
 AGHQDRSNSG QYPARGGPQQ PHNKGCVAPT AGLAALLAV AAGVLL

Seq ID NO: 369 DNA sequence  
 Nucleic Acid Accession #: NM\_005329.1  
 Coding sequence: 1..1662

1 11 21 31 41 51  
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 GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAGAAG 120  
 CACTACCTGT CCTTCGGCT GTACGCGGCC ATCTGGGGCC TGCACTGCTT CATTGAGAGC 180  
 CTTTTCGCTT TCCTGGAGCA CCGCGCATG CGACGTGCGG GCCAGGCCCT GAAGCTGCC 240  
 TCCCGCGGCG GGGGCTCGGT GGCACGTGTC ATTGCCGCT ACCAGGAGGA CCCTGACTAC 300  
 TTGCGCAAGT GCCTGCGCTC GGCACGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCTAT 360  
 GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420  
 GCGGCGACCG AGCAGGCCCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480  
 GGTGAGACCG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TCGGSGATGT GGTGCGGGCC 540  
 AGCACCTTCT CGTGCATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTCTAT GTACACGGCC 600  
 TTCAAGGCCC TCGCGGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660  
 GATCCAGCCT GCACCATCGA GATGCTCGA GTCCCTGGAG AGGATCCCCA AGTAGGGGGA 720  
 GTCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTT CTGAGCAGC 780  
 GTGCGGTACT GGATGGCCTT CAACGTGGAG CGGGCCTGCC AGTCTACTT TGGCTGTGTG 840  
 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900  
 GACTGTGACC ATCAAGAATT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960  
 ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CGCGCGCTC CAAGTGCTCT 1020  
 ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACAGC AAACCCGCTG GAGCAAGTCT 1080  
 TACTTCCGGG AGTGGCTCTA CACTCTCTG TGGTTCCTA AGCACCCTT CTGGATGACC 1140  
 TACGAGTCAG TGGTCAAGGG TTTCTTCCC TTCTTCTCA TTGCCACGGT TATACAGCTT 1200  
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 ATTATCAAG CCACTACGCG CTGCTTCTT CGGGGCAATG CAGAGATGAT CTTGATGTC 1320  
 CTCTACTCCC TCTCTATAT GTCCAGCCTT CTGCGGCCA AGATCTTTC CATTGCTACC 1380  
 ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTCTTGGC 1440  
 CTCTTCTCTG TGTCCATCTG GGTGGCAGTT CTCCTGGAGG GGCTGGCCTA CACAGCTTAT 1500  
 TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCTTGT TCTCTGGGGC TATCTGTAT 1560  
 GGCTGCTACT GGGTGGCCCT CTTCTGCTA TATCTGGCCA TCATCGCCCG GOGATGTGGG 1620  
 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 370 Protein sequence  
 Protein Accession #: NP\_005320.1

1 11 21 31 41 51  
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 VVDGNRQEDA YMLDIFHEVL GGTGAGFFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180  
 STPSCIMQKW GSKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240  
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQGFLE 300  
 DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLWR LNQQTRWSKS 360  
 YFREWLNSL WFKHHLWMT YESVVTGFFP FFLIATVIQL PYRGRIWNIL LFLITVQLVG 420  
 IIKATYACFL RGNAMIFMS LYSLLYMSLL LPAKIFAIAT INKSGWGTSG RKTIVVNFPG 480  
 LIPVSIWVAV LLEGLAYTAY QDLFSETEL AFLVSGAILY GCVWALLML YLAIARROG 540  
 KRPEQYSLAP AEV

Seq ID NO: 371 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 148-7095

1 11 21 31 41 51  
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 CAAAAAATC ATTTCTTCTG CTCCCCCTCC CTCTCCACTC TGAGAGCAG AGGAGCCGCA 120  
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 CAGCTCTCTT GTGTTTGGCG CCGGATTTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTGTAAG AGATTGGCTG GTCCATATCA GGAGCACTGA ATCAAAAAAA TTGGGGAAG 300  
 AAATATCAA CATGTAATAG CCAAAAAACA TCTCTATCA ATATTGATGA AGATCTTCAA 360  
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAACA ATCATTGGAA 420

	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTGAGCGGAG	GAGTTTCAGA	AATGGTGT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAA	ATTTCACCTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
5	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGTGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAACTCAAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTGTG	AAGTCTTAC	AATGCAACAA	960
10	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTATGTA	AGCAGTTTGT	1080
	AGTTCAAGAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTATCA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
15	GGTGCTATTG	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGT	AAGAAAATAT	CAAGGAGGAG	1440
	GAAGAGGGA	AGACATTTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTACAA	1500
	AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
20	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAGAC	ATATTTCCCT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAAGTG	TTCTTAGATC	TCCACATATG	1800
	AACCTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAAACAGAATA	TGAGGAGGAG	1860
25	AGTTTATTTA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTGAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
30	AGCTTTCTCC	AGACTAATTA	CAGTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCCTTCTCG	CAGGCCCACT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCTCA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGCTG	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCCAACG	2400
	GTATACAAAT	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
35	ACCCCTTTGT	TGCTTGACAA	TCAGATCTCT	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TGCGCCTTGC	ATGCTACGCC	TGTATTTCCC	AGTGTGATG	TGTCATTGTA	ATCCATCCTG	2580
	CTCTCTATG	ATGGTGACCC	TTTGCTTCCA	TTTTCTCTG	CTTCTTCTAG	TAGTGAATTT	2640
	TTTGCCCATC	TGCTACAGCT	TTCTCAAAAT	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
	GATAAGGTGC	CCTTGCTATG	TTCTCTGCCA	GTGGCTGGGG	GTGATTGTCT	ATTAGAGCCC	2760
40	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GAGCTGGAA	2820
	TTTGTAGTGT	AAATCGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTATGT	CCATGATGCA	TGCACTGCTT	TCAGGCGCTG	AACCTTCTTA	TGCTTGTGCT	2940
	GATAATGAGG	CTGCCCAACA	CATCTTCACT	GTCTTCTTCA	GTCTGCAAT	ACCTGTGCTAT	3000
	GATTCTGTGG	GTGTAACCTA	TCAGGGTCTC	TTATTAGCG	GCCCTAGCCA	TATACCAATA	3060
45	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCAACT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
	TCTGTGTTTG	TGATGATATA	TAAAGGCGCT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
	ACTGAAGTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAG	CACAGTCATG	3360
50	CCCAACATGT	ATGATAATGT	AAATAAGTGT	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGCGAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAAGTTTCT	3480
	GATCATGAGA	TGATCAAGT	TCCAGAAAAT	AACCTTTTCA	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	CTGGTGACAT	TTGCTTAAAT	CCTGTGCTTA	GTGCAAACTC	AGAGCCGACCA	3600
	TCTCTGACCC	CTGCTTCTAG	TGAATGTTA	TCTCTTCAAT	CTCAGCTCTT	ATTATTATGAG	3660
55	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
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	CCCAAGTTTG	ATAAAATTAG	TTCTACAAAT	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAAAACA	TGCTGCACTG	TACATCTGTA	CCAGTTTTTG	ATGTGTGCGC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTCTCTATG	CAAGTGAGAA	ATATGAACCA	3960
60	GTTTTGTTAA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CITTTGTACAG	TAATGATGAG	4020
	TGTTTCCAAA	CGGCCAATTT	GGAGATTAAC	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAAGTTTATA	4140
	CATTCCGATG	AAATTTTAAAC	CTCCACCAAA	AGTTCTGTGA	CTGGTAAAGT	ATTGTCTGGT	4200
	ATTCCAACAG	TTGCTTCTGA	TACATTGTTA	TCTACTGATC	ATTCTGTTC	TATAGGAAAT	4260
65	GGGCTATGTT	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCTGTAAAC	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTATAAAG	TGTATGTCAT	GCTCATCTTA	TAGAGAATCA	4500
70	CAGGAAAAGG	TAATGAATGA	TTGAGACACC	CAGAAAACA	GTCTTATGGA	TCAGAATAAT	4560
	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
	TCAGACAGTC	AAACTGGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
	CTCTCAGGCC	CTGAATCTAA	AGCATGGGCA	GTCTGACAAA	GTGATGAAGA	AAGTGGATCA	4800
	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATT	CAGTTTGTGA	4860
75	GACACTAATG	AAAAGATGTC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTPCT	4920
	GGATTCCCAAC	AGTCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCCACGTT	4980
	TCAGAGGCGAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
	GAATCCGAGA	AGAAGGCGAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
80	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAGATG	ATGTCCGAGC	AATTTCAATA	AAGCACTTTC	CAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAG	5400
	CACAAGAATC	GATACATAAA	TATGTTGGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460

5 CTTGCTGAAA AGGATGGCAA ACTGACTGAT TATATCAATG CCAATTATGT TGATGGCTAC 5520  
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 TGGAGAAATGA TATGGGAACA TAATGTGGAA GTTATTGTCA TGATAACAAA CCTCGTGGAG 5640  
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 TTTCTGCTCA CTCAGAAGAG TGTGCAAGTG CTGCGCTATT ATACTGTGAG GAATTTTACT 5760  
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 10 CACTGCAGTG CTGGAGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAG 6000  
 CAGATTCAAC ACGAAGGAAC TGTCAACATA TTTGGCTTCT TAAACACAT CCGTTCACAA 6060  
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 20 TTTGTTTACT GGCCAAATAA AGATGAGCCT ATAAATGTGT AGAGCTTTAA GGTCACTTCT 6600  
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 35 GCTGTATTG TAGCAATTAT CAGTTTGTCT AGAAATATAA CTTTAATAC AGTAGCCTGT 7500  
 AAATAAAACA CTCTCCATA TGATATTCAT CATTTTACAA CTGCAATATT CACTTAAAGT 7560  
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 40 TTGTGTTACC TAAGTCATTA ACTTTGTTTC AGCATGTAAT TTTAACTTT GTGAAAAATA 7800  
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Seq ID NO: 372 Protein sequence:  
 Protein Accession #: built from XP\_031379

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 ILFEVGTEN LDFKAIIDGV ESVSFRGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240  
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 55 TGKEEIHAV CSSEPEVQA DPENYTSLLV TWERPRVVD TMIEKFAVLV QQLDGEDQTK 360  
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 65 ILPQVTSATE SDKVPPLHASL PVAGDILLLE PSLAQYSDVL STTHAASETL EFGSESGVLY 900  
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Seq ID NO: 373 DNA sequence

Nucleic Acid Accession #: built from NM\_002851

Coding sequence: 148-4518

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	CTTTGTGAAG	AGATTGGCTG	GTCTATATCA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
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25	TTAGATCCAT	TCATACGTGT	GAACTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTAC	840
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20 Seq ID NO: 374 Protein sequence:  
 Protein Accession #: built from XP\_031379

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50 Seq ID NO: 375 DNA sequence  
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	PKKSPSANGL	SKHNDGKEE	NDIQTSALL	PLSPESKAWA	VLTSDSESGS	GQGTSDSLNE	1560
20	NETSTDFSPA	DINEKODAGI	LAAGDSEITP	GFPQSPSTSV	TSENSEFVHF	SEAEASNSSH	1620
	ESRIGLAEG	ESEKKAIVPL	VIVSALTFFIC	LVLVLGILY	WRKCFQTAHF	YLEDSTSPRV	1680
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGPTTEF	ETLKEFYQEV	QSCITVDLIT	1740
	ADSSNHPDNK	HKNRYINIVA	YDSRVKLAQ	LAEKDGKLT	YINANYVDGY	NRPKAYIAAQ	1800
	GPLKSTADEP	WKMIWENHVE	VIVMITNLVE	KGRKCDQYV	PADGSEBYGN	FLVTQKSVQV	1860
25	LAYYTVRNF	LRNTKIKKGS	QKGRPSGRVV	TOYHYTQWPD	MGVPEYSLPV	LTFVRKAAVA	1920
	KRHAVGPFVV	HCSAGVGRTG	TYIVLDSMLQ	QIQHEGTVNI	FGLPKHRSQ	RNYLVQTEBQ	1980
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	AALKQCNREK	NRTSIIPIVE	RSRVGISSLS	GEGTDYINAS	YIMGYQSNF	FIITQHPLH	2100
	TIKDFWRMIW	DHNAQLVVM	PDGQMAEDE	FVYWPKNDEP	INCESPKVLT	MAEEHKCLSN	2160
30	EEKLIQDPI	LEATQDDVVL	EVRHFQCPKW	PNPDSPISKT	FELISVIKEE	AANRDGPMIV	2220
	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINIM	RPGVFADIEQ	YQFLYKVVLS	2280
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Seq ID NO: 383 DNA sequence

Nucleic Acid Accession #: NM\_005688.1

Coding sequence: 126..4439

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	GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCAGAGAGA	CGGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTGGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCGAGGGGCC	300
	TCTCTCTTGA	TGCCCTCCATG	CATTCTCAGC	TCAGAAATCT	GGATGAGGAG	CATCCCAAGG	360
45	GAAAGTACCA	TCATGGCTTG	AGTGTCTCTG	AGCCCATCCG	GACTACTTCC	AAACACCAAGC	420
	ACCCAGTGGG	CAATGCTGGG	CTTTTCTCT	GTATGACTTT	TTCTGTGCTT	TCTTCTCTGG	480
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	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
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 Protein Accession #: NP\_005679.1

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Seq ID NO: 385 DNA sequence  
Nucleic Acid Accession #: NM\_001327.1  
Coding sequence: 89..631

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10     GACGGGGCAT GCTGATGGCC CAGGAGGCCC TGGCATTCTT GATGGCCAG GGGGCAATGC 180
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15     CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCCGCAA CTGCAGCTCT CCATCAGCTC 540
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      GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCAGCCT GGGCCCTTCT CTAAGGTCTT 660
      GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
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Seq ID NO: 386 Protein sequence  
Protein Accession #: NP\_001318.1

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Nucleic Acid Accession #: Eos sequence  
Coding sequence: 52..459

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Seq ID NO: 388 Protein sequence  
Protein Accession #: Eos sequence

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Seq ID NO: 389 DNA sequence  
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65     GCTTCTGCTC CCTCTGCCG GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
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CAGACGTACG TGATAAAACC GGTGGGGAAC ATCTCTCGGT CTATGCTGTG GTGGTGATTG 1800  
CGTCTGTGGT GGGATTTTGC CTTTGTGTAA TGCTGTTTCT GCTTAAGTTG GCAAGACACT 1860  
CCAAAGTTGG CATGAAGATG TTCTCATGGT TTGGATTGGG GAAAGTAAAA TCAAGACAAG 1920  
GTGTGGCCCC AGCCTCCGTT ATCAGCAATG ATGATGACTC TGCCAGCCCA CTCATCACA 1980  
45 TCTCCAATGG GAGTAACACT CCATCTTCTT CGGAAGGTGG CCCAGATGCT GTCATTATTG 2040  
GAATGACCAA GATCCCTGTC ATTGAAATC CCCAGTACTT TGGCATCACC AACAGTCAGC 2100  
TCAAGCCAGA CACATTTGTT CAGCACATCA AGCGACATAA CATTGTTCTG AAAAGGGAGC 2160  
TAGGCGAAGG AGCCTTTGGA AAAGTGTTC TAGCTGAATG CTATAACCTC TGTCTGAGC 2220  
AGGACAAGAT CTTGTGTGCA GTGAAGACCC TGAAGGATGC CAGTGACAAT GCACGCAAGG 2280  
50 ACTTCCACCG TGAGGCCGAG CTCCTGACCA ACCTCCAGCA TGAGCACATC GTCAAGTTCT 2340  
ATGGCGTCTG CGTGGAGGGC GACCCCTCA TCAATGGTCT TGAGTACATG AAGCATGGGG 2400  
ACCTCAACAA GTTCTCTCAG GCACACGGCC CTGATGCGGT GCTGATGGCT GAGGGCAACC 2460  
CGCCCAACGA ACTGACGAGC TCGCAGATGC TGCAATAGC CCAGCAGATC GCGCGGGGCA 2520  
TGGTCTACCT GGGGTCCGAG CACTTCGTGC ACCGCGATTG GGCCACCAAG AACTGCTGCG 2580  
55 TOGGGGAGAA CTTGCTGGTG AAAATCGGGG ACTTTGGGAT GTCCCGGGAC GTGTACAGCA 2640  
CTGACTACTA CAGGGTCTGT GGCACACAAA TGCTGCCCAT TCGCTGGATG CCTCCAGAGA 2700  
GCATCATGTA CAGGAAATTC ACGACGGAAG GCGACGCTGT GAGCCTGGGG GTGCTGTTGT 2760  
GGGAGATTIT CACCTATGGC AAACAGCCCT GGTACCACTG GTCAAACAAAT GAGGTGATAG 2820  
AGTGATACAC TCAGGGCCGA GTCTGCAGC GACCCCGCAC GTGCCCCAG GAGGTGTATG 2880  
60 AGCTGATGCT GGGGTGCTGG CAGCGAGAGC CCCACATGAG GAAGAATATC AAGGGCATCC 2940  
ATACCCCTCT TCAGAACTTG GCCAAGGCAT CTCGGTCTTA CCTGACATC CTAGGCTAGG 3000  
GCCCTTTTCC CCAGACCGAT CCTTCCCAAC GTACTCTCTA GACGGGCTGA GAGGATGAAC 3060  
ATCTTTTAAAC TCGCGCTGGA GGCCACCAAG CTGCTCTCCT TCACTCTGAC AGTATTAAAC 3120  
TCAAGAGCTC CGAAGAGCTC TCGAGGGAAG CAGTGTGTAC TTCTTCATCC ATAGACACAG 3180  
65 TATTGACTTC TTTTGGCAT TATCTCTTC TCTCTTCCA TCTCCCTTGG TTGTTCTTTT 3240  
TTCTTTTIT AAATTTTCTT TTTCTCTTT TTTTGTCTT TCCCTGCTTC ACGATTCTTA 3300  
CCCTTCTTIT TGAATCAATC TGGCTTCTGC ATTACTATTA ACTCTGCATA GACAAAGGCC 3360  
TTAAACAAAG TAATTTGTTA TATCAGCAGA CACTCCAGTT TGCCCAACCA AACTAACAA 3420  
GCCTGTGTGT ATTCTGCTCT TTGATGTGGA TGAATAAAGG GGAATAACAA TATTTCACCT 3480  
70 AAACITTTGTC ACTTCTGCTG TACAGATATC GAGAGTTTCT ATGGATTAC TTTCTATTAT 3540  
TTATTATTAT TACTGTCTCT ATTGTTTTTG GATGGCTTAA GCCTGTGTAT AAAAAGGAAA 3600  
ACTTGTGTTT AATCTGTGAA GCCTTTATCT ATGGGAGATT AAAACACAGG AGAAGAGAGA 3660  
TTTATTATGA ATCCGATATG GGGAGGAACA AAGACAACCA CTGGGATCAG CTGGTGTGAG 3720  
75 TCCTACTTAA GGAATACTC AGCAACTGTT AGCTGGGAAG AATGATTTCC GCACCTTCCC 3780  
CTGAGGACCT TTTCTGAGGAG TAAAAAGACT ACTGGCCTCT GTGCCATGGA TGATTCTTTT 3840  
CCCATCACCA GAAATGATAG CGTGCACTAG AGAGCAAGA TGGCTTCCGT GAGACACAAG 3900  
ATGGCGCATA GTGTGCTCGG ACACAGTTT GTCTTCTGAG GTTGTGATGA TAGCACTGGT 3960  
80 TTGTTTCTCA AGCGCTATCC ACAGAACCTT TGTCAACTTC AGTTGAAAAG AGGTGGATTG 4020  
ATGTCCAGAG CTCATTTCGG GTTCAGGTGG GAAAGCC

Seq ID NO: 396 Protein sequence  
Protein Accession #: AAL67965.1

1 11 21 31 41 51

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MSSWIRWHGP	AMARLWGFCW	LVVGFWRAAF	ACPTSCCKCSA	SRIWCSDPSP	GIVAFPRLEP	60
NSVDPENITE	IFIANQKRLE	IINEDDVEAY	VGLRNLITVD	SGLKFVAHKA	FLKNSNLQHI	120
NFTRNKLTSL	SRKHPRHLDL	SELILVGNPF	TCCSDIMNIK	TLQEAKESSPD	TQDLYCLNES	180
SKNIPLANLQ	IPNCGLPSAN	LAAPNLVTEE	GKSITLSCSV	AGDPVFNMYW	DVGNLVSKHM	240
NETSHTQSSL	RITNISSDDS	GKQISCVAE	N	LVGEDQDSVN	LTVHFAPIT	300
WCIPFTVKGN	PKPALQWFYN	GAILNESKYY	CTKIHVTNHT	EYHGCLQLDN	PTHMNGDYT	360
LIAKNEYGKD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSNEIPST	420
DVTDKTGREH	LSVYAVVVIA	SVVGFCLLVM	LFLKLARHS	KFGMKDFSFW	GFGKVKSRQG	480
VGPASVISND	DDASPLPHHI	SNGSNTPSSS	EGGPDVAIIG	MTKIPVIENP	QYFGITNSQL	540
KPDTFVQHIA	RHNIVLKRRL	GEGAFKQVFL	AECYNLCPEQ	DKILVAVKTL	KDASDNARKD	600
FHREALLTN	LQHEHIVKFY	GVCVGDPLI	MVFEYMKHGD	LNKFLRAHGP	DAVLMAEGNP	660
PTELTQSQML	HIAQQAAGM	VYLASQHFVH	RDLATRNCLV	GENLLVKIGD	FGMSRDVYST	720
DYRVGGHTM	LPIRMPPES	IMYRKPTTES	DVWSLGVVLW	EIFTYKQFPW	YQLSNNEVIE	780
CITQGRVLQR	PRTCPQEVYE	LMLGCHQREP	HMRKNKIGH	TLQLNLAKAS	PVYLDILG	

Seq ID NO: 397 DNA sequence  
Nucleic Acid Accession #: AB052906  
Coding sequence: 74..814

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1	11	21	31	41	51	
AAAACCTTGA	GGTGATTGAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
CTCTGGGTCC	TTAATGGCAG	CAGCGGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
GATCCTGCTG	TCCGGCTGTG	CCCGGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
CATCACCGTC	ATCCCTAAGT	TCAGAACCTGG	ACCAAGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
GGATGAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCAAC	CTGTCACTCC	300
CCTGGGGAAG	AACTCAATAG	TCACAACGGC	CTGGAAAGCA	CAGAACCCAG	TACTGAGAGA	360
GGTGGTGAC	ATACTTACAG	AGCAACTGCG	TGACATTGAG	CTGGAGAATT	ACACACCCAA	420
GGAAACCCCT	ACCCTGCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
TGGATCTTGG	CAGTTGAGT	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
AAATGTGGACA	ACGGTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAGAGTGGG	AGAATGACAA	600
GGTTGTGGCC	ATGTCCTTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
CTTCTTGATG	GGCATGGACA	GCACCTGGGA	GCCAAGTGCA	GGAGCACCAC	TGCCCATGTC	720
CTCAGGCACA	ACCCAATCTA	GGGCCACAGC	CACCACCTCT	ATCCTTTGCT	GCCTCCTCAT	780
CATCTCCCCC	TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
CCAGCTGGCC	ACGACCTAGC	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
TGGACCCCAAT	AGCTCATTCA	CTGCCTTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGTACCTGTA	TGGAATTCCT	GCACCTTAAG	1080
TTCTGCTGTA	CAAAACAGAA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAAATCAA	1140
GTACTTCTTT	GAATGATGAT	CTCTTTCTTG	CAAAATGATAT	TGTCAAGTAA	ATAATCAAGT	1200
TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGTCTGAAAG	GAGAATTTTT	AAATTATTTA	1260
ATAAGAAAAA	ATTTATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTC	TGTACTGATA	1320
TTTAAATAAA	GAGTTCATT	TCCCAAAAAA	AAAAAATAAA	AA		

Seq ID NO: 398 Protein sequence  
Protein Accession #: BAB61048.1

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55

1	11	21	31	41	51	
MAAAATKIL	LCLPLLLLLL	GWSRAGRADP	HSLCYDITVI	PKFRPGPRWC	AVQGQVDEKT	60
FLHYDCGNKT	VTFVSPGLGK	LNVTAWKAQ	NPVLREVVDI	LTEQLRDIQL	ENYTPKEPLT	120
LQARMSCEBK	ABGHSSGSWQ	FSFDGQIFLL	FDSEKRMWTT	VHFGARKMKE	KWENDKVVAM	180
SFHYFSMGDC	IGWLEDFLMG	MDSTLEPSAG	APLAMSSGTT	QLRATATTLI	LCCLLIILPC	240
FILPGI						

Seq ID NO: 399 DNA sequence  
Nucleic Acid Accession #: NM\_001898.1  
Coding sequence: 57..482

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1	11	21	31	41	51	
GGCTCTCACC	CTCCTCTCCT	GCAGCTCCAG	CTTGTGCTC	TGCTCTGAG	GAGACCATGG	60
CCCAGTATCT	GAGTACCTG	CTGCTCTGCT	TGGCCACCCT	AGCTGTGGCC	CTGGCCTGGA	120
GCCCCAAGGA	GGAGGATAGG	ATAATCCCGG	GTGGCATCTA	TAACGCAGAC	CTCAATGATG	180
AGTGGGTACA	GCGTCCCTT	CACCTCGCCA	TCAGCGAGTA	TAACAGGCGC	ACCAAGATG	240
ACTACTACAG	ACGTCCGCTG	CGGGTACTAA	GAGCCAGGCA	ACAGACCGTT	GGGGGGGTGA	300
ATTACTTCTT	CGACGTAGAG	GTGGGCGGCA	CCATATGTAC	CAAGTCCCAG	CCCAACTTGG	360
ACACCTGTGC	CTTCCATGAA	CAGCCAGAAC	TGCAGAGGAA	ACAGTTGTGC	TCCTTCGAGA	420
TCTACGAAGT	TCCCTGGGAG	AACAGAGGTT	CCCTGGTGAA	ATCCAGGTGT	CAAGAATCCT	480
AGGGATCTGT	GCCAGGCCAT	TGCGACCCAG	CACCAACCC	TCCACCCCC	TGTAGTGCTC	540
CCACCCCTGG	ACTGGTGGCC	CCCACCTGCG	GGGAGGCTC	CCCATGTGCC	TGCGCCCAAGA	600
GACAGACAGA	GAAGGCTGCA	GGAGTCTTTT	GTTGCTCAGC	AGGGCGCTCT	GCCCTCCCTC	660
CTTCTCTCTT	GCTTCTAATA	GCCCTGGTAC	ATGGTACACA	CCCCCCCACC	TCTTGCATTT	720
AAACAGTAGC	ATCGCC					

Seq ID NO: 400 Protein sequence  
Protein Accession #: NP\_001889.1

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1	11	21	31	41	51	
MAQYLSTLLL	LLATLAVALA	WSPKEEDRII	PGGIYNADLN	DEWVORALHF	AISEYNKATK	60
DDYYRRLPLRV	LRARQQTIVG	VNYFFDVEVG	RTICTKSQPN	LDTCAFHEQP	ELQKKQLCSF	120

EIVEVPWENR RSLVKSRCQE S

Seq ID NO: 401 DNA sequence  
Nucleic Acid Accession #: NM\_003976.2  
Coding sequence: 299..961

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1 11 21 31 41 51  
CTCTGAGCTT CTCTGAGCCT TGTITGCTCA TCTGGAAGAA GGGGATTAAA CCATTACCT 60  
CATGGAGTTG TGAAGAATA GCTGCAAGC ACCTAACACA TAGTAAGTT CCCAGTGCAG 120  
CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCTCTG TTCCTCACCT GGAGAAACTG 180  
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTTCGAA GCTGCCTCAA 240  
CAGGAGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTGTGTGT TGATAGAGAT 300  
GGAACCTGGA CTGAGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360  
TGCCCTGTGG CCCACCTTGG CCGCTCTGGC TGTGCTGAGC AGCGTCGCAG AGGCTCCCT 420  
GGGCTCCGCG CCCCGCAGCC CTGCCCCCGG CGAAGGCCCC CCGCTGTCC TGGCGTCCCC 480  
CGCGCGCAC CTGCGGGGGG GACGCACGCG CCGCTGTGTC AGTGAAGAG CCGGCGGGCC 540  
CGCGCGCAG CCTTCTCGGC CCGCGCCCCC GCGCCTGCA CCCCCATCTG CTCTTCCCG 600  
CGGGGGCGCG GCGGCGCGGG CTGGGGCCCC GGGCAGCGCG GCTCGGGCAG CGGGGGCGCG 660  
GGGTGCGCGC CTGCGCTGCG AGCTGGTGCC GGTGCGCGCG CTGCGCTGGG GCGACGCTC 720  
CGACGAGCTG GTGCGTTTCC GCTTCTGCGC CGGCTCCTGC CGCGCGCGCG GCTCTCCACA 780  
CGACCTCAGC CTGGCGAGCC TACTGGGCGC CGGGGCGCTG CGACCGCCCC CGGGCTCCCG 840  
GCGGTCAGC CAGCCTCTGT CCGACCCAC GCGCTACGAA CGGCTCTCCT TCTATGACGT 900  
CAACAGCACC TGGAGAAGCG TGGACCGCCT CTCGCGCACC GCTGCGGCT GCTTGGGCTG 960  
AGGGCTGCTT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCTTGGGAC 1020  
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCTT CAAAGCTGAG 1080  
AGGCCCTTAC CGGTGGGTGA TGGATATCAT CCCGGAACAG GTGAAGGAG AACTGACTAG 1140  
CAGCCCCAGA CGCCTCAGC TGGGATCCCG AGCCTAAAG ACACGAGAGA CCTCAGCTAT 1200  
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCGCTG AACCTGGGAC 1260  
CCCTCTCTCT ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGCGCCAG CCCTGTAGGG 1320  
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTGGTTGAA AGTGCCTGTG CTGGAACCTG 1380  
CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 402 Protein sequence  
Protein Accession #: NP\_003967.1

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1 11 21 31 41 51  
MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60  
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAGA 120  
RGCLRLRQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLIG AGALRPPPGS 180  
RPVSGPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 403 DNA sequence  
Nucleic Acid Accession #: NM\_057091.1  
Coding sequence: 783..1445

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1 11 21 31 41 51  
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60  
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCAA CGCAGGGACC GGCCTACCCC 120  
TCGCTCCCGC CCTCACTCA CTCTTCCCGC CCTCGGCCCG GGCCTCCAG CTCTCTACTT 180  
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCCTTC CACCGCTCGA GTTCTCTACT 240  
CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCGCTC CCAACCTCGG GGGACCTAGC 300  
CAAGCTAGGG GGAAGCTGGT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAGGTGGGG 360  
CGGGGACAGG GCGCTCCAG CCCCACCCCG GAGTCTGGTG ACGCTGGGCG TGGAAATTGA 420  
CACCGGACGG CTGCGGCGCG GGGCAGGAG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCG 480  
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGGCCAGACC CTGCTGCCA 540  
CCCGGGCCTG GAGCCCAACA CCGAGGGGTG CAGACTGGCT GCCAAGGCCA CACTTTGGC 600  
TAAAGAGGCG ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTITGAGCT TCGGGGAGA 660  
GCCAGCACT GGTCCCCGGA AAGGTGCCCTA GAAGAACAAG GTGCAGGACC CCGTGTCTGC 720  
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GCGCTCCTGT GTGTGTATAG 780  
AGATGGAACT TGAAGTTGGA GGCCTCTCCA CGCTGTCCCA CTGCCCCTGC CTTAGGCGGC 840  
AGCCTGCCCT GTGGCCACCC CTGGCGCTC TGGCTCTGCT GAGCAGGCTC GCAGAGGCTT 900  
CCCTGGGCTC GCGCCCCCGC AGCCCTGCCG CCGCGGAAGG CCCCCCGCT GTCTGGGCT 960  
CCCCCGCGCG CCACTTGCAG GGGGAGCGCA CGGCCCGCTG GTGCAGTGA AGAGCCCGGC 1020  
GGCGCGCGCG GCAGCTTCT CCGCCCGCGC CCGCGCGCGC TGCACCCCA TCTGCTCTT 1080  
CCCGCGGGGG CCGCGCGCGG CGGGCTGGGG GCGCGGGCAG CCGCTCTCG GCAGCGGGGG 1140  
CGCGGGGCTG CCGCTGCGC TCGCAGCTG TCGCGGTGCG CGCGCTCGGC CTGGGCCACC 1200  
GCTCCGACGA GCTGGTGGCT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGGCTCTCT 1260  
CACACGACCT CAGCTGGGCC AGCCTACTGG GCGCGGGGCG CCTGCGACCG CCGCGGGCT 1320  
CCCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGCT TCCTTCATGG 1380  
ACGTCAACAG CACTGGAGA ACCGTGGACC GCGCTCCGCG CACCGCTCG GCGTGGCTGT 1440  
GCTGAGGGCT CGCTCCAGGG CTTGCGAGAC TGAACCTTA CCGGTGGCTC TTCTGCTCTG 1500  
GGACCCCTCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCG AGGGACGAAG GCCTCAAGC 1560  
TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACCTGA 1620  
CTAGCAGCCC CAGAGCCCTC ACCCTGCCGA TCCAGCCTA AAAGACACCA GAGACCTCAG 1680  
CTATGGAGCG CTTGGAGCCC ACTTCTCACA GACTCTGSCA CTGGCCAGGC CTGGAACCTG 1740  
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800  
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860  
CTGGCTGTGA CTCACCTATG GGAGCTGGCC CC

Seq ID NO: 404 Protein sequence  
Protein Accession #: NP\_003967.1

1 11 21 31 41 51  
5 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60  
PAGHLPGGRT ARWCSGRARR PPPQSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120  
RGCLRLSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180  
RPVSPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGLG

10 Seq ID NO: 405 DNA sequence  
Nucleic Acid Accession #: NM\_057160.1  
Coding sequence: 1..714

1 11 21 31 41 51  
15 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCAAGACC 60  
CACTGGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGCTC TCTCCGCGCA GCCTGCCCTG 120  
TGGCCACACC TGGCCGCTCT GGCTCTGCTG AGCAGCGTGC CAGAGGCCTC CCTGGGCTCC 180  
GCGCCCCGCA GCGCTGCCCC CCGGAGAGGC CCCCGGCTG TCTGGGCTC CCGCGCGGCC 240  
20 CAGCTGCCGG GGGGACGCAC GGGCCGCTGG TGCAGTGGAA GAGCCCGCG GCGCGCGGCC 300  
CAGCCTTCTC GGGCCGCGCC CCGCGCGCTC GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360  
GCGCGGGGCG GGGCTGGGGG CCGCGGCAGC GCGCTCGGG CAGCGGGGCG GCGGGGCTGC 420  
CGCTGCGCT CGCAGCTGGT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480  
CTGGTGGGT TCGCTTCTG CAGCGCTCC TCGCGCGCG GCGCTCTCC ACACGACCTC 540  
25 AGCCTGGCCA GCCTACTGGG GCGCGGGGCC CTGCGACGCG CCGCGGGCTC CCGCGCGCTC 600  
AGCCAGCCCT GCTGCCGACC CAGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660  
ACCTGAGAAA CCGTGGACCG CCTCTCCGCC ACCGCTGCG GCTGCTGGG CTGAGGGCTC 720  
GCTCCAGGCG TTTGCAGACT GGACCCCTAC CGGTGGCTCT TCTGCTGGG GACCTCCCG 780  
30 CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAG CCTCAAAGCT GAGAGGCCCC 840  
TACCGTGGG TGATGGATAT CATCCCGAA CAGGTGAAG GACAACTGAC TAGCAGCCCC 900  
AGAGCCCTCA CCTGCGGAT CACAGCCTAA AAGACACCAG AGACCTCAGC TATGAGCCCC 960  
TTGGAAGGCA CTCTCAGAG ACTCTGGCAG TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020  
CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCGCGGCC AGGCCCTGTA GGGACAGCAT 1080  
35 TTGAAGGACA CATATTGAG TTGCTTGGT GAAAGTGCT GTGCTGGAAC TGGCCTGTAC 1140  
TCATCATGG GAGCTGGCCC C

Seq ID NO: 406 Protein sequence  
Protein Accession #: NP\_476501.1

1 11 21 31 41 51  
40 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SVAEASLGS 60  
APRSAPREG PPPVLASAPG HLPGRRTARW CSGRARRPPF QPSRPAPPPP APPSALPRGG 120  
45 RAARAGGPGS RARAAGARGC RLRLSQLVPR ALGLGHRSD LVRFRFCSSG CRRARSPHDL 180  
SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TAGCLG

Seq ID NO: 407 DNA sequence  
Nucleic Acid Accession #: NM\_057090.1  
Coding sequence: 29..715

1 11 21 31 41 51  
50 CTGATGGGGC CTCTCGGTGT TGATAGAGAT GGAAGTTGGA CTTGGAGGCC TCTCCAGCT 60  
GTCCCACTGC CCCTGCGCTA GCGGCGAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120  
55 GTGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCTC CCTGGGCTC 180  
CGCGCCCCGC AGCCCTGCCC CCGCGAAGG CCCCGGCTG GTCTGCGCT CCGCGCGGCC 240  
CTACCTGCGC GGGGACGCA CCGCGCTG GTGAGTGA AGAGCCGCG GCGCGCGGCC 300  
GCAGCCTTCT CCGCGCGCG CCGCGCGGCC TGACCCCGCA TCTGCTCTC CCGCGGGGG 360  
60 CCGCGCGCG CCGCTGGGG GCGCGGCGC CCGCTCGG GCAGCGGGG GCGCGGGCTG 420  
CGCCTGCGC TCGCAGTGG TGCCGCTGCG CGCGCTCGG CTGGGCGACC GCTCCGACGA 480  
GCTGGTGGT TTCGCTTCT GCAGCGGCTC CTGCGCGCG GCGCGCTCT CACACGACCT 540  
CAGCCTGGCC AGCCTACTGG GCGCGGGGC CTGCGACCG CCGCGGGCT CCGCGCGCT 600  
CAGCCAGCCC TGCTGCGGAC CACGCGCTA CGAAGCGGTC TCTTCTATGG AGCTCAACAG 660  
65 CACCTGAGA ACGTGGACC GCCTCTCGC CACCGCTGC GGTGCTGCT GCTGAGGGCT 720  
CGCTCCAGG CTTTGCAGC TGGACCTTA CCGGTGGCTC TTCTGCTG GAGACCTCCC 780  
GCAGAGTCCC ACTAGCCAGC GCGCTCAGCC AGGACGAAG GCCTCAAAGC TGAGAGGCC 840  
CTACCGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900  
CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGAGGCC 960  
70 CTGCGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTGAACTCG GAGACCTCCT 1020  
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCGCGC CAGGCCCTGT AGGACAGCA 1080  
TTTGAAGGAC ACATATTGCA GTTGTGCTG TGAAGTGCC TGTGCTGGA CTGGCCTGTA 1140  
CTACTCATG GAGCTGGCCC C

75 Seq ID NO: 408 Protein sequence  
Protein Accession #: NP\_476431.1

1 11 21 31 41 51  
80 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60  
GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQSRPAPPPP PAPPALPRG GRAARAGGPG 120  
SRARAAGARG CLRLSQLVPR RALGLGHRSD ELVRFRFCSSG SCRRARSPHD LSLASLLGAG 180  
ALRPPPGSRP VSPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGLG



Seq ID NO: 409 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1746

5	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCAAC	120
	GGGGCAGCGA	TTGTGCGGT	GCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
10	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCGCTTCC	TCAATATCTC	AGCCCTCATC	240
	CCCTGAGGAG	TTGAGAAGAA	TGAGCTGTG	CGCATCACGC	CTGGGGCCCT	CCGAAACCTG	300
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Seq ID NO: 416 Protein sequence  
 Protein Accession #: NP\_077740.1

20 1 11 21 31 41 51  
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTILHPV SKLDAEKLVG RVNLKECFDA 60  
 25 ANLIHSSDDP FOILEDGSVY TINTILLSSE KRSFTILLSN TENQKKKIF VFLEHOTKVL 120  
 KKRHTKEKVL RRAKRRWAPI PCSMLNSLG PPFLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180  
 EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240  
 PIFTEETYTF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300  
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMQG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360  
 30 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTNIEGVLGVV 420  
 KPLNYEEKQK MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGE CNPPIQTVRM 480  
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWTI DENTGSIKVF RSLDREAETI 540  
 KNGIYNITVL ASDQGGRTCT GTLGILLQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600  
 EPIHGPPPDF SLESSTSEVQ RMWRLLKAIND TAARLSYQND PPFSGYVVEI TVRDLGMSS 660  
 35 VTSLDVLTCD CITENDCTHR VDPRIGGGVG QLGKMAILAI LLGIALLFCI LFTLVCGASG 720  
 TSKQPKVIPD DLAAQNLIYS NTEAPGDDKV YSANGPTTQT VGASAGQVCG TVGSGIKNGG 780  
 QETIEMVKGQ HQTSESCRGA GHHTLIDSCR GHTEVDNCR YTYSEHNSPT QPRLGEKVYL 840  
 CNQDENHKHA QDVVLTYNVE GRGSVAGSVG CCSERQBEDG LEFLDNLEPK FRTLAECMK 900  
 R

Seq ID NO: 417 DNA sequence  
 Nucleic Acid Accession #: NM\_004949.1  
 Coding sequence: 202..2745

45 1 11 21 31 41 51  
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 CTCTCGCGCG GCCCCACCTC CTCGCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120  
 GCTCGCGCGG CGGCCCTCGC CCGCGCGAGC CCTCCTACCC CGGCCCGAGC CTCGCGCGCG 180  
 50 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTC CCGCTCCTG GAACGGAGCC 240  
 CTCTCGCGCG TGCTCCTGCT GACCCCTCGG ATCTTAATAT TTGCCAGTGA TGCCCTGCAA 300  
 AATGTGACAT TACATGTTC CTCCAAACTA GATGCCGAGA AACTTGTGTG TAGAGTTAAC 360  
 CTGAAGAGGT GCTTTACAGC TGCAAACTTA ATTCATTCAA GTGATCTCTG CTTCCAAATT 420  
 TTGGAGGATG GTTCAGTCTA TACACAAAT ACTATTCTAT TGCTCTCGGA GAAGAGAAGT 480  
 55 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540  
 GAGCATCAA CAAAGGTCTT AAAGAAAAGA CATACTAAAG AAAAGTTCTT AAGGCGCGCC 600  
 AAGAGAAGAT GGGCTCCAAT TCCTTGTTGG ATGTAGAGAA ACTCCTTGGG TCCTTTTCCA 660  
 CTTTCTCCTC AACAGGTTC ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720  
 AGAGGTCTCG GAGTTGACCA AGAACCTCGG AATTTAATTT ATGTGGAGAG AGACACTGGA 780  
 60 AACTGTGATT GTACTCGTCC TGTAGATGTT GAGCAGTATG AATCTTTTGA GATAATTGCC 840  
 TTTGCAACAA CTCCAGATGG GTATACTCCA GAACITCCAC TGCCCTAAT AATCAAATA 900  
 GAGGATGAAA ATGATAACTA CCCAATTTT ACAGAAGAAA CTTATACTTT TACAATTTT 960  
 GAAATATGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020  
 GACACGATCG ACACACGCTT GAAGTACTCC ATCATTTGGC AGGTGCCACC ATCACCACC 1080  
 65 CTAATTTCTA TGATCCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140  
 GAGTTAATTG ACAAGTACCA GTTGAAAATA AAGTACAAG ACATGGATGG TCAGTATTTT 1200  
 GGTCTACAGA CAACCTCAAC TTGTATCATT AACATTGATG ATGTAATGA CCACTTGCCA 1260  
 ACATTTACTC GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATTC 1320  
 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAAGTGGAG AGCTAATTAT 1380  
 70 ACCAATTTAA AGGGCAATGA AATGGCAAT TTTAAATTTG TAACAGATGC CAAAACCAAT 1440  
 GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500  
 CAAATTTGTT TAGTTAATGA AGCTCCATTT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560  
 AGCAGCAGCA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAAACCT 1620  
 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAGTGG GAACAACAAG CAATGGATAT 1680  
 75 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAACGTAT 1740  
 CCAACAGGGT GGTCCACCAT TGATGAAAAT ACAGGATCAA TCAAGTTTT CAGAAGCCTG 1800  
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 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920  
 AGCCCATTTA TCTTAAAAA GACAGTGATC ATCTGCAAAC CCACCATGTC ATCTGCGGAG 1980  
 80 ATTGTTGCGG TTGATCTCTA TGAGCCTATC CATGGCCAC CTTTGACTT TAGTCTGGAG 2040  
 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100  
 GCTCTTCTCT ATCAGAAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160  
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 GAAATGTGCG GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGG 2280  
 AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCAATGC TCTTTTGCAT CCGTTTACG 2340

5 CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC 2400  
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 ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCCGT 2700  
 CTTGGTGAAG AATCCATTAG AGGACACACT CTGATTAATA ATTAACAAT GAAAGAAAGT 2760  
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 10 CTATGAAGGA AGAGGATCGG TGGCTGGGTC TGTAGGTGT TGCAGTGAAC GACAAGAAGA 2880  
 AGATGGGCTT GAATTTTGGG ATAATTGGA GCCCAATTT AGGACACTAG CAGAAGCATG 2940  
 CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000  
 AAAAAATTAC AAACCAAGAA TTTTAAAG CAGAAGATGC TATTGTGGG GGTTTTCTC 3060  
 TCATTATTG GATGGAATCT CTTTGGTCAA ATGCACATT ACAGAGAGAC ACTATAAACA 3120  
 15 AGTACACAAA TTTTCAATT TTTACATATT TTTAAATTAC TTATCTCTA TCCAGGAGG 3180  
 TCTACAGAAA AATTAAAGTC TGCCTTATT GTTACATTG GGTATAATGA CAACAGCCAA 3240  
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 CCTAATGGAA AATGTAGAG ACCITGCTTT AACATTATCT CCAGTTAATT AAGTGTTCAT 3360  
 20 GTGGTGCTTG GAAACTGTTG TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420  
 ATTATTTTAT TCTGTAATG TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480  
 TTGACTATTA CAATTCATT

Seq ID NO: 418 Protein sequence  
 Protein Accession #: NP\_004940.1

25 1 11 21 31 41 51  
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFDA 60  
 ANLIHSSDPD FQILEDGSVY TTNILLSE KRSFTILLSN TENQEKKIF VFLEHQTKVL 120  
 30 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQVQV SDTAQNYTII YSIRGPGVDQ 180  
 EPRNLFFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240  
 PIFTEETYP TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIQVPP SPTLFSMHFT 300  
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360  
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KINEGVLCVV 420  
 35 KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATIV NVEDQDEGPE CNPIQTVRM 480  
 KENAEEVGTTS NGKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540  
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600  
 EPIHGPFPDF SLESSTSEVQ RMWRLLKAIND TAARLSYQND PPFSGYVVP I TVRDLRGMS 660  
 VTSLDVTLCD CITENDCTHR VDRPGRGGV QLKGWAILAI LLGIALLFPI LFTLVCGASG 720  
 40 TSKQPKVIED DLAQQNLIVS NTEAPGDDKV YSANGPTTQT VGASAGVCG TVSGSIKNGS 780  
 QBTIEMVKGK BQTSSESCRA GHHTLDSCR GGHTEVDNCR YTYSEWHSFT QPRLGESIR 840  
 GHTLIKN

Seq ID NO: 419 DNA sequence  
 Nucleic Acid Accession #: NM\_002722.1  
 Coding sequence: 14..301

45 1 11 21 31 41 51  
 ACTCTGGACT CGGATGGCT GCGGCAGGCC TCTGCCTCTC CTGCTGCTC CTGTCCACCT 60  
 50 GCGTGGCTCT GTTACTACAG CCAGTGTCTG GTGCCAGGG AGCCCCACTG GAGCCAGTGT 120  
 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCAGTA TGCAGCTGAT CTCCTAGAT 180  
 ACATCAACAT GCTGACCAGG CAGGATATG GGAAGAAGCA CAAAGAGGAC ACGCTGGCCT 240  
 TCTCGGAGTG GGGTCCCGG CATGCTGCTG TCCCAGGGA GCTCAGCCCG CTGGACTTAT 300  
 55 AATGCCACCT TCTGTCTCT ACGACTCCAT GAGCAGCGCC AGCCAGCTC TCCCCTCTGC 360  
 ACCCTTGGCT CTGGCCAAAG CTGTCTCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420  
 AAGCC

Seq ID NO: 420 Protein sequence  
 Protein Accession #: NP\_002713.1

60 1 11 21 31 41 51  
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPQMAQYA ADLRRYINML 60  
 65 TRPRYGRKHK EDTLAFSEWG SPHAAVPREL SPLDL

Seq ID NO: 421 DNA sequence  
 Nucleic Acid Accession #: NM\_032545.1  
 Coding sequence: 46..718

70 1 11 21 31 41 51  
 AAATGATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA 60  
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 75 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTG CCACTCAGAA 180  
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240  
 CGAGGGCTGG GGGCCGGAGG AGCGCTCCC CTACTCCCGG GCTTTCGGAG AGGGTGCCTC 300  
 CGGCGGCGG CTGTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG 360  
 CCGGCGCCAC TTACCGGCGC GCTACTGCGA GCATGACCA AGGCGCAGTG AATGCGGCGC 420  
 80 CCTGGAGCAC GGAGCCTGGA CCTCCGCGC CTGCCACCTC TGCAAGTGA TCTTCGGGGC 480  
 CCTGCACTGC CTCCCCCTCC AGAGCGCTGA CCGCTGTGAC CCGAAGACT TCTGCGCTC 540  
 CCAGCTCAC GGGCCGAGCG CCGGGGCGC GCCCAGCTG CTACTCTGCG TGCCCTGCGC 600  
 ACTCCTCAG CGCTCTCTG GCGCGGATG GCGCGCGAC CCTCGGTCCC TGGTCCCTTC 660  
 CGTCTCCAG GGGAGCGCG GCGCTGCGG AAGGCCGGA CTGGGCATC GCCTTTAATT 720  
 TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780

TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840  
AAAAAA

Seq ID NO: 422 Protein sequence  
Protein Accession #: NP\_115934.1

1 11 21 31 41 51  
MTWRHHVRL LFTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSHFGE 60  
VTGSAEGWGP EEPLPYSRAP GEGASARPRC CRNGGTCVLG SFCVCPAHFT GRYCEHDQRR 120  
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTFDRCDPK DFLASHAHGP SAGGAPSLLL 180  
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPCGRFGLG HRL

Seq ID NO: 423 DNA sequence  
Nucleic Acid Accession #: NM\_006533.1  
Coding sequence: 72..467

1 11 21 31 41 51  
AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60  
CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120  
TCTCCGGACC TGGTGTGTCAG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180  
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGCTGTGGC CCTTCAGGAC TACATGGCCC 240  
CCGACTGCCG ATTCCTGACC ATTCACGGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300  
AGGCGCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360  
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG 420  
GCAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480  
CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAAAATC AATCAGCCCA GTGCAAAAC

Seq ID NO: 424 Protein sequence  
Protein Accession #: NP\_006524.1

1 11 21 31 41 51  
MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISSMAVA LDYMAPDCR 60  
FLTIRHQGVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120  
VKTDKWFYFC Q

Seq ID NO: 425 DNA sequence  
Nucleic Acid Accession #: NM\_080870.1  
Coding sequence: 3..710

1 11 21 31 41 51  
AGATGACACA AGTCACAGAA AAGTCCACAG AACACCCAGA AAAGACCAGG TCAACCCACG 60  
AGAAACACAC AGAAGACCCA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCAACA 120  
AAGGGAAAAA CACACCACTC CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCCACTCTGA 180  
CCACTGAGAC CATAAAGCC CCACTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240  
TCACAAAGAC TATAAACCCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300  
CTTCTCATCT AAATAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCACCTCTC 360  
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAAAG CACAGGAAAC GAGAGCCATC 420  
CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAAATG 480  
ATTCACTCCC TGCAATGGCC ATAGTTATTG TGGTCTCTGT GGCTGTGATT CTCCTCTCTG 540  
TGTTCCTTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCGC ACCTAACCCT 600  
AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAACTCTCTC CCGGTCTACT 660  
TGATGAGGCA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGAGTA 720  
GGCGCCACGC CCTGGCTCTT CCATGCTCTG CCCCTTCTCT GGATGAGGAA CCGGACTCAC 780  
AATTTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAAAC 840  
CTTCATCTGT TCTTGAAACT GGTGGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT 900  
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TGAGTCTCAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080  
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140  
TTATTTCCAT TCACATTATC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTTCTC 1200  
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AAGAAGAAAA GAGAATTAT TCCCTTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320  
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TTAGTTTTCC TAAATGTCTA CAGTGGACGC CCTGTTGGTT TGGCTTGCTG GGTGTGGGTT 1440  
GGACACGCAA GGAGGGGATT TTTATTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500  
GACCTTCCTT GATTGGTCTC TCAGCATTTA TTTTCTGTCT TCTTCCACCA AAAGCCAGCT 1560  
GTAGCTTTAT CTCGTAAAGG TTACCCATCT TCTCTACTGT CCCCATTCTC TCTCTCCCA 1620  
CCTTCAACCC AGATTCAAGT TTTCTCTCTT GTAGGCATTI CATCTGTGTG TGTTTCTCTG 1680  
ATTTTCTCTC TCTCTCTCTA TGGCCATTTC ACCTTATTAC TGATTGGGTA GAGGGGGAAA 1740  
AGGAGAATGA TGATGATAGT TTCCTTCTGT CTATTGACCT TTTTATAAT AAGTATAAC 1800  
ATGTT

Seq ID NO: 426 Protein sequence  
Protein Accession #: NP\_543146.1

1 11 21 31 41 51  
MTQVTEKSTE HPEKTTSTTE KTTTPEKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60  
TETIKAPVKS TENPEKTAIV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSFTLI 120  
TSRTKLSSIT SEATGNESHF YLNKDGSQLG IHAGQMGEND SPPAWAIVIV VLVAVILLLV 180

FLGLIFLVSY MMRTTRTLTQ NTQYNDAEDE GGPNSYPVYL MEQONLGMGQ IPSPR

Seq ID NO: 427 DNA sequence  
Nucleic Acid Accession #: XM\_069480.1  
Coding sequence: 1..4383

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1 11 21 31 41 51

ATGGACACTG TGCTGGTGCT GTCCTGGGGC CTGCAGGCCCT TGGCCCGACC CAGTCCGAAG 60  
CCCCAGAAGG ACTCTGTCTC AGACTGGGGC ATTGTGTGTA TCACTCTCAC TTTGGTGGCA 120  
GCAATTGTCA GCCTAATGTA CGGTATCAAG AAGGCCTGCC AGTTCCGGAG GGAGATGAGT 180  
CTGGGGTGTG GCTGTGGCTC TGTGACCCCT TACAGCAGCC ACCATGAGGG GGAGGCTGCC 240  
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GAATATCAGA AAATCGGGGA ACTCTCAACA TCCGATCACA TATTTCCCT CACTCCAGGC 360  
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CTCCCTAAAT CTACAGAAAT CCAATGAGCA AAACGCCACT GCAACACCAK ACGCCATTCT 480  
AAGCCAACTG ACAAGCCTAC AGGCACTCC AAAACTATAG ACCACAAAG CTCTACAGAT 540  
AATCATGAGG CTCTCCAC TTCTGAAGAA AACTCCAGCA ACCAAGGAA AGACCCAATG 600  
ATCCGGAACC AGCGCTCTGT TGATCCTGCT GACTCCACTA CCACACATAA AGAATCCGCT 660  
GGAAAAAACA ATATAAGCC AGCACCAGAG AGCAAAATAA ACTGTCTGTA GTCCACRACA 720  
GGCAATCAAA CGTAAACAAG AAAATCAGAT AAACTGGAA GACCTTTGGA AAAGTCCATG 780  
AGTACTTTGG ATAAGACAAG TACCAGCTCA CATAAGACTA CACTTCTT CCACAACTCA 840  
GGCAATTCAC AGACCAAGCA AAAAAGCACA TCTTTTCCAG AAAAATCAC AGCAGCCTCA 900  
AAAAACAAT ACAAGACCA AGGAACCCCA GAAGAGTCAG AAAAACTGA AGATTCCAGA 960  
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TCAGCCAAATG AGCTCAGACA ATCTCTAGCA GAGCCTACAG AACATGGAGG AAGGACAGCC 1080  
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TCCCCAGCAG AGCCTACAGA AAATGGACAA AGGACCCCAT TTGCCAATGA GAAAACCA 1740  
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CCATCCCCAG CAGAGCCTAC AGAAAATGGA GACAGGACTC CTTTGGCCAA TGAGAAGACC 1920  
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ACCACATCAT CCTCAGCAGA GCCTACAGAA CACGAAGAAA GGACTCCACT GGCCAATGAG 2040  
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ACCACACCAT CCCCAGCAGG GCCTACAGAA AATAGAGAAA TGACAGCCAA CGAGAAGACC 2160  
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TCATCCCCAG CAGAGCCTAC AGAAAATGGA CAAGGACCC CATTTGCCAA TGAGAAGACC 2280  
ACATCATCCC CAGCAGAGCC TACAGAACAC GGAGAAAGGA CCCACTGGC CAATGAGAAC 2340  
ACCACATCAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA GGACAGCCAA TGAGAAGACC 2400  
ACACCATCCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAACACCACA 2460  
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ACCACATCAT CCTCAGCAGA GCCTACAGAA CACGAGAAA GGACTCCACT GGCCAATGAG 2640  
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ACCACACAT TCCCAGCAGA GCCTACAGAA AATAGAGAAA GCACAGCCAA TGAGAAGACC 2760  
ACACCATCCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAACACCACA 2820  
CTATCCCCAG CAGAGCCTAC AGAACATGAA GAAATGACCC CATTTGCCAA TGAGAAGACC 2880  
ACACTATCCC CAGCAGAGCC TACAGAAAAT GGAGAAAGGA CCCCATTGCG CAATGAGAAG 2940  
ACCACACCAT CCTCAGCAGA GCCTACAGAA CATGGAGAAA GGACCCCACT GGCCAATGAG 3000  
ATCACCACAC CATCCCCGCG AGAGCCTACA GAACATGGAG AAAGGATAGC CAATGAGAAG 3060  
GCCACACCAT CCCCAGCAA GCCTACAGAA CATGGAGAAA CGACAGTCAA TGAGGACACC 3120  
ACACCATCTC CAGCAGAGCC TACAGAAAAT GGAGAAAGGA CCCCATTGCG CAATGAGAAC 3180  
ACCACACAT CCCCAGCAGA GTCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAAGACC 3240  
ACACCATCCC CAGCAGAGCC TACAGAACAT GGAGAAAGGA CACCATCAGC CAATGAGAAG 3300  
ACCATACCAT CTCCAGCAAA GCCTACAGAA CACGAAGAAA TGACCCCATC GGCCAATGAG 3360  
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TCAGCCAATG TGATCACACC AGCCCCAGCA GAGCCTATAA AACATGCAA AAGGACCACA 3660  
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 FGSRCLSCSP ENTSTVKRGA VNISACGVPC PEGKPSRSLG MPCHPCPRDY YQPNAGKAPC 1140  
 LACPTFYGTP FAGSRITTEC STSVLNTITF GGFHLELLN CPSEVFHECF FNPCHNSGTC 1200  
 75 QQLGRGYVCL CPLGYTGLKC ETDIDECSPL PCLNNGVCKD LVGEFICECP SGYTGORCEE 1260  
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 FLCKCPGFL GTRCGNVDE CLSQPKNGA TCKDGANSFR CLCAAGFTGS HCELNINECQ 1380  
 SNPCRNQATC VDELNSYSCK QQPGFSGKRC ETEQSTGFNL DFEVSGIYGY VMDGLMPLSL 1440  
 80 HALTCTFMK SSDDMNYGTP ISYAVDNGSD NTLILLTDYNG WLYVNGREK ITNCPVNDG 1500  
 RWHHIAITWT SANGIKWYVI DGKLSGGAG LSVGLPIPGG GALVLGQEQD KKGEGFSPA 1560  
 SFVGSISQLN LNDYVLPQK VKSLATSCPE ELSKGNVLAW FDLSGIVGK VKIDSISIFC 1620  
 SDCPRLGGSV PHLRTASEDL KPGSKVNLFC DPGFQLVGNP VQYCLNQQGW TQPLPHCERI 1680  
 SCGVPPPLEN GFHSADDPYA GSTVTYQCN GYLLGDSRM FCTDNGSWNG VSPSCLDVDE 1740  
 CAVGSDCEH ASCLNVDGYS ICSCVPPYTG DGKNCAPFK CKAPGNFENG HSSGEITYVG 1800  
 AGVTFPSQEQ YQLMGVTKIT CLESGEWNHL IPYCKAVSCG KPAIPENGCI BELAFTFGSK 1860

VTYRCNKGYT LAGDKESSCL ANSSWSHSP VCEPVKCSSP ENINNGKYIL SGLTYLSTAS 1920  
 YSCDTGVSILQ GPSIIETAS GIWDRAPPAC HLVFCGEPPA IKDAVITGNN FTFRNTVTYT 1980  
 CKEGYTLAAG DTIECLADGK WSRSDQQLA VSCDEPIVD HASPETAHRL FGDIAPFYCS 2040  
 DGYSIADNSQ LLCNAQGWV PPEGQDMPRC IAHFCEKPPS VSYSILESVS KAKFAAGSVV 2100  
 SFKCMGFFVL NTSAKIECMR GGQWNPSPMS IQCIPVRCGE PPSIMNGYAS GSNYSFGAMV 2160  
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 YQCNPGYKVS GSPVFVQAN RHWSESPLM CVPLDCGKPP PIQNGFMKE NFEVGSKVQP 2280  
 FCNEGVELVG DSSWTCQKSG KWNKSNPKC MPAKCEPPL LENQLVLKEL TTEVGVVTF 2340  
 CKEGHVLQGP SVLKCLPSQK WNDSPFVCKI VLCTPPPLIS FGVPISPASL HFGSTVKYSC 2400  
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 GFELVGNITT LCGENGHWLG GKPTCKAIEC LKPKELNGK FSYTDLHYGQ TVTYSNCRGF 2520  
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 IPVDCSSPPV SANGQVRGDE YTFQKEIET CNEGFLLEGA RSRVCLANGS WSGATPDCVP 2880  
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 TPVIEYGTVN GTDFDCGKAA RIQCFKGFKL LGLSEITCEA DGQWSSGPFH CEHTSCGSLP 3060  
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 ANAVATGEAH TYSEVKLR C LEGYTMDDT DTFTQKDG R WFERISCS KKCPLPENIT 3180  
 HILVHGDDFS VNRQVSVSCA EGYTFEGVNI SVQLDGTWE PPSDESCSP VSCGKSPESV 3240  
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 KADIENRTTG PNVSYSNCRG YSLEGPSEAH CTENGWNSHP VPLCKPNPC VPVPIPENAL 3360  
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 GVHYQYGDMI TYSYCSGYML EGFLRSVCLB NGTWTSPIC RAVCRFPQN GGICQRFNAC 3480  
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 PNRCHCLSSW TGHNCNR

Seq ID NO: 431 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..390

1 11 21 31 41 51  
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 CAGTGTCTGT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCGGCCAATG TGGTCCCCC 240  
 TGCACCTTCT GGCCCTGCTT TGAGCTCTGC TGTCTGATT CCTTTGGCCT CACAAACGAT 300  
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Seq ID NO: 432 Protein sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLC PREVIAPAGS EPWLQCPAPR CGDKIYNPLE 60  
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Seq ID NO: 433 DNA sequence  
 Nucleic Acid Accession #: NM\_007231.1  
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 GTGCAGGGAG AAGGAGAAAG TGTGCGCTTC ATCAGAGAAT TTCCATGTTG GTGAAAATGA 180  
 TGAGAATCAG GACCGTGTA ACTGGTCCAA AAAATGSGAT TATCTTCTAT CTATGATTGG 240  
 ATACGCACTG GGATTAGGAA ATGTGTGGAG ATTTCATAT CTGACCTACA GCAATGGTGG 300  
 AGGCGCCTTC TTGATACCTT ATGCAATTAT GTTAGCATG GCTGGTTTAC CTTTGTCTCT 360  
 TCTGGAGTGT TCACTGGGAC AATTGTCTAG CTAGGTCCA GTTTCAGITT GSAGGATTCT 420  
 TCCATTGTTT CAAGGTGTGG GAATTACAAT GGTCTGTATC TCCATTTTGT TGACAATCTA 480  
 TTACAATGTC ATAATTGCTT ATAGTCTTTA CTACATGTTT GCTTCTTTTC AAAGTGAAC 540  
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 CTGGGTAGAC ATCAACAATT TTACCTGCAT CAACGGCAGT GAAATTTATC AGCCAGGGCA 720  
 GCTTCCCACT GAACAATATT GGAATAAAGT GGCCTCCCAA CGGTCAAGTG GAATGAATGA 780  
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 AGCAGCACTA TTTAAAGGAA TCAATCTGTC TGCCAAGGTG GTATATTITA CAGCTCTTTT 900  
 CCCCTATTGT GTCCCTACTCA TCCTGTTAGT ACGAGGTGCA ACTCTGGAGG GTGCTTCAA 960  
 AGGCATTTC TACTATATTG GAGCCCACTC AAATTTTACA AAACCTAAGG AAGCTGAGGT 1020  
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 TGCTCTATCA TCTTACAATA AGTTCRAAAA CACTGCTTC TCTGATGCCA TTGTGGTTTG 1140  
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 CACAAACACA ATTCAAGATT TATTTCCCAA AGTGATGAAG AAAATGAGGG TTCCCATAAC 1440  
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 GTTTAAGCAT CATAGCCTAT GATGATAAAC ACTGCCTATA TATGTAAATA GCTTTTCATC 3180  
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 TTGTAGGGTG CTCATGGTG GTTTTTATTA TTATTACTCA GATTCCACAG TGGCAAGAAA 4380  
 CATCATCTA CATAATGGAA AACATTTACA TCAATCCCA CTACTTTAA TCGCAACTTG 4440  
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Seq ID NO: 434 Protein sequence  
Protein Accession #: NP\_009162.1

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 MVLISIFVTI YYNVILAYSL YMFASFQSE LPWKNCSWS DNKCSRSPIV THCNVSTVNK 180  
 GIQEIQMNK SWVDINNFTC INGSEIYQPG QLPSEYWNK VALQRSSGMN ETGVIWVYLA 240  
 LCLLLAWLIV GAALFKGIKS SGKVVFYFAL FPYVLLILL VRGATLEGAS KGISYYIGAQ 300  
 SNPTKLKEAE VWKDAATQIF YSLSVANGGL VALSSYNKFK NNCFSDAIVV CLINCLTSVF 360  
 AGFAIFSILG HMAHISGKEV SQVVKSGFDL AFIAYPEALA QLPQGPFWSI LFPFMLLTIG 420  
 LDSQFASIEI ITTTIQDLFP KVMKQMRVPI TLGCCLVLEL LGLVCVTQAG IYVWHLIDHF 480  
 CAGWGLLIAA ILELVGIWI YGGRPIEDT EMMIGAKRWI FWLWRACWF VITPILLIAI 540  
 FIWSLVQFHR PNYGAIPYFD WGVALGWHI VFCLIWIPIM AIKIIQAKG NIFQRLISCC 600  
 RPASNNGPYL EQHRGERYKD MVDPKKEADH EIPTVSGSRK PE

Seq ID NO: 435 DNA sequence  
Nucleic Acid Accession #: M18728.1  
Coding sequence: 51..1085

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1 11 21 31 41 51  
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5 CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
 GCCTCCCGGT CAGTCCACAG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660  
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACCGCACTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780  
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840  
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
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 15 GCAAAACATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
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 20 AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTTCTAGACT CACCTGTCTT CACTCCCTGT 1680  
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 25 CTCTTGGTAT TACCTCCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
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 35 TAGCTCTATA ACT

Seq ID NO: 436 Protein sequence  
 Protein Accession #: AA59907.1

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 TLQVAKSLDL NEBATGQFHV YPELPKPSIS SNNSNPVEDK DAVAFTECEP VQNTTYLWNV 180  
 45 NQQLPVSFPR LQLSNGNMTL TLLSVKRNDK GSYECRIQNP ASANRSDPVT LNVLYGPDVP 240  
 TISPSKANYR PGENLNLSC AASNPPAQYS WFINGTFQQS TQELFIFPNIT VNNSGSMYMQ 300  
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Seq ID NO: 437 DNA sequence  
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5 GGCTGGAATT ACAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTAAAAA AAAAAAAGA 2280  
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340  
10 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
TGTTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460  
CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520  
TAGCTCTATA ACT

Seq ID NO: 438 Protein sequence  
Protein Accession #: AAA59908.1

1 11 21 31 41 51  
| | | | |  
20 MDSPSQDVKT RLLIMIRLLP PFNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV 60  
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

Seq ID NO: 439 DNA sequence  
Nucleic Acid Accession #: M18728.1  
Coding sequence: 2370..2501

1 11 21 31 41 51  
| | | | |  
30 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
CCTCAGCCCC TCCTCTCAGA TTGCATGTCC CCTGGAAGGA GGTCCGTGCTC ACAGCCCTCAC 120  
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG 240  
GTTACAGTGC GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
TAGGAATCA ACAAGCTACC CCAGGGCCCG CATAAGTGG TCGAGAGACA ATATACCCCA 360  
ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
35 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480  
TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540  
CCTTCACTGT TGAACCTGAG GTTCAGACA CAACCTACCT GTGGTGGSTA AATGGTCAGA 600  
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCT ACTCTACTCA 660  
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
40 ACCGAGTGA CCGAGTCAAC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780  
CCTCAAGGCG CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCTCTA 840  
ACCCACCTGC ACAGTACTCT TGGTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
45 TCCTCTCAGC TGTGGCCACC GTGGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
TATAGCAGCC CTGGTGTATT TTGATATT TCGGAAGACT GGCAGATTGG ACCAGACCT 1140  
GAATTCTTCT AGCTCCTCCA ATCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200  
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260  
ACCCCTCAGG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320  
50 GCAAAAGATG GTGAGAAATG GACGACTTCA CACTATGAC AGCTTTTCCC AAGATGTCAA 1380  
AACAAGACTC CTATCATGTA TAAGGCTCTT ACCCCCTTTT AATTGTTCCT TGCTTATGCC 1440  
TGCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAAAAG 1560  
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
55 AAATGTACAG TGGTCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTCTC CACTCCCTGT 1680  
TTTAATTCAA CCCAGCCTAG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800  
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860  
CTGACTCAIT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
60 CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
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TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
65 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTAAAAA AAAAAAAGA 2280  
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340  
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
TGTTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460  
70 CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520  
TAGCTCTATA ACT

Seq ID NO: 440 Protein sequence  
Protein Accession #: AAA59909.1

1 11 21 31 41 51  
| | | | |  
75 MLTNVPIVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 441 DNA sequence  
Nucleic Acid Accession #: NM\_002381.2  
Coding sequence: 64..1524

1 11 21 31 41 51

5	AAATCCGAGC	CTCGCGTGGG	CTCCTGGCCC	CCGACGGACA	CCACCAGGCC	CACGGAGCCC	60
	ACCATGCCGC	GCCCCGCCCC	CGCGGCGCGC	CTCCGCGGAC	TCCTCCTGCT	GCTCTGGCCG	120
	CTGCTGCTGC	TGCCCTTCGC	CGCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG	180
	GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCGCCCTT	CTCCTGCGGC	TCCCGACGGC	240
	GCGCCGCTT	CCGGGACGAC	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
	AGACCCCTGG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
	ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
	ACGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TCGAGTTCCA	ACTCCAGGCC	480
10	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGAA	TCACACCCCT	GTCAACAGGC	540
	ACCATGTGAG	GCCTAGCCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCAGGG	600
	GCTGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC	660
	CAGGACCAAG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
	GTGGGCGTGG	ACCGGGCAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTTAGAG	780
15	GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCATTGAGA	AACTTTCCTC	TAGATTCCAG	840
	GAAACCTTCT	GTGCGCTGGA	CCCCTGTGTG	CTTGGAACAC	ACCAGTGCCA	GCAGCTCTGC	900
	ATCAGTGATG	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
	GACAAGAAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
20	ATCTGTGTGA	ATGACAGAGG	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
	AATGAAGACA	GGAAACTTTG	TTCAAGCTCA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
	CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
	ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
	GGTGGCCAGC	ACATTTTGTG	GAGTGTGGGG	GCGGCATCCT	ACCAGTGTGA	TGCTATCTCT	1320
25	GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTACGCCA	CTGAGGAAGC	ACGAAGACTT	1380
	GTTCCTCAGT	AAAGTGTCTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTCAGC	1440
	TCGTATCTTC	AAAGACTGAA	CACATAAATT	GATGACATTT	TGGAGAAGTT	GAAATAAAT	1500
	GAATATGGAC	AAATACATCG	TTAAATTGCT	CCAATTTCTC	ACCTGAAAAT	GTGGACAGCT	1560
	TGGTGTACTT	AATGACTCAT	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCCTGTAA	1620
30	TAAATTGGCA	TTATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTGTA	TGAAGATCTT	1680
	CTGCAGAACT	AGCATGATTT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
	CTTTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAT	GAAAGTTTAA	1800
	GTGTTCTTTT	ATCTACTAAT	TGAGCCATTT	AAATTTTAAA	TGTTTATATT	AGATAACCAT	1860
	ATTACAATGG	GAAACTTTAG	GCTCTAGTTT	TTTTGATAGT	ATTATATAATA	TAAATCAATC	1920
35	TTATTAATGA	GAGTGCATAA	TGTACAAAGT	ATTACACAT	ACAACTTCAT	ATAACTGAGA	1980
	TGAATGTAAT	TTTGAACCTG	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG	2100
	TGAACATTAC	ATTGCCATTT	TTAATTCATT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
	AGCACTAGTT	GTGAATTTAG	GGTGTAAAC	TTTTTACCAA	GTACAAAAAT	CCCAAAATTA	2220
40	CTTTATTTAT	TTGCTTCAGG	ATCCAAGTGA	CAAGTTTATA	TATTTATAAA	ATTGCTATAA	2280
	ATCGACAAAA	TCTAATGTTG	TCITTTTAAAT	GTTAGTGATC	CACCTGCCTC	AGCCTCCCAA	2340
	AGTGCATGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
	AAATCTTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AAATTTGCAC	2460
	TGCTCAATTC	TGTTTTCGCT	TTGCAATGTC	TTTAATATAA	TAAAGGTTAT	TACCTTTACA	2520
45	TATTATCATG	TCTATTTTGG	ATGACTCATC	AAATTTGTCT	ATTAAAGATA	TTTCTTTAAA	2580
	TTAAAAA	AAAAA					

Seq ID NO: 442 Protein sequence  
 Protein Accession #: NP\_002372.1

50	1	11	21	31	41	51	
	MPRPAPARRL	PGLLLLLLWPL	LLLPSAAPDP	VARPGFRRLR	TRGPGGSPGR	RPSPAAPDGA	60
	PASGTSEPRG	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRRI	DTLDIGPADT	120
55	RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIGTAM	DEAFTVEAGA	180
	REPSSNIPKV	ALIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
	HVFVYETVYV	TEKLSRRFQE	TFCALDPCVL	GTHQQHVCII	SDGBGKHICE	CSQGYTLNAD	300
	KKTCALDRIC	ALNTHGCEHI	CVNDRSGSYH	CEBYEGYTLN	EDRKTCASQD	KCALGTHGCG	360
	HICVNDRTGS	HHCECYBGYT	LNADKKTCSV	RDKCALGSHG	CQHICVSDGA	ASYHCDCTPG	420
60	YTLNEDKKTC	SATEEARRLV	STEDACGCEA	TLAFQDKVSS	YLQRLNKLID	DILEKLKINE	480
	YQIHR						

Seq ID NO: 443 DNA sequence  
 Nucleic Acid Accession #: NM\_016639.1  
 Coding sequence: 40..429

65	1	11	21	31	41	51	
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	CGGTGCTGCG	GGCTCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCCGGG	120
70	GAGCAAGCGC	CAGGCACCGC	CCCCTGCTCC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
	AAGTGATGCG	ACTGCGGCTC	TTGCAGGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
	GCTGCAGCAG	CTCTGCCCCC	CTTCCGCGTG	CTTTGGCCCA	TCCTTGGGGG	CGCTCTGAGC	300
	CTGACCTTCG	TGCTGGGGCT	GCTTTCTGGC	TTTTTGGTCT	GGAGACGATG	CGCAGGAGAG	360
	GAGAAGTTCA	CAACCCCAT	AGAGGAGACC	GCGCGAGAGG	GCTGCCGAGC	TGTGGCGCTG	420
75	ATCCAGTGAC	AATGTGCCCC	CTGCCAGCGG	GCGCTCGCCC	ACTCATCAIT	CATTATCCAA	480
	TTCTAGAGCC	AGTCTCTGCC	TCOCAGACGC	GCGGGGAGCC	AAGCTCTCTC	AACCAACAGG	540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTGAGGG	GAACCTTCCA	600
	AGGTGTCTGG	TGCTGGCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
	ACAAAACAGC	TGACACTGAC	TAAGGAACCT	CAGCATTTGC	ACAGGGGAGG	GGGGTGCCTT	720
80	CCTTCCTTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
	TCACCTCAGAT	GTCCCTGAAT	TCCACACCGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
	TTAACACTAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCAACTC	900
	CCCAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAAATTTAT	960

AATAAAGAA TCTTTAACTT TAAAAA AAAA

Seq ID NO: 444 Protein sequence  
Protein Accession #: NP\_057723.1

1 11 21 31 41 51  
MARGSLRRLL RLLVLGLNLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60  
SDFCLGCAAA PPAPFRLWLP ILGGALSLTF VLGLLSGFLV WRRCCRREKF TTPIETTGGE 120  
GCPAVALIQ

Seq ID NO: 445 DNA sequence  
Nucleic Acid Accession #: AF322916.1  
Coding sequence: 50..4300

1 11 21 31 41 51  
GCACTCCGCA GCCTTTAAGG TTGCGCGGG GGCAGGCAA GAGTTAGCCA TGAAGAGCCT 60  
CAAGTCCCOC CTGAGGAGGC AGGACGTGCC CGGCCCGCG TCGTCTGGCG CCGCCGCCGC 120  
CAGCGGCGCAT GCAGCAGATT GGAATAAATA TGATGACCGA TTGATGAAAG CAGCAGAAAG 180  
GGGGGATGTA GAAAAAGTGA CCTCAATCCT TGCTAAAAAG GGGGTCAATC CAGGCAAACT 240  
AGATGTGGAA GGCAGATCTG TCTTCCATGT TGTGACCTCA AAGGGGAATC TTGAGTGTTC 300  
GAATGCCATC CTTATACATG GAGTTGATAT TACAACCAGT GACACTGCAG GGAGAAATGC 360  
TCTTCACTGS GCTGCTAAGT ATGGACATGC ATTGTGCCTA CAAAACTTC TACAGTACAA 420  
TTGTCCCACT GAGCATGCAG ACCTGCAGGG AAGAACTGCA CTTCAAAAA AAGCAATGGC 480  
AGATTGTCTT TCTAGCATAC AGCTGCTTTG TGACCATGGG GCCTCTGTGA ATGCCAAAGA 540  
TGTAAGAGGG CGGACACCACT TTGTTCTGGC TACTCAGATG AGTAGGCCAA CAATATGTCA 600  
ACTGCTGATA GATAGAGGAG CGGATGTTAA TTCCAGAGAC AAACAAACCA GAACTGCCCT 660  
CATGCTAGGT TGCGAATATG GTTGACAGAGA TGCAGTAGAA GTCTTAATTA AAAATGGTGC 720  
TGATATAAGC TTGCTGGATG CGCTTGGCCA TGATAGTTCT TACTATGCAA GAATTGGTGA 780  
CAATCTGGAC ATTCTAACCT TGTGAAGAC TGCATCGGAA AATACCAACA AAGGAGAGA 840  
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AAATGTGAAG TCAGATCAGA GGGAGCATCA AAATATTGAG GATTGGAGA TTGAAATGA 960  
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AAGTCATTTC AGTAACCGAA AAGAGATAT GCTTCTTAAA CAAGGTGAGA TGTATATGGC 1260  
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ACCTCTGAAA CTATCTTTAC CCAGTCAAAC GTCTACTCTT GAAAAAGAAA TTTTAAAGAA 1380  
AGAGTTAGAA GCAATGCGAA CTTTCTGTGA GTCAGCAAAA CAAGACCGAC TGAAGCTCCA 1440  
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AGAACACTTA ACAAGTGAAG CAGCCTCAGG GAATCACAGA CTAACCGAGG AACTGAAGGA 1680  
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GATAGAAGAA AATAAGCGAT TACAGAAGGA ACTTAGTATG TGTGAAATGG AGCGAGAGAA 1860  
GAAAGGAAGA AAGGTCACAG AGATGGAAGG CCAGGCAAAA GAATTGTGAG CGAAGTTGGC 1920  
CCTTTCCATT CCAGCTGAAA AATTTGAAAA CATGAAGAGC TCATTATCAA ATGAAGTGA 1980  
TGAGAAAGCA AAAAAATTAG TAGAAATGGA AAGAGAACAT GAAAAATCAC TTAGTGAAT 2040  
TAGACAGTTA AAGAGAGAAC TTGAGAATGT TAAGGCCAAG CTTGCTCAGC ACCTCAAAAC 2100  
AGAGGAACAT GAACAGGTTA AGAGCAGATT AGAACAGAAA TCAGGAGAAA TTGGGAAGAA 2160  
GATCACTGAG TTAACATTGA AAAATCAGAC ACTACAAAAG GAAATTGAAA AAGTTTATTT 2220  
GGATAATAAG CTCCTCAGG AGCAAGCACA TAACTTAACT ATTGAATGA AAAATCATT 2280  
TGTTCCTTTA AAAGTAAGTG AAGACATGAA AAAGTCACAT GATGCAATTA TTGATGATCT 2340  
TAATGAAAGG CTTTATAGTG TAACACAAA ATATACAGAA AAGAAGTTGG AAATGGAGAA 2400  
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ACCTCTGAG AAACATGAAA AAGAGATAAT AGCTCTGAAA TCCAATATTG TTGAACCTTA 2520  
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AGATGTGAAG AAAAAATTG AAGATATAAA TCAGGAATTT GTAAAAATAA AAGATAAGAA 2760  
TGAATATTA AAAAGAAACC TGGAAAAAC TCAGAACCAA ATAAAGCTG AGTACATCAG 2820  
CCTGGCAGAG CAGCAGGCAA AGATGAGCTC GCTAAGTCAG AGCATGAGAA AGGTGCAGGA 2880  
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TGCCGAAATT AAAGCCGAGA AGAAGGAGCT CGACACAATA CAAGAAATGCA TTAAGGTAAA 3000  
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AACAGACGAG CTAAACAAAC AGTTAAAGAA CTGTCTCAG AAATACACGG AAGTAAAGAA 3300  
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5 GCTTAATGAT GTGGAAGAT TAAACAGGC ACTCAATGGC CTTTCCAAC TCACCTACAC 4080  
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 ATCTCTGGAG CAACAGCTGG CCGATGCTGA CAGACAGCAC CAAGAAGTAA TTGCAATTAA 4200  
 TCGGACACAC CTTCTTAGTG CTGCACAGGG TCACATGGAT GAAGATGTTC AGGAGGCTCT 4260  
 GCTCCAGATG ATACAAATGC GGCAGGGGCT TGTGTGCTAG COGTTAGCAC TGACTGCCAG 4320  
 TATCTGTTT ATCTTGCTGG TGCTGAACAT TCTTTGTGCA ACTCCATGGT CTTTCTGGGC 4380  
 CTTACTGTGC TGGTATAAT AAAATAAAT ATATTTTGT CTGGGTGT

10 Seq ID NO: 446 Protein sequence  
 Protein Accession #: AAG49577.1

1 11 21 31 41 51  
 15 MKSLKSLRR QDVPGPASSG AAAASAHAAD WNKYDDRLMK AAERGDVEKV TSILAKKGVN 60  
 PGKLDVEGRS VFHVVTSKGN LECLNAILIH GVDITTSDTA GRNALHLAAK YGHALCLQKL 120  
 LQYNCPTEHS DLQRTALQK KAMADCPSSI QLLCDHGASV NAKDVKGRTP LVLATQMSRP 180  
 TICQLLIDRG ADVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSSTYA 240  
 RIGDNLILT LKTASENTN KGRELWKKGP SLQQRNLTHM QDEVNVKSHQ REHQNIQDLE 300  
 20 IENEDLKERL RKIQEQEQRIL LDKVNGLQIQ LNEEVMVADD LESEREKLKS LLAKEKQHE 360  
 ESLRTIEALK NRPKYFESDH LGSGSHFSNR KEDMLLKQGG MYMADSQCTS PGIPAHMQSR 420  
 SMLRPLELSL PQQTSYSENE ILKKELEAMR TFCESAKQDR LKIQNELAHK VAECKALALE 480  
 CERVKESDE QIKQLEDALK DVQKRMYESE GKVKQMOTHF LALKEHLTSE AASGNHRLTE 540  
 ELKDQLKDLK VYEGASAEV GKLRNQIKQN EMIVEEPKRD EGKLIENKR LQKELSMCEM 600  
 25 EREKGRKVT EMEGQAKELS AKLALSIPAE KFNEMKSSLS NEVNEKAKKL VEMEREHEKS 660  
 LSEIRQLKRE LENVAKLQAO HVKPEEHEQV KSRLEQKSSE LGKKITELTL KNQTLQKEIE 720  
 KVVLDNKLK EQAHNLTIEM KNHYVPLKVS EDMKSHDAI IDDLNRKLLD VTQKYTEKKL 780  
 EMEKLLLEND SLKSDVSRLE TVFVPPKEHE KEIIALKSNI VELKKQLSEL KKKCGEDQEK 840  
 IHALTSENTN LKHMMSNQYV PVKTHEEVKM TLNDTLAKTN RELLDVKKKF EDINQEFVKI 900  
 30 KDKNEILKRN LENTQNIKA EYISLAHEHA KMSLSQSMR KVQDSNAEIL ANYRKQOEI 960  
 VTLHAEIKAO KKELDITQEC IKVYAPIVS FECEKRFKA TEKELKDQLS EQTKYSVSE 1020  
 EEVKNKQEN DLKKKEIFTL QKDLRDKTVL IEKSHEMERA LSRKTDELNK QLKDLQSKYT 1080  
 EVKNVKEKLV EENAKOTSEI LAVONLLQKQ HVPLEQVEAL KKSNGTIEN LKEELKSMQR 1140  
 CYEKQQTVT KLHQLENOK NSSVPLAEHL QIKEAFEKEV GIHKASLREK EESQNKME 1200  
 35 VSKLQSEVQN TKQALKLET REVVDLSKYK ATKSDLETQI SSLNEKLANL NRKYEEVCEE 1260  
 VLHAKKEIS AKDEKELLHF SIEQEIQDK ERCDKSLTTI TELQRRIQES AKQIEAKDNK 1320  
 ITELNDVER LKQALNGLSQ LTYTSGNPTK RQSLDITLQ HQVKSLEQL ADADRQHEV 1380  
 IAIYRTHLS AAQGHMEDV QEALLQIQM RQGLVC

40 Seq ID NO: 447 DNA sequence  
 Nucleic Acid Accession #: NM\_003020.1  
 Coding sequence: 29..664

1 11 21 31 41 51  
 45 CGCTCTCGG GCTGCCCTC GGTGACAAT GGTCTCCAGG ATGGTCTCTA CCATGCTATC 60  
 TGGCCTACTG TTTTGGCTGG CATCTGGATG GACTCCAGCA TTGCTTACA GCCCCCGGAC 120  
 CCCTGACCGG GTCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT 180  
 GGGCATKTCG AGGCCCGGAG TGAATATCC AGCTCACCAG GCCATGAATC TTGTGGGCC 240  
 50 CCAGAGCATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGGTCTCT TTGGCAACAT 300  
 CCCCAACATC GTGGCAGAGT TGACTGGAGA CAACATTCTT AAGGACTTTA GTGAGGATCA 360  
 GGGGTACCCA GACCCCTCAA ATCCCTGTCC TGTGTGAAAA ACAGATGATG GATGCTAGA 420  
 AAACACCCCT GACACTGCAG AGTTCAGTCG AGAGTTCCAG TTGCACCAGC ATCTCTTTGA 480  
 TCCGGAACAT GACTATCCAG GCTTGGGCAA GTGGAACAAG AAACCTCTTT ACGAGAAGAT 540  
 55 GAAGGGAGGA GAGAGACGAA AGCCGAGGAG TGTCAATCCA TATCTACAAG GACAGAGACT 600  
 GGATAATGTT GTTGCAAGAAG AGTCTGTCCC CCATTTTTC AATGAGGATCA AGGATCCAGA 660  
 GTAAAGAGAA GATGCTAGAC GAAACCCAC ATTACCTGTT AGGCCTCAGC ATGGCTTAGT 720  
 TGACGCTGTA AATGGAGTCC CTGTGAATGA CAGCATGTTT CTTACATAGA TAATTATGGA 780  
 TACAAAGCAG CTGTATGATG ATAGTGTATT GTCTTCACAC CGATGATTC TCTTTTGCT 840  
 60 AAATTAGAAT AAGAGCTTTT TTGTTTCTTG GGTTTTAAA ATGTGAATCT GCAATGATCA 900  
 TAAAAATTAA AATGTGAATG TCAACAATAA AAAGCAAGAC TATGAAAGGC TCAGATTCT 960  
 TGCAGTTTAA AATGTTGTCT GAGGTTGTAC TATTTTGGCC AAGTCTGTAG AAAGCTGTCA 1020  
 TTTGATTTTG ATTATGATG TCATCCAGCC CTGGGCGATT GTTATACACC AGTAAAGAAG 1080  
 GCTGTACTCA AGAGGAGGAG CTGACACATT TCACCTGGCT GCGTCTTAAT AAACATGAAT 1140  
 65 GCAAGCATTG GC

70 Seq ID NO: 448 Protein sequence  
 Protein Accession #: NP\_003011.1

1 11 21 31 41 51  
 70 MVS RMVSTML SGLLPWLASG WTPAFAYSFR TPDRVSEADI QRLHGVMBQ LGIARPRVEY 60  
 PAHQAMNLVG PQSIEGGAHE GLQHLGPFNG IPNIVAEITG DNIPKDFSED QGYDPDPNFC 120  
 FVGKTDGCL ENTPTDAEFS REFQLHQHLE DPEHDYPGLG KWNKKLLYEK MKGGERRKR 180  
 75 SVNPLYQQR LDNVVAKKSV PHFSDKDP E

80 Seq ID NO: 449 DNA sequence  
 Nucleic Acid Accession #: NM\_003816.1  
 Coding sequence: 79..2538

1 11 21 31 41 51  
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60  
 CCGCGGAAT CGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCGCGGGAC CTTCTGTGTC 120  
 CGGTGGTTCG TGTGCTTGG CCTGGTGGGC CAGTCTCTCG GTGCGGCGCG GCCAGGCTTT 180

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CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTTGGAGATT AACTAGAGAA 240  
 AGAAGAGAA CCCCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300  
 AAAGAGCATA TTATTCACCT GGAAAGGAAC AAAGACCTTT TGCCGAAGA TTTTGTGGTT 360  
 TATACTTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420  
 CATTATCGGG GCTATGTGGA GGGAGTTTCA AATTTCATCCA TTGCTCTTAG CGACTGTTTT 480  
 GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC 540  
 AGCTCTCATT TTGAGCAGAT CATTTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600  
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660  
 CCCAGCATGA CTCAGTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG 720  
 GAGCTGTGTA TTGTCGTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780  
 GTGAGAGAA AGATGATTCT CTGGCAAAC TACTTGGATA GTATGTATAT TATGTTAAAT 840  
 ATTOGAATTG TGCTAGTTGG ACTGGAGATT TSGACCAATG GAAACCTGAT CAACATAGTT 900  
 GGGGGTGTCT GTGATGTGCT GGGGAACTTC GTGCAGTGGC GGGAAAAGTT TCTTATCACA 960  
 CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAAGAAAG GTTTTGGTGG AACTGCAGGA 1020  
 ATGGCATTTG TGGGAACAGT GTGTTCAAGG AGCCACGCGAG GCGGGATTAA TGTGTTTGA 1080  
 CAATCACTG TGGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAATCTTGA 1140  
 ATGAATCAG AGATGAGGAG AGATTGTTC TGTGGAGCAA AGAGCTGCAT CATGAATCA 1200  
 GGAGCATCG GTTCCAGAAA CTTTAGCAGT TGCAGTGCAG AGGACTTTGA GAAGTTAACT 1260  
 TTAATAAAG GAGGAAACTG CCTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320  
 CCTCTCTGTG TGAATAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380  
 GAATGTGAAT TGGACCTCTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440  
 TGTGCATATG GTGACTGTG TAAAGACTGT CGGTTCCTTC CAGGAGGTAC TTTATGCCGA 1500  
 GGAAAAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTCTCA GTTCTGTGAG 1560  
 CCAGATGTTT TTATTAGAAA TGGATATCCT TGCCAGAAATA ACAAGCCTTA TTGCTACAAC 1620  
 GGCATGTGCC AGTATTATGA TGCTCAATGT CAAGTCACTT TTGGCTCAAA AGCCAAAGCT 1680  
 GCCCCCAAG ATTGTTTTCAT TGAAGTGAAT TCTAAAGGTG ACAGATTGG CAATTGTGGT 1740  
 TTCTCTGGCA ATGAATACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800  
 TGTGAGAAAT TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCT 1860  
 AGTCGAGGCA CAAATGTTG GGGGTGTGGT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920  
 GGGATGTTTA ACGAAGGCAC AAAATGTGGT GCTGGAAGA TCTGTAGAAA CTTCAGTGT 1980  
 GTAGATGCT GTGTTCTGAA TTATGACTGT GATGTTTCA AAAAGTGTCA TGGCATGGG 2040  
 GTATGTAATA GCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCCC AAATGTGAG 2100  
 ACTAAAGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAAT GAATACTGCA 2160  
 TTAGGGGACG GACTCTGCTT CTCTCTCTTC CTAATTGTTC CCTTATTGT CTGTCTATT 2220  
 TTTATCTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACA 2280  
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTTCCT 2340  
 CGACATGTTT CTCCAGTGAC ACCTCCAGCA GAAGTTCCTA TATATGCAAA CAGATTGCA 2400  
 GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCTAT CAGGCCACC TCCACCACA 2460  
 CCGAAAGTAT CATCTCAGGG AAACCTAATT CCTGCCGCTC CTGCTCCTGC ACCTCCTTTA 2520  
 TATAGTCCC TCACCTGATT TTTTAACTT TCTTTTGTCA AATGCTTCA GGGAACTGAG 2580  
 TCAATCTTTT TTTTCTTCT TGATGTTTC TTGAAAAGCC TTTCTGTTGC AACTATGAAT 2640  
 GAAAAACAAA CACCACAAA CAGACTTCAC TAACACAGAA AACAGAAAC TGAGTGTGAG 2700  
 AGTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC 2760  
 CATCATGAA TAAATCTTAT TCAGTCAATG GTGAGGTAAA TGCACTAATC ATGGATTTTT 2820  
 TGAACATGTT ATTGCAAGTA TTCTCAAAAT AACTGTATTG GTGAAGATT TTTGTCAAT 2880  
 AGTGTGTAAT TGTATTCTG AATTCTTAC CTTAGTTATC ATTAATGTAG TTCTCATG 2940  
 AACATGTGAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000  
 TTTTTCATCA TGCAGGAATT AATAATCATC ATACTCTAGA ATCTTGTCTG TCACTCACTA 3060  
 CATGAATAAG CAAATATTGT CTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA 3120  
 TATTTTGAA AGTACAAAAT AATAAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT 3180  
 TCCATTCTTA TGACCTTTCA ACTATAGGTA ATAACCTTA GAGAAATTA TTTAATATTA 3240  
 GAATTTCTAT TATGAATCAT GTGAAGCAT GACATTCGTT CACAATGACA CTATTTTAAA 3300  
 TAAATATATA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAAAAT GTTGATTCAT 3360  
 GGCATATAA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420  
 CTTGAGAAAT TCATGAGCAC TTTAAATCT GAACTTCAA AGCTTGCTAT TAAATCATTT 3480  
 AGAATGTTTA CATTTACTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540  
 CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAAG 3600  
 TTAATGTGTT ATCTATGAGT TATCATCTTA GCTGTGTTAA AAATGAATTT TTACTATGTC 3660  
 AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAAT TTTTATAAC CTTTCATAAT 3720  
 AAGTTTAAAT AATAGGTTTA TTAAGTGAAT TTCATTAGTT TTTTAAAGT GTTTTGTGTT 3780  
 TGTGTATATA TACATATACA AATACACAT TTACAATAAA TAAATACCT GAAATCTCA 3840  
 AAAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 450 Protein sequence

Protein Accession #: NP\_003807.1

65  
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1 11 21 31 41 51  
 | | | | |  
 MSGGARPPSG TLRVRWLLLL GLVGPVLGAA RFGPQQTSHL SSYEIITPWR LTRRRREAPR 60  
 PYSKQVSYVI QAEKGEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHYRGYV 120  
 EGVHNSIAL SDCLRLRGLL HLENASYGIE PLQNSHFEH ILYRMDVYK EPLKCGVSNK 180  
 DIEKETAKDE EEEPPSMTQL LRRRAVLQP TRYVELFIVV DKERYDMNGR NOTAVREEMI 240  
 LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300  
 AQLVLKKGFG GTAGMAFVGT VCSRHAGGI NVFQITVET FASIVAHGL HNLGMHHDG 360  
 RDCSCGAKSC INNSGAGSSR NFSSCSAEDF EKLTLNKGGN CLINIPKPE AYSAPSCGNK 420  
 LDVAGEECDC GTPKECELDP CCEGSTCGLK SFAECAYGDC CKDCRFLPGG TLRCRGTSEC 480  
 DVPEYCNSS QFCQPDVFIQ NGYPCQMNKA YCYNMCQYY DAQCQVIFGS KAKAAPKDCF 540  
 IEVNSKGRDF GNCGFSGNEY KKCATGNALC GKLCQENVQE IPVFGIVPAI IQTPSRGKTC 600  
 WGVDFQLGSD VPDPMGVNEG TKCGAGKICR NFQCVDA SVL NYDCDVQKKC HGHGVCNSNK 660  
 NCHCENGWAP FNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLVPLI VCAIFPIKR 720  
 DQLWRSYRKP KRSQTYESDG KNQANPSRQP GSVPRHVSFV TPPREVPYA NRPVAPTYAA 780  
 KQPQQFSPRP PPPQPKVSSQ GNLIPARPAP APPLYSLLT

Seq ID NO: 451 DNA sequence  
Nucleic Acid Accession #: NM\_016650.1  
Coding sequence: 196..789

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5      1      11      21      31      41      51
      |      |      |      |      |      |
GGTTTCAATA TATGCAGATG TCTCGATATA GGAATGAAAT TACGTCTTTG GAACAACTTA 60
AATAAGTCAA ATATACCTGG AGCTTTAAAA ATTAAAAAGG GAGAGATTCG AGCACCTTTT 120
CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGTGTGT 180
10     CCCCAGCTGG GAAACATGGC TGTATACAT TCACATCTGT GGAAGAGATT GCAAGAGAAG 240
TTCTTGAAGG GAGAACCCTAA AGTCCTTGGG GTTGTGCAGA TTCTGACTGC CTTGATGAGC 300
CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCCCTATT 360
TCCGTGCATA TCGGGTACAC AATTGGGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG 420
15     TCAATTGCAG CAGGAATTAG AACTACAAAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT 480
ATCACCAGCT CTGTACTGGC TGCATCAGGG ATCTTAATCA ACACATTTAG CTTGGCGTTT 540
TATTCAATTC ATCACCCTTA CTGTAACCTAC TATGGCAACT CAAATAATTG TCATGGGACT 600
ATGTCCATCT TAATGGGTCT GGAATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTCTGC 660
ATGTCTGTGT CCGCTCTCTG CTTTGGATGT AAAGTGCTCT GTTGTACCCC TGGTGGGGTT 720
20     GTGTTAAATC TGCCATCACA TTCTCACATG GCAGAAACAG CATCTCCAC ACCACTTAAT 780
GAGGTTTGAG GCCAACAAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
ACACAGAGAG CTCACATGAG AAATTACCAG TATCCAACTT CGATACTGAT AGACGTGTTG 900
ATATTATTAT TATATGTAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC 960
AAAATTATGT TCTCATTTT TTCCCTGGAA CTCAATAACT CACTTCACTG GCTCTTTATC 1020
25     GAGAGTACTA GGAGTTAAAT TAATAAATAA TGCATTTAAT GAGGCCACAG GAAAAA
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Seq ID NO: 452 Protein sequence  
Protein Accession #: NP\_057734.1

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30     1      11      21      31      41      51
      |      |      |      |      |      |
MAVIHSHLWK GLQEKFLKGE PKVLGVVQIL TALMSLSMGI TMMCMASNTY GSNPISVHIG 60
YTIWGSVMFI ISGSLSIAAG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH 120
PYCNYVGNEN NCHGTMISLM GLDGMVLLLS VLEFCIAVSL SAFGCKVLCC TPGGVVLILP 180
35     SHSHMAETAS PTPLENEV
```

Seq ID NO: 453 DNA sequence  
Nucleic Acid Accession #: NM\_002091.1  
Coding sequence: 56..503

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40     1      11      21      31      41      51
      |      |      |      |      |      |
AGTCTCTGCT CTTCACAGCC TCTCCGCGCG GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCTCT TGCTAGCGC CCGGGGGGCG 120
45     AGCGGTCCCG CTGCCTGGCG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
GAATTGTCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
GGCCTTGGGC AATCAGCAGC CTTGTGGGA TTCAGAGGAT AGCAGCAACT TCAAGATGT 420
50     AGGTTCAAAA GGCAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
CCCCAGCTG ACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAACCCCC 540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA 600
AAATATTGTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
CTTCTGTTT AAACCTGTTT GCTGTGAACA ATTGTGAAAA AGAGTCTTCC AATTAATGCT 720
55     TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAGGCCCC CGAGCTGTTA CCATTCAAA 780
TAAAGCTTA AACACAT
```

Seq ID NO: 454 Protein sequence  
Protein Accession #: NP\_002082.1

```
60     1      11      21      31      41      51
      |      |      |      |      |      |
MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTKMYPR GNHWAVGHLM GKSTGESS 60
VSEKSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPQ PKALGNQPS WDSESSNFK 120
65     DVGSKGVKGR LSAPGSQREG RNPQLNQQ
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Seq ID NO: 455 DNA sequence  
Nucleic Acid Accession #: NM\_016522.1  
Coding sequence: 265..1299

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70     1      11      21      31      41      51
      |      |      |      |      |      |
GCGGAAGCAG CGAGGAGGGA GCCCCCTTTG GCGTCTCTCC GTGGAACCGG TTTTCCGAGG 60
CTGGCAAAAG CCGAGGCTGG ATTGGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGGCG 120
TTTCTCTCTC CCGCGGCTCT CCGGTGCGCG CGGGTTCACC GCTCAGTCCC CGCGCTCGCT 180
75     CGCAACCCCA CCCACTTCTT GTGCTCGCCC GGGGGGCGTG TGCGTGCGCG CTGCGCGAGT 240
TCGGGGAGGT TGTGGCTGTC GAGAAATGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
TGCCCTGCTG TCGTCTCTCT CAGGCTGCTG TTCCTTGTAC CCACAGGAGT GCCCGTGC 360
AGCGGAGATG CCACTTCCC CAAAGCTATG GACAACGTGA CGGTCCGCGA GGGGGAGAGC 420
GCCACCTCTA GGTGCACTAT TGACAACCGG GTCAACCGGG TGGCTGTGCT AAACCGCAGC 480
80     ACCATCTCTT ATGCTGGGAA TGACAAGTGG TGCTGTGATC CTCGCTGGT CTTCTGAGC 540
AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
TACACCTGCT CGGTGCAAGC AGACAACACC CCAAGAGACT CTAGGTTCCA CCTCATTTG 660
CAAGTATCTC CAAAATGTG AGAGATTTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
ATTAGCTCTA CTGCATAGC AACTGGTAGA CCAGAGCTCA CGGTACTTTG GAGACACATC 780
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5 TCTCCCAAG CGGTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840  
 CGGGAAACAGT CAGGGGACTA CGAGTGCACT GCCTCCAATG ACCTGGCCGC GCCCGTGGTA 900  
 CGGAGAGTAA AGGTACCCGT GAACTATCCA CCATACATTT CAGAAGCCAA GGTACAGGT 960  
 GTCCCGGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020  
 TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080  
 AACAGACCTT TCCTCTCAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140  
 TACACTTGGC TGGCCTCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGTGT 1200  
 CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260  
 10 CTGCTCTTTC TGGTCTTGCA CTGCTTCTC AAATTTTGAT GTGAGTGCCA CTTCGCCACC 1320  
 CGGGAAAGGC TGCGCCACC ACCACCACCA ACACACAGC AATGGCAACA CCGACAGCAA 1380  
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAG CTCATGGGAC AGAAATTGTA 1440  
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAAATTG 1500  
 CCTTGACAGT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560  
 15 CCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620  
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CAGCTGGAAC ATTCTGGAGC TGGCCATCCC 1680  
 AAATTCAAAT AGTCTGGGCA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740  
 CCGGCCCAAG CGTGGCGCTG CCGGCACTTT GGTAGACTGT GCCACCAAGG CGTGTGTGT 1800  
 GAAACGTGAA ATAAAAAGAG CAAAAAATA AAAAAAATA

Seq ID NO: 456 Protein sequence

Protein Accession #: NP\_057606.1

25 1 11 21 31 41 51  
 MGVCGLFLP WKCLVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60  
 NRVTRVANLN RSTILYAGND KWCLDPRVVL LSNTQTQYSI EIQNVDVYDE GPYTCSVQTD 120  
 NHEKTSRVEL IVQVSKIVE ISSDISINEG NNISLTCIAT GRPEPTVTWR HISPKAVGFV 180  
 SEDEYLEIQG ITRQSGDYE CSASNDVAAP VRRVKVTVN YPPYISEAKG TGVPEVGKGT 240  
 30 LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VENRPFSLKL IFFNVSEHDY GNYTCVASNK 300  
 LGHTNASIML FPGPAVSEVS NGTSRRAGCV WLLPLLVHLH LLKF

Seq ID NO: 457 DNA sequence

Nucleic Acid Accession #: NM\_012261.1

Coding sequence: 203..1045

35 1 11 21 31 41 51  
 GATTGTCTCT GCCAGCAGCT GTGGGTGCGG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60  
 ACAGAAATAG CGCTCCCTCC CTCGCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120  
 40 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCCGC CTCTGCAGCA GCACAGCCGG 180  
 CCTCATTCGG GGCACCTGGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240  
 ACTTCAGATT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAAAGAT 300  
 GGAATATCTC TCAGGCTTTT CCACTAACCC TGAAAAAGAT ATATTGTGG TCGGGGAAAA 360  
 TGGGACGAGG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420  
 45 GGCACGCAAC TACGTAGATC TGATCAGAGA ACAGGCCGAT ATCGCATTGA CCGGGGGAGC 480  
 TGAGGTGAGG GCGCGCTGTG GCCACAGCCA GTCCGAGCTG CAAGTGTCTT GGGTGGATCG 540  
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAGGCCAC AACATGTCCA AGGGACCTGA 600  
 GCGCACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660  
 CAAAGACGCA GTCAGTCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCTTGGT 720  
 50 CACCCCGCT GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCTCTAG 780  
 TGATCCGAGG AAGACGGTCA CCATGATCCT GTCTGGGTTC CACATCCAAC CTTTGGACAT 840  
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900  
 GGAAGAAACC TTGCCCCCTG TTTTGGGGCT CATCTTGGGC CTGTCATCA TGGTAACACT 960  
 CGGATTTTAC CAGTCCACC ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020  
 55 ATCCAGTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGTCTCC 1080  
 CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTCCATC TTGTACAGCA GATACACCAA 1140  
 CATAGCTACA ATCAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200  
 AACCCACGGA AGCGGGAGAG TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260  
 ATGCTGGGGA GGAGGGGAGG AGGCTCTCAG ACAGCTTTCG TGCTCATGCT GCTTGGCTT 1320  
 60 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380  
 TTGAAAACAT GCTTCTTTGA GGAGGAAACC CTTTAGGTT CAGAAGAATA TGGGGTGTCT 1440  
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500  
 TCATGCTCCC TGCAGCAAGA CCCCAGAAAG TGATTATGTC TTCTGGCTGG CATTCTGCAT 1560  
 65 GTTTAGTGTAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCA 1620  
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680  
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AATGAAATA AAACACACTA 1740  
 TTCTCTGCC

Seq ID NO: 458 Protein sequence

Protein Accession #: NP\_036393.1

75 1 11 21 31 41 51  
 MDLQGRGVPS IDRLRVLLML PHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60  
 EPAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML 120  
 FVKESHNSK GPBATWRLSK VQFVYDSEK THFKDAVSAG KHTANSHLS ALVTPACKSY 180  
 EQAQQTISL ASSDPKTYT MILSAVHIQ FDIISDFVFS EEHKCPVDER EQLEETLPLI 240  
 LGLILGLVIM VTLAIYHVH KMTANVQIP RDRSQYKMG

Seq ID NO: 459 DNA sequence

Nucleic Acid Accession #: NM\_001169.1

Coding sequence: 85..870

1 11 21 31 41 51

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TAGGAGATAA	GAGTATCTTG	CACAGCAGGT	GCAGGTTTCC	CAGCAGCTCA	GGCAAGAGTC	60
CGATGTTTGT	GCCATCTGAT	CCTGATGTCT	GGAGAGATAG	CCATGTGTGA	GCCTGAATTT	120
GGCAATGACA	AGGCCAGGGA	GCCGAGCGTG	GGTGGCAGGT	GGCGAGTGTG	CTGTACGAA	180
CGGTTTGTGC	AGCCATGTCT	GGTCGAACCTG	CTGGGCTCTG	CTCTCTTCAT	CTTCATCGGG	240
TGCCTGTGCG	TCATTGAGAA	TGGGACGGAC	ACTGGGCTGC	TGCAGCCGCG	CCTGGCCAC	300
GGGCTGGCTT	TGGGCTCGT	GATTGCCACG	CTGGGGAATA	TCAGTGGTGG	ACACTTCAAC	360
CCTGCGGTGT	CCCTGGCAGC	CATGCTGATC	GGAGGCCCTCA	ACCTGGTGAT	GCTCCTCCG	420
TACTGGGTCT	CACAGCTGCT	CGGGGGGATG	CTCGGGGCTG	CCTTGGCCAA	GGTGGTGAGT	480
CCTGAGGAGA	GGTTCTGGAA	TGCATCTGGG	CGCGCCTTTG	TGACAGTCCA	GGAGCAGGGG	540
CAGGTGGCAG	GGGCGTGTGT	GGCAGAGATC	ATCCTGACGA	CGCTGCTGGC	CCTGGCTGTA	600
TGCATGGGTG	CCATCAATGA	GAAGACAAAG	GGCCCTCTGG	CCCGTCTCTC	CATCGGCTTT	660
GCCTGACCGG	TGGATATCCT	GGCTGGGGGC	CCTGTGTCTG	GAGGCTGCAT	GAATCCCGCC	720
CGTGTCTTTG	GACCTGCGGT	GGTGGCCAAAC	CACCTGGAAC	TCCACTGGAT	CTACTGGCTG	780
GGCCCACTCC	TGGCTGGCCT	GCTTGTGGA	CTGCTCATT	GGTGTTCAT	TGGAGATGGG	840
AGAGCCCGCC	TCATCTGAA	GGCTCGGTGA	GCAGAGCTCG	TGGGATTCCT	GCTGTCCAG	900
GTGTCTCAG	CTCACCTGTC	CCAGACTGAG	GACAGGGGAG	TTCCTGCATT	TCCTGCCAGG	960
GCAGAGGCCC	AGAGGAGCGA	CCCCCTGCTT	CCACTGCTTG	GGCCTGCTTT	CTCAGATAGA	1020
CTGACTGTCTG	AGGAGGCTCT	AGGTTCTTGG	AATTCTTTTG	TGCTCATCAG	AGACCCACAG	1080
CTGGGGAACA	CGCTGCCCGC	ACTGCCCAAG	GAGCAGTGCA	AACACCAACA	CACGAGCGTG	1140
TTTCTTGAGA	GGAAATGTCC	CGAGTTGGAC	AAGGAGGCTG	TTTCTGCACA	TCAGCTCATT	1200
TCCCGCACCC	CATTCTTCTG	TTGATTGCTT	TGTTGGGGGC	CTGGCCACTT	CCTTGTCTCT	1260
CAAGCTGACA	ATTCTCACTT	TGCAATAAAT	AGTCCAGTGT	TTCCTTCAT		

Seq ID NO: 460 Protein sequence  
Protein Accession #: NP\_001160.1

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MSGEIAMCEP	EFNGDKAREP	SVGGRWRVSW	YERFVQPCLV	ELLGSALFIF	IGCLSVIENG	60
TDTLGLQPAL	AHGLALGLVI	ATLGNISGGH	FNPVSLAAM	LIGGLNLVML	LPYVWSQLLG	120
GMLGAALAKV	VSPEERFVNA	SGAAFTVQVE	QQVAGALVA	EIILTLTLLAL	AVCMGAINKEK	180
TKGLAPFISI	GFATVTDILA	GGPVSGGCMN	PARAFGPAVV	ANHNWPHWIY	WLGPLLALGLL	240
VGLLIRCFIG	DGKTRLILKA	R				

Seq ID NO: 461 DNA sequence  
Nucleic Acid Accession #: NM\_003226.1  
Coding sequence: 2..226

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GATGCTGGGG	CTGGTCTCGG	CCTTGTCTGT	CTCCAGCTCT	GCTGAGGAGT	ACGTGGGCCT	60
GTCTGCAAAAC	CAGTGTGCCG	TGCCGGCCAA	GGACAGGGTG	GACTGCGGCT	ACCCCCATGT	120
CACCCCCAAG	GAGTGCACAA	ACCGGGGCTG	CTGCTTTGAC	TCCAGGATCC	CTGGAGTGCC	180
TTGGTGTTC	AAGCCCCCTGA	CTAGGAAGAC	AGAATGCACC	TTCTGAGGCA	CCTCCAGCTG	240
CCCCGGGAT	GCAGGCTGAG	CACCCCTGCC	CGGCTGTGAT	TGCTGCCAGG	CACGTTCAT	300
CTCAGTTT	CTGTCCCTTT	GCTCCCGGCA	AGCTTCTCTG	TGAAAGTTCA	TATCTGGAGC	360
CTGATGCTT	AACGAATAAA	GGTCCCATGC	TCCACCCG			

Seq ID NO: 462 Protein sequence  
Protein Accession #: NP\_003217.1

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MLGLVLALLS	SSSAEYVGL	SANQCAVPAK	DRVDCGYPHV	TPKECNNRGC	CFDSRIPIGVF	60
WCFKPLTRKT	ECTF					

Seq ID NO: 463 DNA sequence  
Nucleic Acid Accession #: NM\_002993.1  
Coding sequence: 64..408

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GGCAGGAGCC	AGTCTCCGCG	CCTCCACCCA	GCTCAGGAAC	CCGCGAACC	TCTCTGACC	60
ACTATGAGCC	TCCGTCCTAG	CGCGCGGGCC	CGTGTCCCGG	GTCCTTCGGG	CTCCTTGTC	120
GCGCTGCTCG	CGCTGCTGCT	CCTGCTGACG	CGCGCGGGG	CCCTCGCCAG	CGCTGGTCCT	180
GTCTCTGCTG	TGCTGACAGA	GCTGCGTTCG	ACTTGTCTAC	CGCTTACGCT	GAGAGTAAAC	240
CCCAAAACGA	TTGTAAACT	GCAGGTGTTC	CCCGCAGGCC	CGCAGTGCTC	CAAGGTGSA	300
TGGTAGCCT	CCCTGAAGAA	CGGGAAGCAA	GTTTGTCTGG	ACCCGGAAGC	CCCTTTTCTA	360
AAGAAATGCA	TCCAGAAAT	TTTGACAGT	GGAAACAAGA	AAACTGAGT	AACAAAAAAG	420
ACCATGCATC	ATAAAATTGC	CCAGTCTTCA	CGGAGCAGT	TTTCTGGAGA	TCCTGGACC	480
CAGTAAGAAT	AGAAGGAAG	GGTTGGTTTT	TTTCCATTTT	CTACATGGAT	TCCTACTTT	540
GAAGAGTGTG	GGGGAAGCC	TACGCTTCTC	CCTGAAGTTT	ACAGCTCAGC	TAATGAAGTA	600
CTAATATAGT	ATTTCACCTA	TTTACTGTTA	TTTACCTGA	TAAGTTATTG	AACCTTTTGG	660
CAATTGACCA	TATTGTGAGC	AAAGAATCAC	TGTTTATTAG	TCTTTCATG	AATATTGAAT	720
TGAAGATAAC	TATTGTATTT	CTATCATACA	TTCTTAAAG	TCTTACCGAA	AAGGCTGTGG	780
ATTTGATATG	GAAATAATGT	TTTATTAGTG	TGCTGTTGAG	GGAGGTATCC	TGTTGTTCTT	840
ACTCACTCTT	CTCATAAAT	AGGAAATATT	TTAGTTCTGT	TTTCTTGGGG	AATATGTTAC	900
TCCTTACCTT	AGGATGCTAT	TTAAGTTGTA	CTGTATTAGA	ACACTGGGTG	TGTCATACCG	960
TTATCTGTGC	AGAATATATT	TCCTTATTCA	GAATTTCTAA	AAATTTAAGT	TCTGTAAGGG	1020
CTAATATATT	CTCTTCTCAT	GGTTTATGAT	GTTTATGTC	TCTTAGTAT	GGCATAATGT	1080
CATGATTAC	TCATTAACT	TTGATTTTGT	ATGCTATTTT	TTCATATAG	GATGACTATA	1140

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ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCAAAAAACA GATAAATTC 1200  
 TGATTGCTAA TTTACATAGA AATGTAITCT CTGGGTTTT TAAATAAAG CAAAATTAAC 1260  
 AATGATCTGT GCTCTGCAAA GTTTTGAAA TATATTGAA CAATTGAAT ATAAATTCAT 1320  
 CATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380  
 TTTAAAGGTT TTGACCATTT TGTTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440  
 AAATTGCAT TTTATTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT 1500  
 TGGAGAAACA ATAAAGATT TCTAAACCA AAAAAA AAAAAA

Seq ID NO: 464 Protein sequence  
 Protein Accession #: NP\_002984.1

1 11 21 31 41 51  
 MSLPSSRAAR VPGPSGSLCA LLALLLLTP PGPLASAGPV SAVLTELRCR CLRVTLRVNP 60  
 KTIGKLQVFP AGPQCSKVEV VASLKNKQV CLDPEAPFLK KVIQKILDSG NKKN

Seq ID NO: 465 DNA sequence  
 Nucleic Acid Accession #: NM\_002038.2  
 Coding sequence: 108..500

1 11 21 31 41 51  
 GAACCGTTTA CTGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGCTGAA GATTGCTTCT 60  
 CTTCTCTCCT CCAAGGTCTA GTGACGGAGC CCGCGCGCGG CGCCACCATG CGGCAGAGG 120  
 CGGTATCGCT TTTCTTGTC TACCTGCTGC TCITCACTTG CAGTGGGGTG GAGGCAGGTA 180  
 AGAAAAAGCT CTGGAGAGC TCGGACAGCG GCTCCGGGTT CTGGAAGGCC CTGACCTTCA 240  
 TGGCCGTCGG AGGAGGACTC GCAGTCGCGG GGCTGCCCGC GCTGGGCTTC ACCGGCGCGG 300  
 GCATCGCGGC CACTCGGTG GCTGCTCTGC TGATGAGCTG GTCTGCGATC CTGAATGGGG 360  
 CGGGCGTGCC CGCGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA 420  
 CGGTGTCAT AGGTAATATT GGTGCCCTGA TGGGCTACGC CACCCACAAG TATCTCGATA 480  
 GTGAGAGGA TGAGGAGTAG CCAGCAGCTC CCAGAACCTC TTCTTCCTTC TTGGCTTAAC 540  
 TCTTCCAGTT AGGATCTAGA ACTTTGCCCT TTTTITTTTT TTTTITTTTT TTGAGATGG 600  
 GTTCTCACTA TATGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660  
 ACTGCAGCT CCAACTCTTA GCCTCAAGTG ATCCTCTGT CTCAACCTCC CAGTAGGAT 720  
 TACAAGCATG CGCCGACGAT GCCCAGAAAT CAGAATCTTG TCTATCACTC TCCCAACAA 780  
 CCTAGATGTG AAAACAGAAT AAACCTCACC CAGAAAA

Seq ID NO: 466 Protein sequence  
 Protein Accession #: NP\_002029.3

1 11 21 31 41 51  
 MRQKAIVSLFL CYLLLFCTSG VEAGKKKCSE SSDSGSGFEWK ALTFMAVGGG LAVAGLPALG 60  
 FTGAGIAANS VAASLMSWSA ILNNGGVVPAG GLVATLQSLG AGGSSVVIGN IGALMGYATH 120  
 KYLDSEEDDE

Seq ID NO: 467 DNA sequence  
 Nucleic Acid Accession #: NM\_003469.2  
 Coding sequence: 92..1945

1 11 21 31 41 51  
 GAAACGGCCC GAGAAGCTCG CCGGAGAAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60  
 CATATAAACA AAAAGAGGAA ATCTTTTCAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG 120  
 AGCAGCCCTG TCTCTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180  
 TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAAAAATG TCCAAAAGTT 240  
 TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAAGCTCA 300  
 TAAGGAAGAA AGCAGCCGAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360  
 AAAAGAAAT GGCGATGAAA GGCACCTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420  
 GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA 480  
 AGAAATAAG CCCTATGCTT TGAATTGAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540  
 TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTC CTCTATGTA 600  
 TGAAGAGAAT TCCAGGGATA ACCCTTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660  
 TACTCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG 720  
 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTTATA CGGATGATGA 780  
 AGATGATATC TACAAGGCTA ATAACTTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840  
 GAACCCAGTA GAGGAGAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900  
 GAATATAGGA AAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960  
 CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCACTC TCAGATGATG TCTCCAAAGT 1020  
 AATTGCTAT TTGAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080  
 AAATGGGGA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTTATCA 1140  
 GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGGAA GACTTAATTG AGATGCTCAA 1200  
 AACTGGGGAG AAGCCGATG GATCAGTGA ACCGAGCGG GAGCTTGACC TTCTGTGTA 1260  
 CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAA ATAGGATGCT 1320  
 CTCCAAGAGT GGCTACCTTA AAACACCTGG TGTGCTGGG ACTGAGGCC TACCAGACG 1380  
 GCTCAGTGT GAGAGTATT TAAATCTTT AGGGATGGAG AGTGAGCAA ATCAGAAATC 1440  
 GTGATTTTT CCCATCCAT ATAACCAGGA GAAAGTCTG CCAAGGCTCC CTATGCTGTC 1500  
 TGAAGATCT AGATCGAACC AGCTTCCCAA AGCTGCTGG ATTCCACATG TTGAAAACAG 1560  
 ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620  
 GATGCTAGTT AAATACCTG AGATCATTA TTCAAACCAA GTGAAGCGAG TTCCTGGTCA 1680  
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAGAGCA 1740  
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC 1800  
 TGTGGGGCCC CGAAGAAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860  
 AATGAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGAAGGG AGCATATTGC 1920

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TAAGAGAGCA ATGAAAAATA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCTCTC 1980  
CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTGA CTCTATCCT GTTAACACTG 2040  
TAATATCTTT AATGATGTA CAGGCAGATG AAACCAAGTC ACTGGGGAGT CTGCTTCATT 2100  
TCCTCTGAGC TGTATCTTG TGTATGGATA TGTGTAAATG TTATGACTCC TTGATAAAAA 2160  
ATTTATTATG TCCATTATTG AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT 2220  
GGCTGTGGCA TTGTTGATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280  
TTTTTAATAT TTATTGAATT ATTTTGTTAC TGTCTGTAGC GTTTTGTGGA GTACTGGACC 2340  
AAAAAATAA AGCATTATAA ATATA

Seq ID NO: 468 Protein sequence  
Protein Accession #: NP\_003460.1

1 11 21 31 41 51  
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MAEAKTHWLG AALSLIPLIF LISGAEAAAF QRNQLLQKEP DLRLNVQKF PSPMIRALE 60  
YIENLRQQAH KEESPDPYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120  
AENEPSAPK EMKPYALNSE KNFPMDSDD YETQOWPERK LKHMOPPMY EENSNDNPFK 180  
RTNEIVEBQY TPQSLATLES VPQELGKLTG PNNQKRERMD EEQKLYTDDE DDIYKANNIA 240  
YEDVVGGEDW NFVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQQLGI QEEDLRKESK 300  
DQLSDVSVKV IAYLRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRLQI 360  
PPEDLIEMLK TGEKNGSVSE PERELDLFVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420  
RAGTEALPDG LSVEDILNLL GMESAANQKT SYFFNPYNQE KVLPRLPYGA GRSRSNQLPK 480  
AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPQ GSEDDLQEE 540  
EQIEQAIKEH LNQSSSQETD KLAPVSKRFP VGPPKNDDTP NRQYWEDELL MKVLEYLNQE 600  
KAEKGREHIA KRAMENM

Seq ID NO: 469 DNA sequence  
Nucleic Acid Accession #: NM\_006398.1  
Coding sequence: 19..516

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1 11 21 31 41 51  
GGCCCCCTGT CTGCAGAGAT GGCTCCCAAT GCCTCCTGCC TCTGTGTGCA TGTCCGTTCC 60  
GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120  
GAACATGTCC GGCTCAAGAC CAAGGTTTCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180  
AAGATCTTAA AGCCAAGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240  
CACCTTACCC TGAAGTGGT GAAGCCCACT GATGAGGAGC TGCCCTTGTT TCTTGTGGAG 300  
TCAGGTGATG AGGCAAGAG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACAA 360  
GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420  
AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGCCATCAG AAAGGGCAAC 480  
TTACTCTTCC TGCCATCTTA TTGTAATTGA GGGTGACCAC CCTGGGATG GGGTGTGGC 540  
AGGGGTCAA AAGCTTATT CTTTAACTCT CTTACTCAAC GAACACATCT TCTGATGATT 600  
TCCCAAAAT AATGAGAATG AGATGAGTAG AGTAAGATT GGGTGGGATG GGTAGGATGA 660  
AGTATATTGC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720  
TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAATAG AGCATTTC

Seq ID NO: 470 Protein sequence  
Protein Accession #: NP\_006389.1

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1 11 21 31 41 51  
MAPNASCLCV HVRSEEWDLN TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60  
RSLSSYGIDK ERTIHLTKLV VKPSDEELPL FLVESGDEAK RHLQVRRSS SVAQVKAMIE 120  
TKTGIIPETQ IVCNGKRLE DGKMMADYGI RKNLLFLAS YCIGG

Seq ID NO: 471 DNA sequence  
Nucleic Acid Accession #: XM\_094741.1  
Coding sequence: 1..948

60  
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1 11 21 31 41 51  
ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTTCCTCTGC TGGGTTTCTC GACTGGCCT 60  
TCCCTGCAGC CGGTCTCTTT CGCCTTGTC CTCTGTGCT ACCTCCTGAC CTTGACGGGC 120  
AACTCGGCGC TGGTGCTGCT GCGCGTGCGC GACCGCGGCC TGACACGCC CATGTACTAC 180  
TTCTCTGCC ACCTGGCCTT GGTAGACGCG GCGTTCACCT CTAGCGTGGT GCCGCGGCTG 240  
CTGGCCAACC TGCGCGGACC AGCGCTCTGG CTGCGCGGCA GCCACTGCAC GGCCCGAGCTG 300  
TGCGCATCGC TGGCTCTGGG TTGCGCGGAA TGCGTCTCTC TGGCGGTGAT GGCTCTGGAC 360  
CGCGCGGCGG CAGCTGTGCG CCGCTGCGC TATGCGGGGC TGGTCTCCCC GCGCCTATGT 420  
CGCAGGCTGG CCAGCGCCTC CTGGCTAAGC GGCCTCACC ACTCGGTGCG GCAAAACGCG 480  
CTCTGGCTG AGCGGCGGCT GTGCGCGGCC CGCTCTCTG ACCACTTCAT CTGTGAGCTG 540  
CCGGCTTGC TCAAGCTGGC CTGCGGAGGC GACGAGAGCA CTACCGAGAA CCAGATGTTT 600  
GCGCGCGGCG TGGTCACTCT GCTGCTGCGG TTGCGCGTCA TCCTGGCCTC CTACGGTGCC 660  
GTGGCCGAG CTGTCTGTTG CATGCGGTTG AGCGGAGGCC GAGGAGGGC GGTGGGCAAG 720  
TGTTGGTCCC ACCTGACAGC CGTCTGCGCT TTCTACGGCT CGGCACTCTA CACCTACCTG 780  
CAGCGCGGCG AGCGCTACAA CCAGGCAAGG GGCAGATTCT TATCGCTCTT CTACACGCTG 840  
GTACACCTG CTCTCAACCC GCTCATCTAC ACCCTCAGGA ATAAGAAAGT GAAGGGGGCA 900  
GCGAGGAGGC TGCTGCGGAG TCTGGGGAGA GGCCAGGCTG GGCAGTGA

Seq ID NO: 472 Protein sequence  
Protein Accession #: XP\_094741.1

1 11 21 31 41 51  
MKANYSABER FLLLGPSDWP SLQFVLFAV LLCYLLTLTG NSALVLLAVR DPLRLTPMY 60

FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSRE CVLLAVMALD 120  
 RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLDDHFICEL 180  
 PALLKLACGG DGDITENQMF AARVVILLFP FAVILASYGA VARAVCCMRP SGGRRRAVGT 240  
 CGSHLTAVCL FYGSAIYTYL QPAQRYNQAR GKFVSLFTYV VTPALNPLIY TLRNKKVKGA 300  
 ARRLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence  
 Nucleic Acid Accession #: NM\_001062.1  
 Coding sequence: 76..1380

1 11 21 31 41 51  
 GCTCTCATT CCTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60  
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT 120  
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180  
 CTAAAACCTC TGTGAAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240  
 AATGTTGTTG TGTCCCTCAA ACTTGTGTTGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300  
 ATCCACACAA TCAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCTT AATATATGAT 420  
 TACCACCTGA CTGACAAGCT AGAAAAATAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480  
 CACAATGGCA CTCCTCTGAC TAACTACTAC CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540  
 CTGTTCAATG GGAACACTC AACCCGCGAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600  
 AACTATTATT TTGTTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CTTGGCTCTG 660  
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720  
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAT 780  
 GGTCTCATTT GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840  
 GACTATTATA ATGAAATGA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCACGGAA 900  
 ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960  
 GGAAAGACCT TCTTGGATAT TAACAAAGAC TCTTCTTGGC TCTCTGCTTC AGGTAACCTC 1020  
 AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080  
 GTCAATTACT CTGTGAGAAAT CAATGAAACA TATTTCACCA ATGTCACTGT GCTAAATGGT 1140  
 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200  
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260  
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320  
 GGTAGTTACG TTGTCGCGAA TGGAGAAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380  
 GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCATG TTTATTGTCC 1440  
 TTATGCTTTC TTCTTCATT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500  
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence  
 Protein Accession #: NP\_001053.1

1 11 21 31 41 51  
 MRQSHQLPLV GLLLFSPFIP QLCEICEVSE ENYIRLKLPL NTMIQSNYNR GTSAVNVVLS 60  
 LKLVGIQIT LMQKMIQKIK YNVKSLSDV SSGELALIL ALGVCRNAEE NLIYDYHLTD 120  
 KLENKQAEI ENMEAHNGTP LTNYQLSLD VLALCLFNNG YSTAEVVNHF TPENKNYFYG 180  
 SQFSVDTGAM AVLALTCVKK SLINGQIKAD ESSLKINISY TKSLEKILS EKKENGLIGN 240  
 TFSSTGEAMQA LFSVSSDYNE NDWNCQQLN TVLTEISQGA FSNPNAAQV LPALMGKTFL 300  
 DINKSSSCVS ASGNFNISAD EPITVTTPDS QSYISVNVSV RINETYPTNV TVLNGSVFLS 360  
 VMEKAQRMND TIFGPTMEER SWGPIYITCI GLCANNDRT YWELLSGSEP LSQGAGSYVV 420  
 RNGENLEVRW SKY

Seq ID NO: 475 DNA sequence  
 Nucleic Acid Accession #: NM\_004852.1  
 Coding sequence: 89..1546

1 11 21 31 41 51  
 GCCCCCGCCC GCCCCGGGCC CTGATGGACT GAATGAAGGC TGCCTACACC GCCTATCGAT 60  
 GCCTCACCAA AGACCTAGAA CGTGGCCAT GAACCGGAG CTGACAATGG AAAGTCTGGG 120  
 CACTTTGACG GCGCGCGCGG GCGGCGGCGG TGGCGGGGGG GCGGCGGGGG GCGGCGGGGG 180  
 GCGGCGGGGG GCGGCGGGGG ATGAGCAGGA GCTGCTGGCC AGCCCCAGCC CCCACCAAGC 240  
 GCGGCGGGGG GCGGCTGGCT CGCTGCGGGG CCTCGCGCG CTTCCAACCG CGCACCAGGA 300  
 GCTGGGCAGG GCGGCGCGGG CGGCAGCGGC GCGGTGCGGC TCGGCATGG TCACCAGCAT 360  
 GGCCTCGATC CTGGACGCGG GCGACTACCG GCCCGAGCTC TCCATCCCGC TGCACCAAGC 420  
 CATGAGCATG TCTCGGACT CGTCTCGGCC TGGCATGGGC ATGAGCAACA CCTACACCAC 480  
 GCTGACACCG TCCAGCGCG TGCCACCCAT CTCCACCGTG TCTGACAAGT TCCACCAACC 540  
 TCACCCGCGC CACCATCCGC ACCACCAACA CCACCAACC CACGAGCGCC TGTCCGGCAA 600  
 CGTCAGCGGC AGCTTCACCC TCATGCGCGA CGAGCGCGGG CTCGCGGCA TGAACAACCT 660  
 CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC CTGTCCCGCG TGGCCGCCAC 720  
 GCGGCTGGGC AACGGGCTAG GCGGCTCCA CAACGCGCAG CAGAGTCTGC CCAACTACGG 780  
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5 Seq ID NO: 476 Protein sequence  
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20 Seq ID NO: 477 DNA sequence  
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Seq ID NO: 484 Protein sequence  
 Protein Accession #: NP\_003658.1

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 40 QFNFFETPAL PQDPSLENLS LISYVISSSV ANLTVRNLTR NVTVTLKHIN PSQDELTVRC 540  
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 45 QLCRIKKKKQ LGAQRKTSIQ DLRSIAGLTF LLGITWGFAP FAWGPNVTF MYLFAIFNL 840  
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Seq ID NO: 491 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..3045

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 GATTATTAC CTGTGACCCA CAATGTTCCC TCTCCAATAG GGGAGATTCA ACCCTTTCA 900  
 70 CCCCAGCCTT CAGCTCCCAT AGCTTCCAGC CTGCCCATTG ACATGCCCCC ACAGTCTGAA 960  
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 75 CAAGTCAGCA GACTCTTCA TTCCCGCCT GACATGCTGG CCCCTCTGGC TCAAGATTG 1260  
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5	CAATGATGG	CTCTGACGTT	CATTACATAT	ATTGGTTGTG	GGCTTTCATC	AATTTTCTG	1920
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	ATCCTCATCC	AGCTGTGTGC	TGCTCTGCTT	CTGCTGAACC	TGGTCTTCTT	CCTGGACTCG	2040
	TGGATTGCTC	TGTATAAGAT	GCAAGGCCTC	TGCATCTCAG	TGGCTGTATT	TCTTCATTAT	2100
	TTTCTCTTGG	TCTCATTAC	ATGGATGGGC	CTAGAAGCAT	TCCATATGTA	CCTGGCCCTT	2160
	GTCAAAGTAT	TTAATACTTA	CATCCGAAAA	TACATCCTTA	AATTCTGCAT	TGTGGTTGG	2220
	GGGTACCAG	CTGTGGTTGT	GACCATCATC	CTGACTATAT	CCCCAGATA	CTATGGGCTT	2280
	GGATCCTATG	GGAAATTCCC	CAATGGTTCA	CCGATGACT	TCTGCTGGAT	CAACAACAA	2340
	GCAGTATTCT	ACATTACGGT	GGTGGGATAT	TTCTGTGTGA	TATTTTGTCT	GAACGTCAGC	2400
10	ATGTTCAATTG	TGGTCCCTGG	TCAGCTCTGT	CGAATTAATA	AGAAGAAGCA	ACTGGGAGCC	2460
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	ATAACTTGGG	GCTTTGCCTT	CTTTGCCTGG	GGACCACTTA	ACGTGACCTT	CATGTATCTG	2580
	TTTGCCATCT	TTAATACCTT	ACAAGGATTT	TTTATATTCA	TCTTTTACTG	TGTGGCCAAA	2640
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15	AATTTCTGACT	GGAGTAAATC	TGCTACTAAT	GGTTTAAAGA	AGCAGACTGT	AAACCAAGGA	2760
	GTGTCCAGCT	CTTCAAATTC	CTTACAGTCA	AGCAGTAACT	CCACTAACTC	CACCACACTG	2820
	CTAGTGAATA	ATGATTGCTC	AGTACACGCA	AGCGGGAATG	GAAATGCTTC	TACAGAGAGG	2880
	AATGGGGTCT	CTTTTAGTGT	TCAGAAATGA	GATGTGTGCC	TTCACTGATT	CCTGGAAAA	2940
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Seq ID NO: 492 Protein sequence  
Protein Accession #: Eos sequence

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30	GEIMFQYDKE	STVPQNHIT	NGTLTGVLSL	SELKRSELNK	TLQTLSETYP	IMCATAEAQS	180
	TLNCTFTIKL	NNTMNACAAI	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
	VCLADHPRGP	PFSSSQSIPV	VPRATVLSQV	PKATSPFAEP	DYSPVTHNVP	SPIGEIQPLS	300
	PQPSAPIASS	PAIDMPPQSE	TISSPMQTH	VSGTPPPVKA	SFSSPTVSAP	ANVNTTSAPP	360
	VQTDIVNTSS	ISDLENQVLQ	MEKALSLGSL	EPNLAGEMIN	QVSRLLHSPP	DMLAPLAQRL	420
	LKVVDIGILQ	LNSPNTTISL	TSPSLALAVI	RVNASSFNIT	TFVAODPANL	QVSELTQAPE	480
35	NSIGTTITPLS	SLMNLPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLIS	VVISSVANL	540
	TVRNLTRNVT	VTLKHINPSQ	DELTVRVCFW	DLGRNGGRGG	WSDNGCSVKD	RRLNETICTC	600
	SHLTSFGVLL	DLSTSVLPA	QMMALTFITY	IGCGLSSIFL	SVTLVTYIAF	EKIRRDYPSK	660
	ILIQLCALLL	LLNLVFLDLS	WIALYKMQGL	CISVAVFLHY	FLLVSFYWMG	LEAFHMYLAL	720
	VKVENTYIRK	YILKFCIVGW	GVPVAVVTII	LTISPDNYGL	GSYGKFPNGS	PDDFCWINNN	780
40	AVFYITVVG	FCVIFLLNVS	MFIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFLLG	840
	ITWGAFFFAW	GPVNVTFMYL	PAIFNTLQGE	FIFIPYCAVK	ENVRKQWRRY	LCCGKLRLAE	900
	NSDWSKTATN	GLKKQTVNQG	VSSSSNSLQS	SSNSTNSTTL	LVNNDCSVHA	SGNGNASTER	960
	NGVSFSVQNG	DVCLHDFTKG	QHMFFNEKEDS	CNGKGRMALR	RTSKRGSLSHF	IBQM	

45 Seq ID NO: 493 DNA sequence  
Nucleic Acid Accession #: NM\_015507  
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	CGAGTGAGG	GGAGGACCGG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
	GGGTCCGGCC	GCGGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGGGAGA	240
55	ATGCCCTGTC	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
	GGGAAGCGCG	CCAGTGCAAG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
	TGTCACTATG	GAACATAACT	GGCCTGCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
	TGTGAAGCTA	CATGCGAACC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAATATC	480
	AGATGCTTTC	CAGGATACAC	CGGAAAACC	TGCAGTCAAG	ATGTGAATGA	GTGTGAATG	540
60	AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
	CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATC	660
	ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
	TCAGGACTCC	GCCTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCCTCT	780
	GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTTGAAG	CTACTACTGC	840
65	AAATGTCACA	TTGGTTTCCA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
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	ATCCCTGAAA	ATTCTGTGAA	GGAACTCCTC	AGAGCACCTG	GTACCATCAA	AGACAGAAATC	1080
	AAGAAGTTGC	TTGCTCACAA	AAACAGCATG	AAAGAAGAAG	CAAAAATTAA	AAATGTTTACC	1140
70	CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTTG	AGCCCTTCAA	CTATGAAGAG	1200
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	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
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	CTGGTCCAAA	GGAAAGCGCT	AACITCCAAA	CTGGAACATA	AAGATTTAAA	TATCTCGGTT	1440
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	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACAGATGA	GGATGAAAAG	1740
80	TGGAAGACAG	GGAAAAATCA	GTGTGTATCA	GGAACATGAT	CTACCAAAAG	CATCATTTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAAACGGC	GAAATGSCAG	TGGATGGCGT	CTTGCTTGTT	1860
	TCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
	TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
	TTAGAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040



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Seq ID NO: 494 Protein sequence  
 Protein Accession #: NP\_056322

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 20 PEPTRTPTPK VNLQFFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360  
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CAPPCPNMYF KSDELEFAKS FIGTVSIFCL CATLPTFLTF LIDVRRFRYP ERPIIYSVC 240  
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VILTITWFLA AGRKWSCEAI EQKAVWPHAV AWGTPGFLTV MLLALANKVEG DNISGVCFVG 360  
LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVROVI QHGRNQEKI KCFMIRIGVF 420  
SGLYLVPVLT LLGCVYVEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELAFMIKY 480  
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Seq ID NO: 498 Protein sequence  
Protein Accession #: NP\_005037

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NERWVLTAAH CKMNEYTVHL GSDTLGDRRA QRIKASKSFR HPGYSTQTHV NDLMLVKLNS 120  
QARLSSMAVK VRLPSRCEPP GTTCTVSCWG TTTSPDVTFP SGLMCDVVKL ISFDCTKVY 180  
KDLLENSMLC AGIPDSKKNA CNGDSGGPLV CRGTQLGLVS WGTFFCGQPN DPGVYTQVCK 240  
FTKWINDTMK KHR

Seq ID NO: 499 DNA sequence  
Nucleic Acid Accession #: NM\_007196  
Coding sequence: 182..962

1 11 21 31 41 51  
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GATTCCCACT TAAAGGCTC CAGAATCGTG TACCAGGCAG AGAACTGAAG TACTGGGGCC 120  
TCCTCCACTG GGTCCGAATC AGTAGGTGAC CCCGCCCTG GATTCTGGA GACCTCACCA 180  
TGGGACGCCC CCGACCTCGT GCGGCCAAGA CGTGGATGTT CCTGCTCTG CTGGGGGGAG 240  
CCTGGGCAGG ACATCCAGG GCACAGGAGG ACAAGGTGCT GGGGGGTCT GAGTGCCAAC 300  
CCCATTCGCA GCCTTGGCAG GCGGCCTTGT TCCAGGGCCA GCAACTACTG TGTGGCGGTG 360  
TCCTGTAGG TGGCACTGG GTCCCTACAG CTGCCCCACTG TAAAAACCG AAATACACAG 420  
TAGCCCTGGG AGACCAAGC CTACAGAATA AAGATGGCCC AGAGCAGAA ATACCTGTGG 480  
TTCAGTCCAT CCCACACCCC TGCTACAACA GCAGCGATGT GGAGGACCAC AACCATGATC 540  
TGATGCTTCT TCAACTGCGT GACCAGGCAT CCTGGGGTC CAAAGTGAAG OCCATCAGCC 600  
TGGCAGATCA TTGCACCCAG CCTGGCCAGA AGTGCAACCT CTCAGGCTGG GGCATGTCA 660  
CCAGTCCCCG AGAAGATTTT CCTGACACTC TCAACTGTGC AGAAGTAAA ATCTTTCCCC 720  
AGAAGAAGTG TGAGGATGCT TACCGGGGC AGATCACAGA TGGCATGGTC TGTGAGGCA 780  
GCAGCAAAGG GGCTGACAG TGCCAGGGCG ATTCTGGAGG CCCCTGGTG TGTGATGGTG 840  
CATCCAGGG CATCATCC TGGGGCTCAG ACCCTGTGG GAGGTCCGAC AAACCTGGCG 900  
TCTATACCAA CATCTGCCG TACCTGGACT GGATCAAGAA GATCATAGGC AGCAAGGGCT 960  
GATTCTAGGA TAAGCACTAG ATCTCCCTTA ATAAACTCAC AACTCTC

Seq ID NO: 500 Protein sequence  
Protein Accession #: NP\_009127

1 11 21 31 41 51

MGRPRPRAAK TWMFLLLGG AWAGHSRAQE DKVLGGHECQ PHSQPWQAAAL FQGQQLLCGG 60  
 VLVGNNWVLT AAHCKKPKYT VRLGDHSLQN KDGPEQEIPV VQSIPHPCYN SSDVEDHNMHD 120  
 LMLLQLRDOA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPDT LNCAEVKIFP 180  
 QKKCEDAYPG QITDGMVCAG SSKGADTCQG DSGGFLVCDG ALQGITSMWG DPCGRSDKPG 240  
 VYTINICRYLD WIKKIIGSKG

Seq ID NO: 501 DNA sequence  
 Nucleic Acid Accession #: NM\_006103  
 Coding sequence: 29..406

1 11 21 31 41 51  
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 GAAGACTGGC GTGTGCCCGG AGCTCCAGGC TGACCAGAAC TGACGCGAAG AGTGGGTCTC 180  
 GGACAGCGAA TGCGCCGACA ACCTCAAGTG CTGCAGCGCG GGCTGTGCCA CCTTCTGCCT 240  
 TCTCTGCCCA AATGATAAGG AGGGTTCTTG CCCCAGGTG AACATTAACT TTCCCCAGCT 300  
 CGGCCTCTGT CGGGACCACT GCCAGGTGGA CAGCCAGTGT CCTGGCCAGA TGAATGTCTG 360  
 CGCCTAATGGC TGTGGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGGTC CAGCCACCAC 420  
 CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGGTT CCAGCCACC 480  
 TGCCCTCCCC TTTTTCGGGA CTCTGTATTC CCTCTTGGGC TGACCACAGC TTCTCCCTTT 540  
 CCAACCAAT AAAGTAACCA CTTTCAGCAA AAAAAAAAAA AAAA

Seq ID NO: 502 Protein sequence  
 Protein Accession #: NP\_006094

1 11 21 31 41 51  
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 CCSAGCATFC LLCPNKKEGS CPQVWINFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVCSC 120  
 VTFNF

Seq ID NO: 503 DNA sequence  
 Nucleic Acid Accession #: NM\_002407  
 Coding sequence: 65..352

1 11 21 31 41 51  
 CCTCCACAGC AACTTCCTTG ATCCCTGCCA CGCAGGACTG AACACAGACA GCAGCGCGCT 60  
 CGCCATGAAG CTGCTGATGG TCCTCATGCT GCGCGCCCTC CTCCTGCACT GCTATGCAGA 120  
 TTCTGGCTGC AAATCTCTGG AGGACATGGT TGAAGAGACC ATCAATTCCG ACATATCTAT 180  
 ACCTGAATAC AAGAGAGCTTC TTCAAGAGTT CATAGACAGT GATGCGCGTG CAGAGGCTAT 240  
 GGGGAAATTC AAGCAGTGTG TCCTCAACCA GTCACATAGA ACTCTGAAAA ACTTTGGAAT 300  
 GATGATGCAT ACAGTGTACG ACAGCATTGG GTGTAATATG AAGAGTAATT AACTTTACCC 360  
 AAGGCGTTTG GCTCAGAGGG CTACAGACTA TGGCCAGAAC TCATCTGTTG ATTGTAGAAA 420  
 ACCACTTTTC TTTCTGTGTG TGTCTTTTGA TGTGGAAACT GCTAGACACG TGTGAAACC 480  
 TCAAAATCAT TTCATTTCAT ATAACAACT GCATAATC

Seq ID NO: 504 Protein sequence  
 Protein Accession #: NP\_002398

1 11 21 31 41 51  
 MKLLMVLMLA ALLLHCYADS GCKLLEDMEV KTINSDISIP EYKELLQEFI DSDAAAEAMG 60  
 KFKQCFLNQS HRTLKNFGLM MHTVYDSIWC NMKSN

Seq ID NO: 505 DNA sequence  
 Nucleic Acid Accession #: NM\_014791.1  
 Coding sequence: 171..2126

1 11 21 31 41 51  
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 TCCGCCCCCTC AGGTTCCTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180  
 ATGATGAATC TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA 240  
 AGGTCAAATC TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300  
 AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAAC 360  
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 TGTGAGAAGA GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540  
 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600  
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 CATATCTTGG ATCAGAGGCA GATGTTTGGG GCATGGGCAT ACTGTTATAT GTTCTTATGT 780  
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 GAAAATATGA TGTTCCTCAG TGGCTCTCTC CCAGTAGCAT TCTGCTCTCT CAACAATATC 900  
 TGCAGGTGGA CCCAAGAGAA CGGATTTCTA TGAATAATCT ATTGAACCAT CCTTGGATCA 960  
 TCAAGATTA CAATATCTCT GTTGAAGTGG AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020  
 ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAACAA ATGGAGGATT 1080  
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 AGGCTCGGGG AAAACCAAGT CGTTTAAGGC TTTCTTCTTT CTCTGTGGA CAAGCCAGTG 1200  
 CTACCCCATC CACAGACATC AAGTCAAATA ATTGGAGTCT GGAAGATGTG ACGCAAGTG 1260

5 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320  
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 AATCTAAATC ATTAACCTCA GCCTTATGCA GAACACCTGC AAATAAAATTA AAGAACAAG 1440  
 AAAATGTATA TACTCTAAG TCTGCTGTA AGAATGAAGA GTACTTTATG TTCTCTGAGC 1500  
 10 CAAAGACTCC AGTTAATAAG AACCCAGATA AGAGAGAAAT ACTCACTACG CCAATTCGTT 1560  
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 GCTCAGTGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG 1740  
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 15 GCAAAGGAA GGGTCTGCC AGAGACGGGC CCAGAAGACT AAAGCTTAC TATAATGTGA 1860  
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 20 ACATCCTATC TAGCTGCAAG GTATAATGA TGGATTCTTC CATCTGCCG GATGAGTGTG 2160  
 GGTGTGATAC AGCCTACATA AAGACTGTGA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220  
 CTACCAACTT GTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280  
 GATATTATT TTGTGTGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTT 2340  
 TAATCATGTG GTTTGTGATA TTAATAATTG TTGACTTCT TAGATTCACT TCCATATGTG 2400  
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 TTGTGAATAT

Seq ID NO: 506 Protein sequence  
 Protein Accession #: NP\_055606.1

25 1 11 21 31 41 51  
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 30 LKHLRQHIC QLVHVLLETAN KIFMVLEYCP GGELEFDYIIS QDRLSEEBTR VVFRQIVSAV 120  
 AYVHSQGYAH RDLKPENLLF DEYHKLKID FGLCAKPKGN KDYLQTCQG SLAYAAPALI 180  
 QGKSYLGSEA DVWSMGLILY VLMCGFLPFD DDNVMAlyK IMRGKYDVPK WLSPPSILL 240  
 QQMLQVDPK RISMKNLLNH PWIMQDYNYP VEWQSKNPFH HLDLDCVTEL SVHHRNRQT 300  
 MEDLISLWQY DHLTATYLL LAKKARGKPV RLRLSSFSFG QASATPPTDI KSNHWSLEDV 360  
 35 TASDKNVVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL 420  
 KNKENVYTPK SAVKNEEYFM FPEPKTPVKN NQHKREILT PNYRTTPSKA RNQCLKETPI 480  
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540  
 LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLNEIMS ILPKKHVDFV QGYTLKQQT 600  
 QSDFGKVTMQ FELEVQLQK PDVVGIRQR LKGDWVYKR LVEDILSSCK V

40 Seq ID NO: 507 DNA sequence  
 Nucleic Acid Accession #: NM\_000582  
 Coding sequence: 88..990

45 1 11 21 31 41 51  
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 GGCATCACT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAGAGCAG 180  
 50 CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240  
 CAGAATCTCC TAGCCCCACA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGCCACATG 300  
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 AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420  
 TCTGATGAAT TGATGAACCT GGTCACTGAT TTTCCCAACG ACCTGCCAGC AACCGAAGTT 480  
 55 TTCACTCCAG TTGTCCCACT AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540  
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 GACGAGGACA TCACCTCACA CATGGAAAAC GAGGAGTTGA ATGTGCATA CAAGGCCATC 660  
 CCGGTGCCCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720  
 GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780  
 60 TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCAITCCG ATGTGATGTA TAGTCAGGAA 840  
 CTTTCCAAG TCAGCGGTGA ATTCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900  
 GTTGTAGACC CCAAAGTAA GGAAGAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA 960  
 TTAGATAGTG CATCTTCTGA GTTCAATTAA AAGGAGAAAA AATACAATT CTCACITTGC 1020  
 ATTTAGTCAA AAGAAAAAT GCITTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080  
 65 CTGAGTTTAT TGGTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140  
 ATTAGTTTAT TTTGTGGCTT CATGGAAACT CCCTGTAAC TAAAAGCTTC AGGGTTATGT 1200  
 CTATGTCAT TCTATAGAAG AAATGCAAC TATCACTGTA TTTTAATATT TGTATTCTC 1260  
 TCATGAATAG AAATTTATGT AGAAGCAAC AAAATACTTT TACCACCTTA AAAAGAGAAT 1320  
 70 AATACTTTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TGTGTGTGAT 1380  
 TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGTGTG 1440  
 AATTGCTTAT TTGTTTTCCT ACGTTTGTCC AGCAATTAAT AAAACATAAC CTTTTTATC 1500  
 GCTTAAAAA AAAAAA AAAA

Seq ID NO: 508 Protein sequence  
 Protein Accession #: NP\_000573

75 1 11 21 31 41 51  
 MRIVAVICFL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60  
 80 PSKSNESHDB MDDMDDEDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDESDELVT 120  
 DFPDLPATE VPTPVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYFDA TDEDITSHME 180  
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDQDS AETHSHKQSR LYKRKANDES 240  
 NEHSDVIDSQ ELSKVSREFH SHEPHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN

Seq ID NO: 509 DNA sequence  
Nucleic Acid Accession #: AB051390.1  
Coding sequence: 34..2457

5 1 11 21 31 41 51  
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CTGAGCCCGA CTCGGGCACT GCTGGCCCTG GCGCTGCCCG TGGCCGCGCG GCTGGCCTTC 120  
TCCGACGAGA CCTGGGACAA AGTGGCCCAAG TCAGAGGGCT ACTGCAGCCG TATCCTGCCG 180  
10 GCCCAGGGCA CGCGCGCGGA GGGCTACACC GAGTTCAGCC TCCGCGTGGA GGGCGACCCC 240  
GACTTCTACA AGCCGGGAAC CAGCTACCGC GTAACTCTT CAGCTGCTCC TCCCTCCTAC 300  
TTCAGAGGAT TCACATTAAT TGCCCTCAGA GAGAACAGAG AGGGTGATAA GGAAGAAGAC 360  
CATGCTGGGA CCTTCCAGAT CATAGACGAA GAAGAACTC AGTTTATGAG CAATTGCCCT 420  
15 TTGCAAGTCA CTGAAGCAC TCCACGGAGG AGGACCCGGA TCCAGGTGTT TTGGATAGCA 480  
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TATTTTCAAG ATGAGGGCTC TCTGACCAAG AAACCTTTGT AACAAGATT CACATTTGAT 600  
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ACATTTTATG GGAATTGGTC CGAGAAGACA CACCAAAAGG ATTACCTCG TCGGCCCAAC 720  
20 CACTGGTCTG CGATCATCGG AGGATCCAC TCCAAGAAAT ATGTACTGTG GGAATATGGA 780  
GGATATGCCA GCGAAGGCGT CAAACAAGTT GCAGAATTGG GCTCACCCTG GAAATATGGA 840  
GAAGAAATTC ATGAGGCTC TGATGAGGTC CTCACCGTCA TCAAGGCCAA AGCCCAATGG 900  
CCAGCTGGCG AGCCTCTCAA CGTGAGAGCA GCACCTTCAG CTGAATTTTC CGTGGACAGA 960  
ACGCGCCATT TAATGTCCTT CCTGACCATG ATGGGCCCTA GTCCCGACTG GAACGTAGGC 1020  
25 TTATCTCGAG AAGATCTGTG CACCAAGGAA TGTGGCTGGG TCCAGAAGGT GGTGCAAGAC 1080  
CTGATTCCCT GGGACGCTGG CACCGACAGC GGGGTGACCT ATGAGTCACC CAACAAACCC 1140  
ACCATCCCTC AGGAGAAATC CCGGCCCTG ACCAGCTCG ACCATCTCA GAGTCTTTTC 1200  
TATGACCCAG AGGGTGGGTC CATCACTCAA GTAGCCAGAG TTGTCATCGA GAGAATCGCA 1260  
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CCATGCTCGC CCTGCAGCTC CTCACCTGTG GACAAAGGCA AGAGGATGCG ACAGGCGATG 1440  
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TGCAAGCGCA AGTGGCGAT GGGCATGAAG AAGCGGCACC GCATGATCAA GATGAACCCC 1800  
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TGCCACACCA TCCCATGCTT GCTGTCCCA TGGTCCGAGT GGAGTGACTG CAGCGTGACC 1920  
40 TGCGGGAAGG GCATGCGAAC CCGACAGCGG ATGCTCAAGT CTCTGGCAGA ACTTGGAGAC 1980  
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GAGCTCAAGC CTGCGGCAT GTGGTCCGAA TGTAAACAGT CATGTGGGAA AGGCCACGTG 2100  
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45 CGCTGGAGGG AGGCCGAGGA GAGCCGGCGG AGTGAGCAGC TGAAGGAAGA GTCTGAAGGG 2280  
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50 GCTGTGTTAA GACAATTAA ATGTGTACG CTAGTTTACA TTTTTCAGT GTGGTTCGCC 2580  
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GCATGTATGT TGGGTGGCTT TTGTTCTTTC ACTGAGAAAT TCGGAATACA TTTGTCTCAC 3060  
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65 CAAAGCCCC CCAATGCATT CCTTCAACAA AATACAATCT CTGTACTTTA AAGTTATTTT 3480  
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70 TGCCCTCCCA GCAATTATA GCACACCAGA TTCAGGGAGA CTGACCACCA AGGGATAGTG 3720  
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75 TTTTATATT GTCTCCACC TCCATCATTT TCAATAAAG ATAGGGCTTT TGCTCCCTTG 4080  
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80 CAAGGACAAG CCACCTAGT GTCTCATGTT TGTATTTGGT CCCAGTGGG TACATTTTAA 4380  
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TACCAAAGTC TTGTAGGTT GTTTATAGTT CTTTGGCTA ACAATCATT TTGGAATAA 4560  
AGATTTTTTA CTACAAAAAT G

Seq ID NO: 510 Protein sequence  
Protein Accession #: BAB18461.1

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FSLRVEGDDP FYKPGTSYRV TLSAAPPSTYF RGFTLIALRE NREGDKEDDH AGTFQIIDE 120
ETQFMSNCPV AVTESTPRRR TRIQVFWIAP PAGTGCVLK ASIVQKRIIY FQDEGLTKK 180
LCEQDSTFDG VTDKPIIDCC ACGTAKYRLT FYGNWSEKTH PKDYPRRANH WSAIIGGSHS 240
10 KNYVLWEYGG YASEGVKQVA ELGSPVKMEE EIRQQSDEVL TVIKAKAQWP AWQPLNVRAA 300
PSAEFSVDRT RHLMSFLTMM GPSPDMNVGL SAEDLCTKEC GWVQKVVDL IPWDAGTDSG 360
VTYESPNKPT IPQEKIRPLT SLDHPQSPFY DPEGGSTQV ARVVIETAR KGEQCNIVPD 420
NVDDIVADLA PEEKEDDTP ETCIYSNWSP WSACSSSTCD KGRMRQRL KAQLDLSVPC 480
15 PDTQDFPQCM GPGCSDDEGS TCTMSEWITW SPCSISCGMG MRSRERYVKQ FPEDGVSCTL 540
PTEETEKCTV NEECSPSSCL MTEWGEWDEC SATCGMGMKK RHRMIKMPA DGSCKAETS 600
QAEKCMPECT HTIPCLLSPW SEWSDCSVTC GKGMRTQRM LKSLAELGDC NEDLEQVEKC 660
MLPECPIDCE LTEWSQWSEC NKSCGKHVI RTRMIQMEPQ FGGAPCPETV QRKCKRIRKC 720
LRNPSIQKLR WREARESRRS EQLKEESEGE QFPGRMRPW TANSECTKLC GGGIQERYMT 780
VKGRFKSSQF TSCKDKKEIR ACNVHPC
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Seq ID NO: 511 DNA sequence  
Nucleic Acid Accession #: NM\_003108.1  
Coding sequence: 76..1401

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GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA 60
GCCCTGCAAC GATCATGTGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC 120
30 CGGGAGGCGC TGACACGSA GGAGGGCGAA TTCATGGCTT GCAGCCGGT GGCCCTGGAC 180
GAGAGCGACC CAGACTGGTG CAAGACGCGC TCGGGCCACA TCAAGCGGCC GATGAACGCG 240
TTCATGTAT GGTCCAAGAT CGAACGCGAG AAGATCATGG AGCAGTCTCC GGACATGCAC 300
AACCGCGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAATA TGCTGAAGGA CAGCGAGAAG 360
ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC 420
35 TACAAGTACC GGCCCGGAA AAAGCCCAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC 480
CAGAGCCAG AGAAGAGCGC GGCCCGCGGC GCGCGGCGGA AGGCGCGGCG AGGCGCGGCG 540
GGTGCCAGA CTTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCGCGCGGCC 600
GCGCGCGGCA AGGCGGCGGC GGGCAAGCGC GCCAGTCCG GGGACTACGG GGGCGCGGCG 660
GACGACTACG TGCTGGCGAG CTTGGCGGTG AGCGGCTCGG GGGCGGCGCG CGCGGCGAAG 720
40 ACGGTCAAGT GCGTGTCTCT GGATGAGGAC GACGACGAGC ACGACGACGA CGACGAGCTG 780
CAGCTGCAGA TCAACAGGA GCCGACGAG GAGGACGAGG AACCCCGCA CAGCAGCTC 840
CTGACGCGC CGGGGCGAGC GCGCTGCGAG CTGCTGAGAC GCTACAACT CGCCAAAGTG 900
CCCGCGAGC TCTCGCTGAG CAGCTCGGCG GAGTCCCCCG AGGAGCGAGC CCTCTACGAC 960
GAGGTGCGCG CGGGCGGAC CCGGCGGCC GGGGCGGCA GCGGCTCTA CTACAGCTTC 1020
45 AAGAACATCA CCAAGCAGCA CCGCGCGCG CTGCGCGAGC CCGGCTGTC GCCCGGTC 1080
TCGCGCTCGG TGTCCACCTC CTGCTCCAGC AGCAGCGGCA GCAGCAGCG CAGCAGCGC 1140
GAGGACGCG AGACCTGAT GTTGCACCTG AGCTTGAATT TCTCTCAAG CGCGCACAGC 1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCGGGA ACCTGTCCCT GTGCTGGTG 1260
50 GATAAGGATT TGAATCGTT CAGCGAGGCG AGCCTGGGCT CCCACTCGA GTTCCCGGAC 1320
TACTGACGCG CGGAGCTGAG CGAGATGATC GCGGGGAGT GCGTGGAGC GAACTTCTCC 1380
GACCTGGTGT TCACTATTTG AAAGCGCGCC GCTGCTGCT CTTTCTCTG GAGGCTGCG 1440
AGCTGGGTTT CTTGGGAGGA AGTTGTATGT GTGATGATG TGATGATGAT AATGATGATG 1500
ATGATGGTGG TGTGTATGTT GCGGTGGTA GGGTGGAGGG GAGAGAAGAA GATGCTGATG 1560
55 ATATTGATAA GATGTCGTA CGCAAGAAA TTGGAAGAA TGATGAAAT TTTGGTGGAG 1620
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TCTTTATCG TGTCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA 1800
AAAATGTGTT TTTGTAATTA CTATTTCTTT TTCTGAAAT TCGTGATTGC AACAAAGGCA 1860
GAGGGGGCGG CGGGCGGAG GGGAGGTAGG ACCGCTCCG GAAGGCGCTG TTTGAAGCTT 1920
60 GTCGGCTTT GAAGTCTGGA AGACGCTGCG AGAGGACCTT TTTGGCAGCA CACTGTATC 1980
TCTAGGAGAT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAGAAC TGGTGATTT
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Seq ID NO: 512 Protein sequence  
Protein Accession #: NP\_003099.1

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65      1      11      21      31      41      51
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KIERRKIMEQ SPDMENAEIS KRLGKRWKML KDSEKIPFIR EAERLRLKHM ADYDPYKYRP 120
70 RKKPKMDPSA KPSASQSPER SAAGGCGGSA GCGAGGAKTS KGSSKCKGKL KAPAAAGAKA 180
GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGTKVKCV FLDEDDDDDD DDELQLQIK 240
QEPDEEDEEP PHQQLQPPG QQPSQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVAG 300
ATSGAGGGR LYYSFKNITK QHPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD 360
75 LMPDLNLNFS QSAHSASEQQ LGGAAAGNL SLSLVDKDL D SFESEGLSGH FEFPDYCTPE 420
LSEMIAGDWL EANFSDLVFT Y
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Seq ID NO: 513 DNA sequence  
Nucleic Acid Accession #: CAT Cluster

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80      1      11      21      31      41      51
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ATTGGTAATC TACAGTAAGA TTTTCAGTTA GGATTGAGA TTATGATAAT AACTAATAGA 120
ATATTTCTAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTG 180
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5 GCAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA 240  
AAGGATATCT GTTGTCTCCG AATGAAACAA TTTTCTGTAA ATAGAGGGCC CAGAATTGGT 300  
CTCTGACAAAT TAATAAGAC ATCAAAGATA GCAAATGAT TTTTATATCT TAGGGCCAAT 360  
ACTACCAATT TAATAATTAA ACAAAGTTCT GGTGAGCTCT GAACCTTGGA GAATTGGTGG 420  
CAACATAGAC TTGGATTCTT CCAAATTTCC CACATAAAAC AAAGGGGATC AACTAGATAG 480  
AAAAACCAGA AACCTTTGGA AATATCTGTT TAAAAAAA AAAAAGTCTGA CGCGGGCC

Seq ID NO: 514 DNA sequence  
Nucleic Acid Accession #: CAT cluster

10

1 11 21 31 41 51  
15 GGAGCCACAG TGAAGTCAA GAATGTCAGT GATTCCACAT TTAATATCTA CATTTTGTCA 60  
GGGCAGTTAC TCTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTA GACAAGTGAA 120  
TACAGGATTCT TCTGGGTGTG ATTCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC 180  
CTTGGCTTCA CTCTGACTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT 240  
CCTGCAGTC TTAAGAAGAC CTITCCAAAC TATGAACAG CCCAGCAGCA CTGAGTTAGA 300  
GGTAAATTCT GAACCTTGA ACACATAAAC TATTCTACT GCACATAGAA TTGGCAAGTA 360  
GCATTCTATG TCTATGAACA GTATGTCTTT TCTATATAAC AGAGAAATC TTTTAAAGCA 420  
AACTACTCAG TTTAAACCTT AATTCTTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA 480  
TCAATGCAAC AGTACACTCT TATTGAGGCA TTTGAAAGAA AGAATTCGAG ATCTAGTTTG 540  
TATCAGATAT TATAAATTAG TATGGTTTAG TCTTTGTCTT GAAATTTCTAC TTAATTTTGT 600  
GACTATAGT TTAAGAATGT AAGCAGAAGT TCTGCACCAA TCAGAATAAG CTACATTATG 660  
CTTGAAGTAC AACTACTGTA ATGACAAAAT ATCAGTGGCT TAATACAATG GTTTTCTCT 720  
CATACTTGTT CATAAAGAGT CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG 780  
GGTTGTGGA AGCTCCACCA TTTTAGATAG CTCCCTTCAA AGTCAGCCAT CTTTGGCAGT 840  
CCATGTCCCC CACAGGCTG GCAAATTTG GCTCTGGATG GCTTCAAGGA TTGAGCATCG 900  
GGCAGTTTAA ATGCTTTCAA CATGGAAGT GGACACCGGC CACTCCCACT CACATCCCTT 960  
GGGCCAGAAC TAGGTCAGTG GGCCCGGACC TAACCTGGGA GGGTTGGGGA ATTGTAAATC 1020  
CTCCATGTAC CCAAGTGGGA GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG 1080  
AAATCCATT TACCATTCCT TTTGCCATAA GTGAAAAGAT GAGTACTTTC ATCAATTTGT 1140  
AAACTGTACT TTTGAAGTAA ATCCTGGTAG CTGTCATGGG GGCTGGATT TCCAGAAAGCC 1200  
ATATGTAATT TGGGAATGAC ATTCACCTAA GCTCATAGAA TATCATTATT TGATGTAAAA 1260  
TGCCCTCAT TGCATATACG GACCAAAATG CACTAACAC AAAACCCCC TCCCCACGGG 1320  
GCCCGGGTCC CCAATTCCTC TCCATCCCTT TAAATGAGGC ATCTATGAT TTGGAATGGA 1380  
AGCCAGTGTG TAGTCGTAGG AATTTTACTT AATTCAAGAA TTATTCTCAC TGAATATGTG 1440  
CCAGTTCTGA AGGAATGCA AAGTCAAAAT TTGCATCTTC TTTGCTCAAG GGCCTTTAGA 1500  
TGTAACAACA CAGACATGAT ACAAGGCTGA CAATGACATT ATGATTAAAA TATGTTAAAC 1560  
AATTTATTAA ATTGTGAATC AACAAAAAAT TATGTTCTTT ATTTTATGGT TTTGCTAGT 1620  
CCTGACTCAC TGCCTACATA CCCCTCTGT TCCTCAGTTC TTATCCCTGA TTTCTTACAG 1680  
GATGGCCTAA GACAGCTGTA GATGTTTTTA TTAGCAAAA AAAAAAAA AAAAGTCGAC 1740  
CGCGCCCGA ATTTAGTAG

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Seq ID NO: 515 DNA sequence  
Nucleic Acid Accession #: NM\_012427  
Coding sequence: 43..924

50 1 11 21 31 41 51  
CTTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGCTAC AGCAAGACCC 60  
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GTCTCTGCCA ACAATGATGT TTCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180  
AACCAGGACC TGGGAGCTGG GGCCGGGGAA GACGCCCGGT CGGATGACAG CAGCAGCCGC 240  
ATCATCAATG GATCCGAGTG CGATATGCAC ACCCAGCCGT GGCAGGCCGC GCTGTTGCTA 300  
AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGGTGCATC CACAGTGGCT GCTCAGGGCC 360  
GCCCACTGCA GGAAGAAAGT TTTCAGAGTC CGTCTGGGCC ACTACTCCCT GTCAACAGTT 420  
TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAATCCA TCCCCACCC TGGCTACTCC 480  
CACCTGGGCC ACTCTAACGA CCTCATGCTC ATCAAATGCA ACAGAAGAAT TCGTCCCACT 540  
AAAGATGTCA GACCCATCAA CGTCTCCTCT CATTGTCCCT CTGCTGGGAC AAAGTGCCTG 600  
GTGTCGTGGT GGGGGACAA CAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC 660  
TTGAATATCA GCGTGTCTAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720  
GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG 780  
GGCCTGTGG TCTGCAATGG CTCCTGCAG GGAATGCTGT CCTGGGAGGA TTACCTTGT 840  
GCCCGGCCCA ACAGACCGGG TGCTACAGG AACCTCTGCA AGTTCACCAA GTGGATCCAG 900  
GAAACCATCC AGGCCAACTC CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCACT 960  
GCTGAGGGA CAGCCCTGAC ACTCCTTCA GACCTCATT CCTTCCAGGA GATGTTGAGA 1020  
ATGTTACTCT CTCCAGCCCC TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCCCCAC 1080  
ATTGGGCTGA CGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAA CTGTCAGGG 1140  
CGGGGGTTGC GTCTCAATCT CCCCTGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT 1200  
TCTCTGACGC TCTGACCCAA ATTTAGTCCC AGAATAAAC TGAGAAGTGG AAAAAAAA

75

Seq ID NO: 516 Protein sequence  
Protein Accession #: NP\_036559

80

1 11 21 31 41 51  
MATARPWMV VLCAALITALL LGVWEHVLN NDVSCDHPSN TVPSGNSQDL GAGAGEDARS 60  
DDSSSRIRNG SDCDMHTQPW QAALLLRPNQ LYCGAVLVHP QNLLTAARCR KKVFRVRLGH 120  
YLSLSPVYESG QMPQGVKSI PHPGYSHPHG SNDLMLIKLN RRIIPTKQDR PINVSSHCP 180  
AGTKCLVSGW GTTKSPQVHP PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS 240  
CQDGGGPPV CNGSLQLVLS WGDYPCARP RPVGYTNLCK PTKMIQETIQ ANS

Seq ID NO: 517 DNA sequence  
Nucleic Acid Accession #: NM\_001719  
Coding sequence: 123..1418

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5 1 11 21 31 41 51
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CTGCCACCTG GGGCGGTGCG GGGCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
10 CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACTCCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
GCCAGGGCTT CTCTACCCCT TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
15 GCCTGCAAGA TAGCCATTTC CTCACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCAGAAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
ACATCGGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCGG 780
20 AGGAGGGCTG GCTGTGTTT GACATCACAG CCACAGCAA CCACTGGGTG GTCAATCGCG 840
GGCACAACCT GGGCTGCGAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGCTGGCTT 960
TCTTCAAGGC CACGGAGGTC CACTTCGCGA GCATCCGCTC CACGGGAGC AAACAGCGCA 1020
25 GCCAGAACC GTCCAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACCTGGCAG 1080
AGAACAGCAG CAGCGACCG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGCGAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
AGGGGGAGTG TGCCTTCCCT CTGAATCCTT ACATGAACGC CACCAACCA GCGCTCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCAAGC 1320
30 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCTAT CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTC 1440
TTGGGGCCAA GTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCTCCTCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
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35 TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAACA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCAATTGGT GGGAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC TTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAGGGGT 1800
GGGCACATTG GTGCTGTGCG GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAACG AATGAATG
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Seq ID NO: 518 Protein sequence  
Protein Accession #: NP\_001710

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45 1 11 21 31 41 51
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MHVRSRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQRILS 60
ILGLPHRRPP HLQGHNSAP MMLDLYNAM AVEEGGGPGG QGFSYPYKAV PSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREPRFDL SKIPEGEAVT AAEFRIYKDY 180
IRERFDNETF RISVQVLQGE HLGRESDLFL LDSRTLWASE EGMVLFDITA TSNHWVNVNR 240
HNLGLQLQVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAE FKATEVHFPS IRSTGSKORS 300
50 QNRSTPKPNQ EALRMANVAE NSSSDQRQAC KKHLYVSPFR DLGWDWIIA PEGYAAYTCE 360
GECAPFLNSY MNATNHAIVQ TLVHFNPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
RNMVVRACGC H
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Seq ID NO: 519 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 264..782

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60 1 11 21 31 41 51
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CCCTGCTCCA GTCACACCCG GAAGCTGACT GGTCCACGCA CAGCTGAAGC ATGAGGAAAC 60
TCATCGCGGG ACTAATTTTC CTTAAAATT AGACTTGCAC AGTAAGGACT TCAACTGACC 120
TTCTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC 180
TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC 240
AACTTATCAG CAAGGAGCTC ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG 300
65 TGATCGCGGT GGTGTCCCTC TTCTGTCAGG CCTGCTTCTT CACGCGCATC AACTACCTGC 360
TCAGCAGGCA CATGGCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCCAGGTTT 420
CCAGGCCAG CCTGCGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA 480
CAGAGAGAGA CATCCCAATG TCTGATTCCC TTACAGGCA TGACAGCGAC ACACCTCAG 540
70 ATAGCTTGA TAGCTCTGCG AGTTGSCCTC CTGCTGCCCA GGCCACAGAG GATGTGGATT 600
ACACACAAGT CGTCTTTTCT GACCCCTGGAG AACTAAAAAA TGACTCCCG CTGGAATATG 660
AGAACATAAA GGAATACACA GATTATGTCA ATGTCAATCC AGAAAGACAC AAGCCCAATT 720
TCTGGTATT TGTCAACCTT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT 780
GAATTCACAA TATTTTAAAT GGGGTCCAGT TCTCTATGGA TTCTTACATT TAATTGTAG 840
75 GGAATGCCA TTTTCCCCC TTAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGGC 900
CAAAAAGAA GTGAGAGAAG AAACGTATAA ATACACAGAG GTCCTCAAGA CCCATGGACT 960
CCTGGTCTGT ACCCAAAAAA GCTGTTCGTT CCTCAAAAC AAAACAAGG CTTGGCTGGG 1020
AAAAACAGCC AATGCCCCGG CAAGAAAGGT TGAGATCAGA TGTTAGGAAG AACTTTCAGG 1080
TAAAGTATGA GAACTATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCAAGGGA 1140
80 AAATTTTAAA AAGTTGAAT CAGCTGTGTG AGAGTCTTAT TTGGCAATCT CATGGTTAAA 1200
TGACTTCCTT TTGAGCTCTT TAATTATTGG CAATAACAA CTTCCTTAAA AGTTTAAAA 1260
AAAATAGCAA CCACCACA
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Seq ID NO: 520 Protein sequence  
Protein Accession #: Eos sequence



1 11 21 31 41 51  
 5 MLTEVMEVWH GLVIAVVSFL LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH 60  
 HPPAVKENKE TQTERDIPMS DSYLRHSDST PSDSLDSSCS SPPACQATED VDYTVVFS 120  
 PGELKNDSP L DYENKEITD YVNVNPERHK PSFVYFVNPA LSEPAEYDQV AM

Seq ID NO: 521 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 107..328

1 11 21 31 41 51  
 15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCCA AATATTTTAA 60  
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 CCTTAAACAA GGCATGGGCG TCACAAGTCT ATGGAGACAG GCCAAAAGA ATGTGGAGAA 180  
 GAAATCTGAT AATATCACAG AGGTCTCTCA GACCCATGGA CTCTGGTCT GTACCCAAAA 240  
 AAGCTGTTCG TTCTCTCAAA ACAAAAACAA GGCTTGGCTG GGAAAACAGG CCAATGCCCC 300  
 20 GGCAAGAAAG GTTGAGATCA GATGTAGGA AGAATCTTCA GGTAAAGTAT GAGAACTATG 360  
 GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCCAGG GAAAATTTTA AAAAGGTTGA 420  
 ATCAGCTGTT GTAGATGTTCT ATTTGGCAAT CTCATGGTTA AATGACTTCC CTTTGAAGCTC 480  
 TTTAATTATT GGCAATAAAC AACTTCTTTA AAAGTTTAA ATAAATAGC AACCACCACC 540  
 A

25 Seq ID NO: 522 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 30 MPFFPLKQGM GLTSLWRQAK KNVEKKTDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK 60  
 QANAPARKVE IRC

35 Seq ID NO: 523 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 211..1895

1 11 21 31 41 51  
 40 GGATCTGAGG GGCGCCAGT CACTTCTCTC ACGTTCCTGT GCTGGGCGGG AGGAGCGGAT 60  
 GGGGCTTGGG AGGCAGCGCT CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTGGGA 120  
 GAGGAATTAT CTGATAAAAT TCTGGGTTA ATATTTTAA AAAACGAGAG TTTTAAAAA 180  
 TGATTTTTT CCCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGT C AACCCAGCATA 240  
 GTGCTTTTTC TTTTCTCTTC TTTTCTCTTC ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300  
 45 CACAGGTTCC TTGAACAGCT GGATCTGAT GGCAACATTA CTATAGAGGA GCAGATTGTC 360  
 CTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCAACT CCAGGAGGGA 420  
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 50 GCAATTATT CAGACTGCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660  
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTCTCTG 720  
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 GTAGTCCACT GTACCATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGAA GATTTATCAA 900  
 55 CAAAATTTCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960  
 GTTGTGATGT TTATTTACTT CTTGGCTACA AATTATTAAT GSATCCTGGT GGAAGTCTC 1020  
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 60 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TCTGAATAC GGTTAGAGTT 1260  
 CTAGTACCA AATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320  
 AAATCGGCA AATCGACACT GGTCTGGTC CTAGTCTTTG GAGTGCATTA CATCGTGTTC 1380  
 GTATGCTGCT CTCACTCCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440  
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500  
 65 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAGAGG 1560  
 ACACCCCAT GTGGCAGCG CAGATGCGGC TCAGTGCTCA CCACGTGAC GCACAGCACC 1620  
 AGCAGCCAGT CACAGGTGGC GGCAGCACA GCATGGTGC TTAATCTTGG CAAAGCTGCC 1680  
 AAGATCGCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740  
 TCAGAGCAGG ACTGCCTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800  
 70 CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CCCAGACACT 1860  
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 524 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 75 MLRSSLSSTSI VLFLFSSFSI INESISSRRK HRFLEQLDSD GTTIEBQIV LVLKAKVQCE 60  
 LNITAQLEG EGNCFFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120  
 80 DFMSLNKWT ANYSDCLRFL QPDISIGQBE FFERLYVMT VGSISFSGSL AVAILIIGYF 180  
 RRLHCTRYNI HMHLFVSFML RATSIFVKOR VVHAHIGVKE LESLIMQDDP QNSIEATSDV 240  
 KSOYIGCKIA VVMFIYFLAT NYWILVEGL YLHNLIFVAF PSDTKYLWGF ILIGWGFPA 300  
 PVAAWAVARA TLADARCELWEL SAGDIKWIYQ APILAAIGLN FILPLNTRV LATKIWETNA 360  
 VGHDRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FPNFQGFV 420  
 SIIYCYCNGE VQAEVKQWMS RWNLSVDWKR TPPOGSRRCG SVLTITVTHST SSQSQAAS 480

Seq ID NO: 525 DNA sequence  
Nucleic Acid Accession #: NM\_005048  
Coding sequence: 143..1795

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60

70

75

80

	ACCAGGAAGT	GCTACGTATA	GAATCCGGAA	AACAGAGCCT	TTGCAGACTA	ACTGTGCTTA	480
	TGTTGGTGAC	ATCGTGGACA	TTCCAGGAAC	CTCTGTTGCC	ATCAGCAACT	GTGATGGTCT	540
	GGCTGGAATG	ATAAAAAGTG	ATAATGAAGA	GTATTTTCATT	GAACCCCTGG	AAAGAGGTAA	600
	ACAGATGGAG	GAAGAAAAG	GAAGGATTCA	TGTTGTCTAC	AAGAGATCAG	CTGTAGAACA	660
5	GGCTCCCAT	GACATGTCCA	AAGACTTCCA	CTACAGAGAG	TCGGACCTGG	AAGGCCTTGA	720
	TGATCTAGGT	ACTGTTTATG	GCAACATCCA	CCAGCAGCTG	AATGAAACAA	TGAGACGCCG	780
	CAGACACGGG	GGAGAAAACG	ATTACAATAT	CGAGGTACTG	CTGGGAGTGG	ATGACTCTGT	840
	GGTCCGTTTC	CATGGCAAAG	AGCACGTCCA	AAACTACCTC	CTGACCCTAA	TGAACATTGT	900
	GAATGAAATT	TACCATGATG	AGTCCCTGGG	AGTGCAATATA	AATGTGGTCC	TGGTGCGCAT	960
10	GATAATGCTG	GGATATGCAA	AGTCCATCAG	CCTCATAGAA	AGGGGAAACC	CATCCAGAAG	1020
	CTTGGAGAAT	GTGTGTGCGT	GGGCGTCCCA	ACAGCAAAGA	TCTGATCTCA	ACCACTCTGA	1080
	ACACCATGAC	CATGCAATTT	TTTAAACCAG	GCAAGACTTT	GGACCTGCTG	GAATGCAAGG	1140
	ATATGCTCCA	GTCCACGGCA	TGTGTCTATC	AGTGAGAAGT	TGTACCCCTGA	ATCATGAGGA	1200
	TGGTTTTTCA	TCGTCTTTTG	TAGTAGCCCA	TGAAACGGGC	CATGTGTGGG	GAATGGAGCA	1260
15	TGATGGACAA	GGCAACAGGT	GTGGTGATGA	GACTGCTATG	GGAAGTGTCA	TGGCTCCCTT	1320
	GGTACAAGCA	GCATTCCATC	GTTACCACTG	GTCCCGATGC	AGTGGTCAAG	AACTGAAAAG	1380
	ATATATCCAT	TCTATGACT	GTCTCCTTGA	TGACCCCTTT	GATCATGATT	GGCCTAAACT	1440
	CCCAAGACTT	CCTGGAATCA	ATTATTCTAT	GGATGAGCAA	TGTCTTTTGG	ATTTTGGTGT	1500
	TGGCTATAAA	ATGTGCACCG	CGTTCCGAAC	CTTTGACCCA	TGTAACACGC	TGTGGTGTAG	1560
20	CCATCCTGAT	AATCCCTACT	TTTGTAAGAC	TAAAAGGGA	CCTCCACTTG	ATGGGACTGA	1620
	ATGTGCTGCT	GGAAAATGGT	GCTATAAGGG	TCATTGTCATG	TGGAAGAATG	CTAATCAGCA	1680
	AAAACAAGAT	GGCAATTGGG	GGTCATGGAC	TAAATTGGGC	TCCTGTTCTC	GGACATGTGG	1740
	AACCTGGTGT	CGTTTCAGAA	CACGCCAGTG	CAATAATCCC	ATGCCCATCA	ATGGTGGTCA	1800
	GGATTGTCTC	GGTGTAAATT	TTGAGTACCA	GCTTTGTAA	ACAGAAGAAT	GCCAAAACA	1860
25	CTTTGAGGAC	TTACAGGCAC	AGCAGTGTCA	GCAGCGAAAC	TCCCACTTTG	AATACCGAA	1920
	TACCAAAACAC	CACCTGGTGC	CATATGAACA	TCCTGACCCC	AAGAAAAGAT	GCCACCTTTA	1980
	CTGTCACTGC	AAGGAGACTG	GAGATGTTGC	TTACATGAAA	CAACTGGTGC	ATGATGGAAC	2040
	GCACCTGTTT	TACAAAGATC	CATATAGCAT	ATGTGTGCGA	GGAGAGTGTG	TGAAAGTGGG	2100
	CTGTGATAAA	GAATTTGGTT	CTAATAAGGT	TGAGGATAAG	TGTGGTGTCT	GTGGAGGAGA	2160
30	TAATCCCAAC	TGCCGAACCG	TGAAGGGGAC	ATTTACCAGA	ACTCCCAAGG	AGCTTGGGTA	2220
	CCTTAAGATG	TTTGATATAC	CCCTTGGGGC	TAGACATGTG	TTAATCCAAG	AAGACGAGGC	2280
	TTCTCTCAT	ATTCTTGCTA	TTAAGAACCA	GGCTACAGGC	CATTATATTT	TAAATGGCAA	2340
	AGGGAGGAAA	GCCAAGTCCG	GGACCTTCAT	AGATCTTGGT	GTGGAGTGGG	ATTATAACAT	2400
	TGAAGATGAC	ATTGAAAGTC	TTACACCGA	TGGACCTTTA	CATGATCCTG	TTATTGTTTT	2460
35	GATTATACCT	CAAGAAAATG	ATACCCGCTC	TAGCCTGACA	TATAAGTACA	TCATCCATGA	2520
	AGACTCTGTA	CCTACAAATCA	ACAGCAACAA	TGTCTCCAG	GAAGAATTAG	ATACTTTTGA	2580
	GTGGGCTTTG	AAGAGCTGGT	CTCAGTGTTC	CAAAACCTGT	GGTGGAGGTT	TCCAGTACAC	2640
	TAAATATGGA	TCCGATAGGA	AAAGTGATAA	TAAATGGTTC	CATCCGAGCT	TCTGTGAGGC	2700
	CAACAAAAG	CCGAAACCTA	TTAGACGAAT	GTGCAATATT	CAAGAGTGTG	CACATCCACT	2760
40	CTGGGTAGCA	GAAGAATGGG	AACACTGCAC	CAAAACCTGT	GGAAGTCTCG	GCTATCAGCT	2820
	TGCACTGTGA	CGCTGCCTTC	AGCCACTCCT	TGATGGCACC	AACCGCTCTG	TGCACAGCAA	2880
	ATACTGCTAG	GGTGACCGTC	CCGAGAGCCG	CCGGCCCTGT	AACAGAGTGC	CCTGCCCTGC	2940
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	GAGGCAGGTC	CTCTGCAGGG	CTGGGGACCA	CTGTGATGGT	GAAAAGCCTG	AGTCGGTCAG	3060
45	AGCCTGTCAA	CTGCCTCCTT	GTAATGATGA	ACCATGTTTG	GGAGACAAGT	CCATATTCTG	3120
	TCAAATGGAA	GTGTTGGCAC	GATACGTGCT	CATACCAGGT	TATAACAAGT	TATGTTGTGA	3180
	GTCTGTCAGC	AAGCGCAGTA	GCACCTGCCC	ACCACCATAC	CTTCTAGAAG	CTGCTGAAAC	3240
	TATGATGATG	GTCTCTCTTA	ACCCTAGTGA	CCTCCCTAGA	TCTCTAGTGA	TGCTATACATC	3300
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	TTTACGCCAG	AGGAGTGTCT	AGCAAGCAGG	AAGTAAGACT	GTGAGACTGG	TCACCGTACC	3480
	ATCCTCCCCA	CCCACCAAGA	GGGTCCACCT	CAGTTCAGCT	TCACAAATGG	CTGCTGCTTC	3540
	CTCTTTGCA	GCCAGTGATT	CAATAGGTGC	TTCTTCTCAG	GCAAGAACCT	CAAGAGAAAG	3600
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55	TGAACCAAAA	AGGCTAGAAA	CCAGAGGAAA	ACCTGGACAA	CCTCTCTCTT	CCCATGGTGC	3720
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65	TAATTTTCAA	AGCAGAGTAT	TACAAAAGAG	AAGTTAGAAT	TACAGCTACT	GACAATATAA	4320
	AGGGTTTTGT	TGAATCAACA	ATGTGATACG	TAAATTATAG	AAAAAGAAAA	GAAACACAAA	4380
	AGCTATAGAT	ATACAGATAT	CAGCTTACCT	ATTGCCTTCT	ATACTTATAA	TTTAAAGGAT	4440
	TGGTGTCTTA	GTACACTTGT	GGTCACAGGG	ATCAACGAAT	AGTAAATAAT	GAACCTCGTC	4500
	AAGACAAAAC	TGAACCCCTC	TTTCCAGGAC	CTCAGTAGGC	ACCGTTGAGG	TGTCCTTTGT	4560
70	TTTTGTGTGT	GTGTTGTTCT	TTTTAATTTT	CGCATTTGTT	ACAGATACAA	ACAGTTATAC	4620
	TCATGTACT	GTAATAATCG	CAAGGAAAAA	AGTTTGGGGA	TAACCTATTT	GTATGTTGGT	4680
	AGCTGAGAAA	AATATCATCA	GTCTAGAATT	GATATTGAG	TATAGTAGAG	CTTTGGGGCT	4740
	TTGAAGGCAG	GTTCAGAAAA	GCAATATGCG	ATGGTTGAGA	TATTTATTTT	CCATATGGTT	4800
	CATGTTCAAA	TGTTCAACAC	CACATGCAT	CTGACTGCAA	TAATGTGCTA	ATAATTTATG	4860
75	TCAGTAGTCA	CCTTGCTCAC	AGCAAGGCCA	GAAATGCTCT	CTCCAGGGAG	TAGATGTAAA	4920
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	ATAGTATTTT	TATGACTTAA	ATATTACAC	TAATATCAAT	TACATATTTT	GGTAAACTAG	5040
	AGAGACATAA	TAGAGATGTC	ATGCTTTGTT	CTGTGCATAG	AGACCTTTAA	GCAAACTACT	5100
	ACAGCCAACT	CAAAAGCTAA	AACCTGAACAA	ATTGATGTT	ATGCAAAACAT	CTTGCAITTT	5160
80	TAGTAGTTGA	TATTAAGTTG	ATGACTTGT	TCCCTTCAAG	GAAACATTAA	ATTGTATGGA	5220
	CTCAGCTAGC	TGTTCAATGA	AATTGTGAAT	TAGAAACATT	TTTAAAAGTT	TTTGAAGAG	5280
	ATAAGTGCAT	CATGAATTAC	ATGTACATGA	GAGGAGATAG	TGATATCAGC	ATAATGATTT	5340
	TGAGGTGAGT	ACCTGAGCTG	TCTAAAAATA	TATTATACAA	ACTAAAATGT	AGATGAATTA	5400
	ACCTCTCAAA	GCACAGAATG	TGCAAGAACT	TTTGCAITTT	AATCGTTGTA	AACCTAACGC	5460

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 CCTAAAAATT CCCATAGAAT AAAATTCTCT CTAGTTTACT TGTGTGTGCA TACATCTCAT 5640  
 CCACAGGGGA AGATAAGAT GGTACACAAA ACAGTTTCCA TAAAGATGTA CATATTTCATT 5700  
 ATACTTCTGA CCTTTGGGCT TTCTTTTCTA CTAAGCTAAA AATTCCTTTT TATCAAAGTG 5760  
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10 Seq ID NO: 528 Protein sequence  
 Protein Accession #: XP\_036683

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 TDPINNHPQG SATYRIKTE PLQTNCAVVG DIVDIPGTSV AISNCDGLAG MIKSDNEEYF 180  
 IEPLERGRQM EEEKGRIHVY YKRSAVEQAP IDMSKDFHYR ESDLEGLDDL GTVYGNHQQ 240  
 LNETMRRRRH AGENDYNIEV LLGVDDSVVR FHGKEHVQNY LLTLMNIVNE IYHDESLGVH 300  
 INVVLVRMIM LGYAKSISLI ERGNPSRSLE NVCRWASQQ RSDLNHSEHH DHAIPLTRQD 360  
 FGPAGMGGYA PVTGMCHPVR SCTLNHEDGF SSAPVVAHET GHVLGMEHDG QGNRCGDETA 420  
 MGSVMAPLQV AAFHYHWSR CSGQLKRYI HSYDCLLDDP FDHDWPKLPE LFGINYSMDE 480  
 QCRFDGFGVY KMCTAFRTFD PCKQLWCSPH DNPYFCKTKK GPPLDGTCA AGKWCYKGHC 540  
 MWKNANQKQK DGNWGSWTKF GSCSRTCGTG VRFRTQCMN PMPINGGQDC PGVNFYQLC 600  
 NTEECQKHFE DFRAGCQQR NSHFYQNTK HHWLPYEHDP PKKRCHLYCQ SKETGDAVYM 660  
 KQLVHDGTHC SYKDPYSICV RGECVKVCGD KEIGSNKVED KCGVCGGDNH HCRTVKGTFT 720  
 RTPRKILGKLV MFIPPGARH VLIQDEASP HILAINKQAT GHYILNGKE EAKSRTFIDL 780  
 GVEWDYNIED DIESLHTDGP LHDPIVILII POENDTRSSL TYKIIHEDS VPTINSNNVI 840  
 QEELDTFEWA LKSWSCSKP CGGFGYQTKY GCRKSDNKM VHSFCEANK KPKPIRRMCN 900  
 IQECTHPLWV AEWEHCTKT CGSSGYQLRT VRLCPLLDG TNRVHSHKCY MGDRPESRRP 960  
 CNRVPCPAQV KTGFWSECSV TCGEGTEVRQ VLCRAGDHCD GEKPEVSRAC QLPPCNDEPC 1020  
 LGDKSIFCQM EVLARYCSIP GYNKLCCESC SKRSSTLPPP YLLEAAETHD DVISNPSDLP 1080  
 RSLVMPSTLV PYHSETPAKK MSLSSIISVG GPNAYAAFRP NSKPDGANLR QRSQAQAGSK 1140  
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35 Seq ID NO: 529 DNA sequence  
 Nucleic Acid Accession #: NM\_002774  
 Coding sequence: 246..980

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 GCTGGCTCGC TCTCTCTCTG GGACACAGAG GTCCGGCAGGC AGCACACAGA GGGACCTACG 180  
 GGACGCTGTT CTTTCCCGCG ACTCAAGAA CCCCAGAGGC CCGAGGGCT CGACGAGGAG 240  
 CGGCCATGAA GAAGCTGATG GTGGTGCTGA GTCTGATTGC TGCAGCTGG CGACGAGGAGC 300  
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 TCTACACCTC GGGCCACTTG CTCTGTGGTG GGGTCTTAT CCATCCACTG TGGTCTCTCA 420  
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 ACATCCTGGG CTGGGGCAAG ACAGCAGATG GTGATTTCCT TGACACCATC CAGTGTGCAT 720  
 ACATCCACCT GGTGTCCCGT GAGGAGTGTG AGCATGCCCTA CCCTGGCCAG ATCACCAGGA 780  
 ACATGTTGTG TGCTGGGGAT GAGAAGTACG GGAAGGATTC CTGCCAGGCT GATTCTGGGG 840  
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 GATCAAAAGG GAAGCCAGGA GTCTACACCA ACGTCTGCAG ATACAGAAC TGGATCCAAA 960  
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 TATTTT

70 Seq ID NO: 530 Protein sequence  
 Protein Accession #: NP\_002765

75 1 11 21 31 41 51  
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 LIQPLPLERD CSANTTSCHI LGWGTADGD FPDITIQAYI HLVSRECEH AYPGQITQNM 180  
 LCAGDEKYGK DSCQSDSGGP LVCGDHLRGL VSWGNIPCGS KEKPGVTVNV CRYTNWIKQT 240  
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80 Seq ID NO: 531 DNA sequence  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43..1104

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GACAAGCACA	TGGACTTTT	TTATAATAGG	AGCAACACTG	ATACTGTGCA	TGACTGGACA	120
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TACCTGTGG	CTAATTAGC	TGCTGCCGAT	TTCTTCGCTG	GAATTGCCTA	TGTATTCTCTG	300
ATGTTTAAAC	CAGGCCCACT	TTCAAAAACT	TGACTGTGCA	ACCGCTGGTT	TCTCCGTCAG	360
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AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
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TACCTTGT	TCTGGACAGT	GTCCAACCTC	ATGGCCTTCC	TCATCATGGT	TGTGGTGTAC	660
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AGGCAGTGTG	GCGTGACAGA	TGTGAAAAGG	TGGTTCCTGC	TGCTGGCGCT	GCTCAACTCC	900
GTGCTGAACC	CCATCATCTA	CTCCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
ATGATCTGCT	GCTTCTCTCA	GGAGAAACCA	GAGAGGGGTC	CCTCTCGCAT	CCCCTCCACA	1020
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Seq ID NO: 532 Protein sequence  
Protein Accession #: NP\_036284

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LVIIVERHMS	IMRMVHNSL	TKKRVTLIL	LWVAIAIFMG	AVPTLGNL	CNISACSSLA	180
PIYSRSYLVP	WTVSNLMAFL	IMVVYLRIY	VYVKKRTNVL	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CWTPGLVLL	LDGLNCRQCG	VOHVKRWFL	LALLNSVNP	IYYSYKDEDM	300
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Seq ID NO: 533 DNA sequence  
Nucleic Acid Accession #: NM\_002821  
Coding sequence: 150..3362

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CCATTGTCTT	CATCAAGCAG	CCGTCTCTCC	AGGATGCACT	GCAGGGGCGC	CGGGCGCTGC	300
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CGCTGTGGC	CTACATCAT	GCGGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
AAGCCAAAGC	GCTGCAAGAG	CAGCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAAGC	2400
GAGGGCCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
GCTTGGGCTC	CGGCCCCCGG	GCCACCAACA	AAGCCACAG	CACAAGTGT	AAGATGCAC	2520
TCCACGCTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGAGGTTGT	2580
TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTGGTA	CTTGTGAAGA	2640

GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG 2700  
 GGAAGCTGAA CCAGCGCAAC GTGGTGCGGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC 2760  
 ACTACATGCT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA 2820  
 AGAGCAAGGA TGAAAAATTG AAGTCACAGC CCCTCAGCAC CAAGCAGAAG GTGGCCCTAT 2880  
 5 GCACCCAGGT AGCCCTGGGC ATGGAGCACC TGTCCAACAA CCGCTTTGTG CATAAGGACT 2940  
 TGGCTGCGCG TAACGTGCTG GTCAGTGCCC AGAGACAAGT GAAGGTGTCT GCCCTGGGCC 3000  
 TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCTGGG GTGCCGCTGC 3060  
 GCTGGATGTC CCCCGAGGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGCTGGG 3120  
 10 CCTTCGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCAT GGTGGGCAGG 3180  
 CAGATGATGA AGTACTGGCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG 3240  
 GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GGCCCTCAGC CCCAAGGACC 3300  
 GGCCCTCCTT CAGTGAGATT GCCAGCGCCC TGGGAGACAG CACCGTGGAC AGCAAGCCGT 3360  
 GAGGAGGGAG CCCCTCAGG ATGGCCTGGG CAGGGGAGGA CATCTCTAGA GGGAGGCTCA 3420  
 15 CAGCATGATG GGCAGATCC CTGTCTCTCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA 3480  
 TTGCTGAGGT CTGAGCAGGG CCTGGCCTTT CTCTCTCTTC CTCACCTCA TCCTTTGGGA 3540  
 GGCTGACTTG GACCCAAACT GGGCGACTAG GGCTTTGAGC TGGGCAGTTT CCCTGCCAC 3600  
 CTCTCTCTCT ATCAGGAGCA GTGTGGGTGC CACAGGTAAC CCCAATTCTT GGCCTTCAAC 3660  
 TTCTCCCTCT CACCGGGTCC AACTCTGCCA CTCATCTGCC AACTTTGCCT GGGGAGGGCT 3720  
 20 AGGCTTGGGA TGAGCTGGGT TTGTGGGGAG TTCTTAATA TTCTCAAGT CTGGGCACAC 3780  
 AGGGTTAATG AGTCTCTTGC CCACCTGGTCC ACTTGGGGGT CTAGACCAGG ATTATAGAGG 3840  
 ACACAGCAAG TGAGTCTCTC CCACCTGGG CTGTGCACA CTGACCAGA CCCAGCTCTT 3900  
 CCCCACCTCT CTCTCTTTC CTCATCTTAA GTGCCCTGCA GATGAAGGAG TTTTCAGGAG 3960  
 CATTGTGACAC TATATAAAC GCCCTTTTGT TATGCACCAC GGGCGGCTTT TATATGTAAT 4020  
 25 TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CTGGAGATG AGGAGGGTGG 4080  
 GCCATCCTTA CCCCACACTT TTAATGTGTG CGTTTTTGTG TTGTTTGTGT TTTTGTGTTT 4140  
 TGTTTTGTGT TTTACACTCG CTGCTCTCAA TAAATAAGCC TTTTITA

Seq ID NO: 534 Protein sequence

Protein Accession #: NP\_002812

30  
 1 11 21 31 41 51  
 MGAARGSPAR PRRLLPLSVL LLEPLLGGTQT AIVFIKQPS QDALQRRAL LRCEVEAPGP 60  
 35 VHVYWLDDGA PQVQDTERFA QGSSLFAAV DRLQDSGTFQ CVARDVDTGE EARSANASFN 120  
 IKWIEAGPVV LKHPASEAEI QPQTQVTLRC HIDGHPRTY QWFRDGTPLS DQGSNHTVSS 180  
 KERNLTLRPA GPEHSLGLYC CAHSAPGQAC SSQNFSLISA DESFARVULA PQDVVVARYE 240  
 EAMFHCQFSA QPPPLQWLFP EDETPIITNS RPHLLRRATV FANGSLLLTQ VRPRNAGIYR 300  
 CIGQGQRGPP ILELATLHLA EIEDMPLFEP RVFTAGSBER VTCLPPKGLP EPSVWWEHAG 360  
 40 VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGOR RQDVNITVAT VPSWLKKPQD 420  
 SQLEBKGPGY LDCILTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVIDGTWYR 480  
 CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QOCMEFDKEA TVPCSATGRE KPTIKNERAD 540  
 GSSLPEWYTD NAGTLHFARV TRDDAGNYTC IASNGPQQOI RAHVQLTVAV PITFKVEPER 600  
 TTVYQGTAL LQCEAGGDPK PLIQWKGKDR ILDPKLGPR MHIPQNGSLV IHDVAPEDSG 660  
 45 RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPSPPPYK MIQTIGLSVG AAVAYIIAVL 720  
 GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780  
 KRHSTDKMH FPRSLQPIIT TLGKSEFGEV FLAKAQGLEB GVAETLVLVK SLQTKDEQQQ 840  
 LDFRLELMF GKLHNANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKQSQ 900  
 PLSTKQKVAL CTQVALGMEH LSNRNFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960  
 50 YHFRQAWVPL RWMSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLDLQ 1020  
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP

Seq ID NO: 535 DNA sequence

Nucleic Acid Accession #: NM\_013952

Coding sequence: 161..1357

55  
 1 11 21 31 41 51  
 TTCAGAAGGA GGAGAGACAC CGGGCCCGAG GCACCCCTGC GGGCGGGCGG ACCCAAGCAG 60  
 60 TGAGGGCCTG CAGCGGCGCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGAGGGA 120  
 AGCCCGGAGC CCTCGCGCGG CTGCGAGCGA CTCCCGGCGG ATGCTCTACA ACTCCATCAG 180  
 ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGCTTTT GTGAATGGCA GACCTCTGCC 240  
 GGAAGTGGTC CGCCAGCGCA TCGTAGACCT GGCCCAACAG GGTGTAAGGC CTGCGGCAT 300  
 CTCTCGCCAG CTCCGCGTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA 360  
 65 GACTGGCAGC ATCCGCGCTG GAGTGATAGG GGGCTCCAAG CCCAAGGTGG CCAACCCCAA 420  
 GGTGGTGGAG AAGATTGGGG ACTACAAACG CCAGAACCTT ACCATGTTTG CTGGGAGAT 480  
 CCGAGACCGG CTCTGGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCACTC 540  
 CATTAATAGA ATCATCCGGA CCAAAGTGCA GCAACCATTC AACCTCCCTA TGGACAGCTG 600  
 OGTGGCCACC AAGTCCCTGA GTCCCGGACA CACGCTGATC CCCAGCTCAG CTGTAACTCC 660  
 70 CCGGAGTCA CCCCAGTCGG ATTCCCTGGG CTCCACCTAC TCCATCAATG GGCTCCTGGG 720  
 CATCGCTCAG CCTGGCAGCG ACAAGAGGAA AATGGATGAC AGTGATCAGG ATAGCTGCCG 780  
 ACTAAGCATT GACTCACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC 840  
 CTTACGCCAG CACCACCTCG AGCCGCTCGA GTGCCCATTT GAGCGGCAGC ACTACCCAGA 900  
 GGCTATGTCG TCCGCCAGCC ACACCAAAGG CGAGCAGGGC CTCTACCCCG TGCCCTTGTG 960  
 75 CAACAGCACC CTGACGACG GGAAGGCCAC CTGACCCCT TCCAACACG CACTGGGGCG 1020  
 CAACCTCTCG ACTCACCAGA CCTACCCCTG GGTGGCAGCT CCGCCCTTTT GGATCTGCAG 1080  
 CAAGTGGCTT CCGGGGTCCC GCCCTTCAAT GCCTTTCCCC ATGCTGCTCT CGTGTACGGG 1140  
 CAGTTACCGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCCA GCTGCCCGGA 1200  
 TACCCACCCC ACATCCCCAC CAGCGGACAG GGCAGCTATG CCTCTCTGCG CATCGCAGCG 1260  
 80 ATGGTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCTTA CTCTCTCTAC 1320  
 AGCGAGGCCCT GGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC 1380  
 ACATCAAGGC CGAGTGCAAC GCCCACCCTT GCCAAGGCCCT TTGACCATCT GTAGTTGCCA 1440  
 TGGGACAGT G

Seq ID NO: 536 Protein sequence  
Protein Accession #: NP\_039246

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQOPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD DSDQSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
10    ERQHYPEAYA SPSHTKGBQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAA 300
      PPFWICSKSA PGRSPMPFP MLPPCTGSSR ARPSSQGERW WGPCRCPDTHP TSPPADRAAM 360
      PLPLSQANWQ EVNTLAMPMA TPPTPTARP GASPTPAC

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Seq ID NO: 537 DNA sequence  
Nucleic Acid Accession #: NM\_003466.1  
Coding sequence: 11..1363

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20      1      11      21      31      41      51
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GAATTCGGCG ATGCTCTACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG 60
AGGGGGCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
GGCCACACCA GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCCGCGTCA GCCATGGTTG 180
CGTCAGCAAG ATCCTTGGCA GGTACTACGA GACTGGCAGC ATCCGGCCTG GAGTGATAGG 240
GGGCTCCAAG CCCAAGGTGG CCACCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAACG 300
25    CCAGAACCCT ACCATGTTT CCTGGGAGAT CCGAGACCGG CTCCTGGCTG AGGGGCTCTG 360
TGACAATGAC ACTGTGCCCA GTGTACAGTC CATTAATAGA ATCATCCGGA CCAAGTGCA 420
GCAACCATTC AACCTCCCTA TGGACAGCTG CGTGCCACCC AAGTCCCTGA GTCCCGGACA 480
CAGCTGATC CCAGCTCAG CTGTAACTCC CCGGAGTCA CCCCAGTCGG ATTCCTGGG 540
CTCCACCTAC TCCATCAATG GGCTCCTGGG CATCGCTCAG CTGGCAGCG ACAAGAGGAA 600
30    AATGGATGAC AGTGATCAGG ATAGCTGCCG ACTAAGCATT GACTCACAGA GCAGCAGCAG 660
CGGACCCCGA AAGCACCTTC GCACGGATGC CTTACAGCCAG CACCACCTCG AGCCGCTCGA 720
GTGCCCATTT GAGCGGCGAG ACTACCCAGA GGCCTATGCC TCCCCAGGCC ACACCAAAGG 780
CGAGCAGGCG CTCTACCCGC TGCCCTTGCT CAACAGCACC CTGGACGACG GGAAGGCCAC 840
CCTGACCCCT TCCACACGCG CACTGGGCGC CAACCTCTCG ACTACCCAGA CCTACCCCGT 900
35    GGTGGCAGAT CCTCACTCAC CCTTGSCCAT AAAGCAGGAA ACCCCGAGG TGTCCAGTTC 960
TAGCTCCACC CCTCTCTCTT TATCTAGCTC GCCTTTTTTG GATCTGCAGC AAGTCGGCTC 1020
CGGGGTCCCG CCTTCAATG CCTTTCCCA TGCTGCCTCC GTGTACGGGC AGTTACGGG 1080
CCAGGCCCTC CTCTCAGGCG GAGAGATGGT GGGGCCACG CTCGCCGAT ACCCAACCCA 1140
CATCCCAACC AGCGGACAGG GCAGCTATGC CTCTCTGCC ATCGCAGGCA TGGTGGCAGG 1200
40    AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCTAC TCCTCTACA GCGAGGCGCT 1260
GCGCTTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1320
GAGTGACCG CCCACCACTG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT

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Seq ID NO: 538 Protein sequence  
Protein Accession #: NP\_003457

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50      1      11      21      31      41      51
      |      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQOPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD DSDQSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGBQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAD 300
55    PHSPPAIKQE TPEVSSSSST PSSLSSSAFL DLQVGSVGP PFNAFPAAAS VYQFTGQAL 360
      LSGREMVGPT LPGYPPHIFT SGQGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP 420
      NSSLLSSPY YSSTSRPSAP PTTATAFDHL

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Seq ID NO: 539 DNA sequence  
Nucleic Acid Accession #: NM\_006799  
Coding sequence: 19..963

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65      1      11      21      31      41      51
      |      |      |      |      |      |
GCCGCGGGAG AGGAGGCCAT GGGGCGCGC GGGGGCTGC TGCTGGGCTG GCTGCTGGCT 60
CGGGCTGGAC TCAGGAAGCC GGAGTCGAG GAGGCGGCGC GGTATCAGG ACCATGCGGC 120
CGACGGGTCA TCAGTCGCG CATCGTGGGT GGAGAGGACG CGAAGCTCGG GCGTGGCCG 180
TGGCAGGGGA GCCTGCGCCT GTGGGATTC CACGTATGCG GAGTGAGCCT GCTCAGCCAC 240
CGCTGGGCAC TCACGGCGCG GCCTGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
GGGTGGATG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTTCTGGAG CCTGCAGGCC 360
70    TACTACACC GTTACTTCGT ATCGAATATC TATCTGAGCC CTGCTACCT GGGGAATTCA 420
CCCTATGACA TTGCTTGGT GAAGCTGTCT GCACCTGTCA CCTACATAA ACACATCCAG 480
CCCATCTGTC TCCAGGCCTC CACATTTGAG TTTGAGAACG GGACAGACTG CTGGGTGACT 540
GGCTGGGGGT ACATCAAAGA GGATGAGGCA CTGCCATCTC CCCACACCTC CCAGGAAGTT 600
CAGGTGCCCA TCATAACAA CTCTATGTGC AACCACTCT TCCTCAAGTA CAGTTTCCGC 660
75    AAGGACATCT TTGAGACAT GGTTTGTGCT GGCAATGCC AAGGCGGAA GGATGCGCTG 720
TTGCGTGACT CAGGTGGACC CTTGGCTGT AACAGAATG GACTGTGGTA TCAGATTGGA 780
GTGCTGAGCT GGGGAGTGGG CTGTGGTGG CCCAATCGCG CGGTGTCTA CACCAATATC 840
AGCCACCACT TTAGTGGAT CCAGAAGCTG ATGGCCAGA GTGGCATGTC CCAGCAGAC 900
CCCTCCTGGC CGCTACTCTT TTTCCCTCT CTCTGGGCTC TCCACTCCT GGGGCGGCTC 960
80    TGAGCCTACC TGAGCCCATC CAGCCTGGGG CCACTGCCAA GTCAGGCCCT GGTTCCTCTC 1020
      TGCTCTGTTT GGTAATAAAC ACATTCCAGT TGATGCCCTG CAGGCACTTC TTCAAAA

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Seq ID NO: 540 Protein sequence  
Protein Accession #: NP\_006790

1 11 21 31 41 51  
5 MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPNQGS LR 60  
LWDSHVCGVS LLSHRWALTA AHCFTYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120  
VSNIIYSPRY LGNSPYDIAL VKLSAPVITY KHIQPICLQA STFBFENRTD CNVTGWGYIK 180  
EDEALPSPHT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACFGDSGG 240  
PLACNKNGLW YQIGVVSQGW GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSWPLL 300  
10 FFPILLWALPL LGPV

Seq ID NO: 541 DNA sequence  
Nucleic Acid Accession #: NM\_014344  
Coding sequence: 131..1444

15 1 11 21 31 41 51  
GCGGCCGCGA TGGGGCCGAA GCGCCCGAAG CCCCAGAGCC CACAAACTGC CGGGCCCGCC 60  
TCGCCGCCCG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGGCGC ACCGGCAGAC 120  
20 CCGCGGGAGC ATGGGCAGGA GGATGCGGGG CCGCGCCGCC ACCGCGGGGC TCTGGCTGCT 180  
GGCGCTGGCG TGCTGCTGGG CGCTGTGGGG AGGCTCCTG CCGCGCGGGA CCGAGCTGCC 240  
CGCTCCCGG CCGCCGGAAG ACCGACTCCC ACGGCGCCCG GCCCGGAGCG GCGGCCCGCG 300  
GCCCCGCGCT CGCTTCCCTC TGCCCCCGCC CCTGGCGTGG GACGCCCGCG GCGGCTCCCT 360  
GAAAACCTTC CGGGCGCTGC TCACCCCTGG GCGCGGCGCG GACGCCCGCG CCGGCGAGTC 420  
CCGAGAGCGC CCGAGGTGGC AGGTGTCAGC CAGGCGAGCC CCGCGGAGG AGAGCGCGCG 480  
25 GGTGCACGGG GCGCTCTTCT GGAGCGCGCG CCTGGAGGAG CAGGTGCCCC CGGGCTTTTC 540  
GGAGGCCCGC GCGGCGGCGT GGCTGGAGGC GGCTCGCGGC GCCCGGATGG TGGCCCTTGA 600  
GCGCGGGGGT TGCGGGCGCA GCTCCAAACG ACTGGCCCGT TTTGCGGAGC GCACCGCGCG 660  
CTGCGTGGCG TACGGCATCA ACCCGGAGCA GATTCAAGGC GAGGCCCTGT CTTACTATCT 720  
GGCGCGCTG CTGGGCTTCC AGCGCCACGT GCGCGCGCTG CCACTGGCTC GGGTGGAGGC 780  
30 TCGGCGCGCG CAGTGGGCGC AGGTGCGGGA GGAGCTGCGC GCTGCGCACT GGACCGAGGG 840  
CAGCGTGGTG AGCTGACAC GCTGGCTGCC CAACCTCACG GACGTGGTGG TGCCCGCGCC 900  
CTGGCGCTCG GAGGACGCGC GTCTGCGCCC CTCCCGGAT GCGGGGGGTG AGCTGGCCAA 960  
CCTCAGCCAG GCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTCGACTA 1020  
CCTGACGCGC AACTTCGACC GGCTCGTAAG CAACCTCTTC AGCTCGAGT GGGACCCGCG 1080  
35 CGTCATGCAG CTGTGCCACA GCAACCTGCA CCGCGGTCCG GCGGGGGCGC TGGTCTTTCT 1140  
GGACAATGAG GCGGGCTTGG TGACCGGCTA CCGGGTAGCA GGCATGTGGG ACAAGTATAA 1200  
CGAGCGCGTG TTGACGTGAG TGTGCGTGT CCGGAGCGCG ACCGCGCGCG GCGTCTCTGA 1260  
GCTGCACGCG GCGGAGGAGC CCGCGGCCCG GCTGCTGCGC CTCTACCGCG GCCACGAGCC 1320  
40 TGCTTCTCCC GAGCTGGCGC CCCTTGACGA CCCCCACGCT CAGCTGTCTC AGCGCGCGCT 1380  
CGACTTCTCT GCCAGCACCA TTTTGCATG TAAGGCCAAG TACGGCGCGC GGTCTGGGAC 1440  
TTAGTGTGAC CCGGAGGAAA AGAGAGAGAT CTGGGCGTGG GGTATGGATG ATGGGGGGAA 1500  
GGGCGGTGCG CTCTGCCACT GTCAGGAGCC AGCGGCCCAA CGCCACCCCG CAAAGGTGTC 1560  
TAAAACTTC AGCTTTTTC CCACTGCGCC CTCTCTTTCA ATCCACGCTG GTTTCCTTTC 1620  
45 AAAGTCTGCG GAGGACGAAC TCACCGAGGC GAGAAGTGTA ACATTCTCTC CACCAGCTT 1680  
ATAAAGAGAT TCCTTACTGT GCCAGCAGG GGATTGGATC GGAAGAAACT GGTACTTGGG 1740  
GTTTGGCCCC CGAGTGGCGC TCCTGTGGG AGATGACACC CATCTTGGG CCCCCTCAT 1800  
TCCTTTCCG AAAAAGGAAA ACTTGGTGT GAGCGGTGTA GCTAATTCTG CAATTTTCTA 1860  
CCAAACAGAG CCGTGTGGCG CCGGAGCAG GGCTGTGACA TTGGCTGGTG GAGCCCTTC 1920  
50 CTGTGTTCTC CCTTGTGTC AGCGCCGCGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC 1980  
GGCTCGCAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG 2040  
ACAATTGCGC TGACTCATTC CTGACCTCT GTCATTTTGG CCTGAAGGCT ACAATTGAG 2100  
GGTCAGCTGT ATGCATTAAG TCAATAATG AATTCTCTCC TCCCTCTCGC AACCGACCAA 2160  
AATTGTGACA ACATGATGAT TCACCAAGG GAAAAAATAA TCAGTTTTAT GCACTTTATT 2220  
55 TTGTTTGTAT TTTTATTTT TATTAAGAAA AAATTTTATT TTACAGAAAT TACCTTCTCT 2280  
GTATATATGT GCATAAAGT TGGTGTAAAT ATACTAAACA AACTTATATT TCAATAAAG 2340  
GGAGTTTAAA ATTTAAAAA AAAAAA

Seq ID NO: 542 Protein sequence  
Protein Accession #: NP\_055159

60 1 11 21 31 41 51  
MGRMRGAAA TAGLWLLALG SLLALWGGLL PPRTELPASR PPEDRLPRRP ARSGGPAPAP 60  
65 RFPLPPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHSARQP RPEESAAVHG 120  
GVFWSRGLLE QVPPGFSEAQ AAAMLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180  
YGINPEQIQG EALSYYLARI LGLQRHVPL ALARVEARGA QNAQVOEELR AAEWTEGSVV 240  
SLTRWLPNLT DVVVFAPWRS EDGRRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLT 300  
NFDRLVSNLF SLQWDPRVMQ RATSNLHRGP GGALVFLDNE AGLVHGIRVA GMDKYNEPL 360  
70 LQSVCFRFR TARRVLELHR GQDAARLLR LYRRHEPRFP ELAALADPHA QLLQRLDLFL 420  
AKHILHCKAK YGRRSGT

Seq ID NO: 543 DNA sequence  
Nucleic Acid Accession #: XM\_007652.4  
Coding sequence: 1..1290

75 1 11 21 31 41 51  
ATGGCGCGCT CTGGCGCGTG GAAGCGCCTC AAATCTATGC TAAGGAAGGA TGATGCGCGG 60  
80 CTGTTTTTAA ATGACACAGC CGCCTTGAC TTCTCGGATG AGGCGGGGGA CGAGGGGCTT 120  
TCTCGGTACA ACAAACTTCG AGTTGTGGTG CCGGATGACG GTTCCGAAGC CCGGAAAGG 180  
CCTGTTAACG GGGCGCACCC GACCCTCCAG CCGGACGATG ATTCTTACT GGACCAAGAC 240  
TTACCTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGAGCT CTTGTGACAA CTGCAGCAAA 300  
CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAGCCAGGT TGACCATTGC TGCCGTTCTG 360  
TACTTGCTTT TCATGATTGG AGAACTTGTA GGTGGATACA TTGCAATAG CCTAGCAATC 420



5  
 10  
 15

ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480  
 TTGTGGCTAT CATCAAAATC ACCAACCAAA AGATTACCTT TTGGATTTC TCGCTTAGAG 540  
 GTTTGTGTCAG CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT 600  
 GAAGCTGTGC AAAGAAGTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660  
 ACCGAGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGGT TTCTGTTGAA CCAGTCTGGT 720  
 CACCGTCACT CCCATTCCCA CTCCTGCGCT TCAAATTCCT CTACCAGAGG TTCTGGGTGT 780  
 GAACTGAACC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTGTGTACA TGCTTTGGGA 840  
 GATTGTGTAC AGAGTGTGG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA 900  
 TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA 960  
 TTTGGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTGGAAT 1020  
 GTAGACTATA TCAAAGAAGC CTGTATGAAA ATAGAAGATG TATATTCACT CGAAGATTTA 1080  
 AATATCTGGT CTCTCACTTC AGGAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140  
 GGAAGTTTCA TAAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTATT ATTGAACACA 1200  
 TTTGGCATGT ATAGATGTAC TATTCACTT CAGAGTTACA GGCAAGAAGT GGACAGAAGT 1260  
 TGTGCAAAAT GTCAGAGTTC TAGTCCCTGA

Seq ID NO: 544 Protein sequence

Protein Accession #: XP\_007652.1

20  
 25  
 30

1 11 21 31 41 51  
 MAGSGAWKRL KSMRLKDDAP LFLNDTSAPD PSDEAGDEGL SRFNKL RVVV ADDGSEAPER 60  
 PVNGAHP TLQ ADDSLLDQD LPLTNSQLSL KVDSCDNCSK QREILKQKRV KARLTIAAVL 120  
 YLLFMIGELV GGYIANSLAI MTDALHMLTD LSAILLTLA LMLSSKSPKT RPTFGFHRLE 180  
 VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDIMLI TAAVGVAVNV IMGFLNQS 240  
 HRRSHSHSLP SNSPTRGSGC ERNHGQDSL A VRAAFVHALG DLVQSVGLI AAYIRKPE 300  
 YKIADPICYT VPSLIVAF TT FRIIWDTVVI ILEGVPSHLN VDYIKEALMK IEDVYSEVDL 360  
 NIWSLTSGKS TAIWHIQLIP GSSSKWEEVQ SKANHL LNT FGMRYCTIQL QSYRQEVDRD 420  
 CANCQSSSP

Seq ID NO: 545 DNA sequence

Nucleic Acid Accession #: AB037765.1

Coding sequence: 1..2478

35  
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 50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 ATGTTTTCGG GCTTCAATGT CTTTAGAGTT GGGATCTCTT TTGTCATAAT GTGCATTTTT 60  
 TACATGCCAA CAGTAACTC TTTACCAGAA CTGAGTCCTC AGAAATATTT TAGTACATTG 120  
 CAACCCAGGA AAGCCTCTTT AGCTTATTTT TGTCAAGCTG ATCCCCAAG AACATCTGTA 180  
 TTTCTTGAAG AACTCAATGA GGCTGTTAGA CCTCTGCAGG ACTATGGAAT TTCAGTTGCC 240  
 AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAAA GGATTGTATG 300  
 AAAGCATATT TATTCAGGG CAACATATTG CTCAGAGAA TCCCTACTGA CACCTTGTTT 360  
 GATGTGAATG CCATTGTCCG CCAATGTTCT TTTGCTCTTC TTTTATGTA AGTGAAATAT 420  
 ATTACCAACC TGGAGACCT TCAGAACATA GAAATGCTC TGAAGGAAA AGCAATATTT 480  
 ATATTCTCAT ATGTAAGAGC CATTTGAATA CCAGAGCACA GAGCAGTCAT GGAAGCCGCT 540  
 TTTGTGTATG GGACTACATA CCAATTGTC TTAACACAG AAATTGCCCT TTTGAAAGT 600  
 ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCATTGTAA ACTAGTCTTG 660  
 GACTTGACCC AGCAATGTAG AAGAACATA ATGGAACAGC CATTGACTAC ACTGAACATT 720  
 CACCTGTTTA TTAAGACAA GAAAGCACCT CTGTGACTG AAGTTGCTGA AGATCCTCAA 780  
 CAAGTTTCAA CTGTCCATCT CCAACTGGGC TTACCACTGG TTTTATTTGT TAGCCAACAG 840  
 GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG CTGGCGTCT TCTGGGAAAA 900  
 GCAGGAGTTC TACTCTGTGT AAGGGACTCT TTGGAAGTGA ACATTCCTCA AGATGCTAAT 960  
 GTGGTCTTCA AAGAGGACGA AGAGGGAGTT CCAGTGAAT TTTTGGTATT ACATGATGTT 1020  
 GATTTAATAA TATCTCATGT GGAATAAAT ATGCACATTG AGGAAATACA AGAAGATGAA 1080  
 GACAATGACA TGGAAAGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAACTGTT 1140  
 TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACCTTAC TGGAACTAAC AGAAGAAACA 1200  
 TTTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260  
 GTATCCATGG CATTTTTCGA ATCCTATATT GATGTGGCAG TTAAACTGAA AGGCACATCT 1320  
 ACTATGCTTC TTAAGTAAT AAACTGTGCA GATTGGTCTG ATGTATGTAC TAAGCAAAAT 1380  
 GTTACTGAAT TTCTATCAT AAGATGTAC AAGAAAGGCG AGAACCAGT ATCTTATGCT 1440  
 GGAATGTTAG GAACCGAAGA TCTCCTAAAA TTTATCCAG TCAACAGGAT TTCATATCCA 1500  
 GTGAATATAA CATCGATCCA AGAAGCAGAA GAATATTTAA GTGGGGAATT ATATAAGAC 1560  
 CTCATCTTGA ATTCTAGTGT GTCAGTATTG GGACTATTTA GTCCAACCAT GAAAACAGCA 1620  
 AAGAAGATT TTAGTGAAGC AGGAACTAC CTAAAGGAT ATGTTATCAC TGAATTTAT 1680  
 TCTGAAGAAG ATGTTTTGCT ACTGTCAACC AATATGCTG CAAGTCTTCC AGCCCTGCTG 1740  
 CTGCGCAGAC ACACAGAAGG CAAATAGAG AGCATCCCAC TAGCTAGCAC ACATGCACAA 1800  
 GACATAGTTC AATATTAAC AGATGCACTA CTGGAATGT TTCCGGAAT CACTGTGGAA 1860  
 AATCTTCCCA GTTATTTTCA ACTTCAGAAA CCATTATTGA TTTTGTTCAG TGATGGCACT 1920  
 GTAAATCCTC AGTATAAAA AGCAATATTG ACCTGCTTAA AGCAGAAATA CTGGAATCA 1980  
 TTTACTCCAT GCTGGTTAAA TCTAAGAAAT ACTCCAGTGG GGAGAGGAAT CTGAGGGCA 2040  
 TATTTGTATC CTCTGCCCTC CTCTCCTCTT CTGTGTTTGG TGAATCTGCA TTCAGTGGC 2100  
 CAGATATTGG CATTTCTCTC AGACCAGGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160  
 AAGAAATTAG AAGCAGGACT AGAAATCAT ATCACAATTT TACCTGCTCA AGAATGGAAA 2220  
 CCTCCTCTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280  
 ACTAGGAAAG TTCCCAAGTG TATGAAAGAA ACAGATGTGC AGGAGAATGA TAAGGAACAA 2340  
 CATGAAGATA AATCGGAGT CAGAAAAGAA CCGATTGAAA CTCTGAGAAT AAAGCATTGG 2400  
 AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AATCATTTA GACGTGATAA AGAGTTAGGA 2460  
 TGCTCAAAG TGAACATA

Seq ID NO: 546 Protein sequence

Protein Accession #: BAA92582.1

1 11 21 31 41 51  
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5 MFSGFNVFRV GISFVIMCIF YMPTVNSLPE LSPQKYFSTL QPGKASLAYF CQADSPTS SV 60  
 FLEELNEAVR PLQDYGISVA KVNCVKEEIS RYCGKEKDLN KAYLFPKGNIL LREFFDTLTF 120  
 DVNAIVAHVL FALLFSEVKY ITNLEDLQNI ENALKGKANI IPSYVRAIGI PEHRAVMEAA 180  
 FVYGTTYQFV LTTEIFALLES IGSEDEVYAH LYFFHCKLVL DLTQQCRRTL MEQPLTTLNI 240  
 HLFIKTMKAP LLEVAEDPO QVSTVHLQLG LPLVFIVSQQ ATYEADRRTA EHVAVRLLGK 300  
 AGVLLLLRDS LEVNIPQDAN VVFKRAEEGV PVEPLVLHDV DLIISHVENN MHIEEIQEDE 360  
 DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTEET FNATVMASDS IVLFYAGWQA 420  
 VSMAPLQSYI DVAVKLKGTS TMLLRINCA DWSDVCTKQN VTEFPPIKMY KKGPNVSYA 480  
 10 GMLGTEDLLK FIQLNRISYP VNITSIQEAE EYLSGELYKD LILYSSVSVL GLFSPTMKTA 540  
 KEDFSEAGNY LKGYVITGIY SEEDVLLIST KYAASLPALL LARHTEGKIE SIPLASTHAQ 600  
 DIVQIITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKKAIL TLVKQKYLDS 660  
 FTPCWLNLKN TFPVGRGILRA YFDPLPLPL LVLVNLHSGG QVFAFPSDQA IIBENLVLWL 720  
 KLEAGLENH ITILPAQEWK PPLPAYDPLS MIDAATSQRG TRKVPKCKME TDVQENDKEQ 780  
 15 HEOKSAVRKE PIETLRIKHW NRSNWFKEAE KSFRDRKELG CSKVN

Seq ID NO: 547 DNA sequence  
 Nucleic Acid Accession #: NM\_033102.1  
 Coding sequence: 1..1662

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 25 CCTCTGCTGC TGGAGTGGG GGTAGAGGAG AAGTTTCATGA CCATGGTGCT GGGCATTGGT 180  
 CCAGTGCTGG GCCTGTGCTG TGTCCGCTC CTAGGCTCAG CCAGTGACCA CTGGCGTGGG 240  
 CGCTATGGCC GCGGCGGCGC CTTCATCTGG GCACGTGCTT TGGGCATCCT GCTGAGCCTC 300  
 TTTCTCATCC CAAGGGCGCG CTGGCTAGCA GGGCTGCTGT GCCCGGATCC CAGGCCCCCTG 360  
 GAGCTGGCAG TGCTCATCCT GGGCGTGGGG CTGCTGGA CTCTGTGGCA GGTGTGCTTC 420  
 30 ACTCCACTGG AGGCCCTGCT CTCTGACCTC TTCCGGGACC CGGACCACTG TCGCCAGGCC 480  
 TACTCTGTCT ATGCGCTCAT GATCAGTCTT GGGGCTGCTC TGGGCTACTT CTTGCTGCTC 540  
 ATTGACTGGG ACACCATGTC CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCCCTCTT 600  
 GGCCTGCTCA CCTCATCTT CTCACTGCTG GTAGCAGCCA CACTGCTGGT GGCTGAGGAG 660  
 GCAGCGCTGG GCGCCACCGA GCCAGCAGAA GGGCTGCTGG CCCCCTCCTT GTGCGCCAC 720  
 35 TGCTGTCCAT GCGCGGCGCG CTGGCTTTC CGGAACCTGG GCGCCTGCTT TCCCGGCTG 780  
 CACCAGCTGT GCTGCGCAT GCGCCGACCC CTGCGCGGCT TCTTCTGCTG TGAGCTGTGC 840  
 AGCTGGATGG CACTCATGAC CTTACGCTG TTTTACACGG ATTTCGTGGG CGAGGGGCTG 900  
 TACCAGGGCG TGCCAGAGG TGAGCGGGG ACCGAGGCCC GGAGACACTA TGATGAAGGC 960  
 GTTCGGATGG GCGAGCTGGG GCTGTTCTG CAGTGCGCCA TCTCCTGGT CTTCTCTCTG 1020  
 40 GTCATGGACC GGCTGGTGA GCGATTGCGC ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080  
 GCTTTCCCTG TGGCTGCCG TGCCACATGC CTGTCCCA GTGTGGCGT GGTGACAGT 1140  
 TCAGCGGCC TCACCGGTTT CACCTTCTCA GCCCTGCAGA TCCTGCCCTA CACACTGGCC 1200  
 TCCCTCTACC ACCGGGAGAA GCAGGTGTTT CTGCCCAAT ACCGAGGGGA CACTGGAGGT 1260  
 GCTAGCAGTG AGGACAGCT GATGACCA GCCTTGCAG GCCCTAAGCC TGGAGCTCCC 1320  
 45 TTCCCTAATG GACACGTGGG TGCTGGAGG AGTGGCCTGC TCCCACTCC ACCCGGCTC 1380  
 TGCGGGGCTT CTGCTGTGA TGCTCCGTA CGTGTGGTGG TGGGTGAGCC CACCGAGGCC 1440  
 AGGCTGGTTC CCGGCGGGG CATCTGCTG GACCTCGCCA TCCTGGATAG TGCTTCTCTG 1500  
 CTGTCCAGG TGCGCCATC CCGTGTATG GGTCCATTG TCCAGCTCAG CCACTCTGTC 1560  
 50 ACTGCTATA TGGTGTCTG CGCAGGCTG GGTCTGGTGC CCATTACTT TGCTACACAG 1620  
 GTAGTATTG ACAAGAGCA CTGGCCAAA TACTCAGCT GA

Seq ID NO: 548 Protein sequence  
 Protein Accession #: NP\_149093.1

55 1 11 21 31 41 51  
 MVQLWVSR LRRKQAQLL VNLTFGLEV CLAAGITYVP PLLLEVGVVE KFTMTVLGIG 60  
 PVLGLVCPV LGSASDHWG RYRRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120  
 ELALLILGV LDFCQVCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGLGGLLPA 180  
 60 IDMDTSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGTEPAE GLSAPSLSPH 240  
 CCPCRLARL RNIGALLPRL HQLCCRPRT LRRLFVAELC SMALMTFTL FYTDFVGEGL 300  
 YQGVPRAEFG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG TRAVYLASVA 360  
 APPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420  
 ASSEDSMTS FLPGPKPGAP PPNGHVAGG SGLLPPPPAL CGASACDVSF RVVVGEPTEA 480  
 65 RVVPGRGICL DLAILDSAF L SQVAPSLFM GSIVQLSQSV TAYMVAAGL GLVAIFYATQ 540  
 VVFDKSLAK YSA

Seq ID NO: 549 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1389

70 1 11 21 31 41 51  
 ATGGGCTACC AGAGGCAGGA GCCTGTCTAT CCGCGCAGG GAGATTAGA TGACAGAGAA 60  
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 75 GTTGTCAACT CGATTATAG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180  
 GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACGGA CTTTCCCTT 240  
 GTTTTATTTA TAAAGAGAG GGCCTCTCTT GGAACAGATA CCTACCAGTC TTGTGTCAT 300  
 AAAACTTTTG GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTAGTTTCTT GTATCTTTT 360  
 80 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420  
 ATCCAGGAG TTATCTCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTTC 480  
 ACAGTTACCT TTAGCTGCTC TTTATCTGTC TACCGAAATA TAGCAAGCT TGGAAAGTTC 540  
 TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600  
 TCACCTGGTC CACACATACC AAAACAGAA GACGCTTGGG TATTTCGAAA GCCCAATGCC 660  
 ATTCAGCGG TCGGGGTAT GTCTTTTGA TTTATTGTC ACCATACTC CTCTTAGTT 720

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TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTATCCA TATGTCCATC 780  
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TTCAACCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTTGGA 900  
AGATTTTGTG ATGGTGTCAC TGTCAATTTG ACATACCCTA TGGAAATGCT TGTGACAAGA 960  
GAGGTAATG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTCCA CATTGTTGTA 1020  
ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGGATA 1080  
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTATCAT TCCATCAGCC 1140  
TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTC 1200  
ATGCTTCCCA TTGGTGCTGT GGTGATGGTT TTTGGATTCC TCATGGCTAT TACAAATACT 1260  
CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATTT CTCTCTCACA 1320  
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC 1380  
TTCAATGA

Seq ID NO: 550 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
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MGYQRQEPVI PFQRLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60  
GFPLGILLFF WVSIVTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPYGLL LSVLQFLYPF 120  
IAMISYNIIA GDTLSKVQFR IPGVDPENVF IGRHFIIGLS TVTFLPLSL YRNIKLGKV 180  
SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKFA IQAVGVMSFA FICHNSFLV 240  
YSSLEETVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLFENY CRNDLVTGTC 300  
RFCYGVTVIL TYPMECFVTR EVIANVFEGG NLSSVFHIV TVMVITVATL VSLIDCLGI 360  
VLELNGVLC TPLIFIPSA CYLKLSEEP THSDKIMSCV MLPIGAVMV FGFVMAITNT 420  
QDCTHGQEMF YCFPDNPSLT NTSESHVQQT TQLSTLNISI PQ

Seq ID NO: 551 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1284

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AAGCAAGCTG GGTTCCTTT GGAATATTG CTTTATTCT GGGTTTCATA TGTACAGAC 120  
TTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180  
TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTGTG 240  
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300  
TTTCAAGAA TCCAGGAGT TGATCTGAA AACGTGTTA TTGGTCGCCA CTTCATTATT 360  
GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTGT ACCGAAATAT AGCAAAGCTT 420  
GGAAAGGTCT CCTCATCTC TACAGGTTA ACAACTCTGA TTCTTGAAT TGTAAATGGCA 480  
AGGCAATTT CACTGGGTCC ACACATACCA AAACAGAGG ACGCTTGGGT ATTTGCAAG 540  
CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTGCGCA CCATAACTCC 600  
TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660  
ATGTCATCG TGAATTCGT ATTTATCTGT ATATTCTTG CTACATGTGG ATACTTGACA 720  
TTTACTGGCT TCACCAAGG GGAATTATT GAAATTACT GCAGAAATGA TGACCTGTA 780  
ACATTGGGAA GATTTTGTTA TGGTGCTACT GTCATTTGA CATACCTAT GGAATGCTT 840  
GTGACAAGAG AGGTAATTGC CAATGTGTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900  
ATTGTGTAA CAGTAGTGT CATCACTGTA GCCACGCTG TGTCATTGCT GATTGATTGC 960  
CTCGGATAG TTCTAGAACT CAATGGTGT CTCTGTGCA CTCCCTCAT TTTTATCATT 1020  
CCATCAGCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCA TAAGATTATG 1080  
TCTTGTGCTA TGCTTCCAT TGGTGCTGT GTGATGGTT TTGGAATCGT CATGGCTATT 1140  
ACAAATACCA AAGATGACAC CCATGGGCAG GAAATGTTCT ACTGCTTTC TGACAATTC 1200  
TCTCTCACA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACTTC TACTTTAAAT 1260  
ATTAGTATCT TTCAACTCGA GTAA

Seq ID NO: 552 Protein sequence  
Protein Accession #: Eos sequence

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1 11 21 31 41 51  
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVSIVTD FSLVLLIKGG ALSGDTYQS 60  
LVNKTGFFPG YLLSVLQFL YPFIAMISYN IAGDTLSKV PQRIPGVDP NVPIGRHFII 120  
GLSTVTFLE LSLYRNIKLV KSVSLISTGL TTLILGIVMA RAISLGHIP KTEDAWVFAK 180  
PNAIQAVGVV SFALICHNS FLVYSSLEEP TVAKWSRLIH MSIVSVFIC IFFATCGYLT 240  
FTGTTQGDLE ENYCRNDLV TFGRCYGVV VILTYPMECF VTREIVANVF FGNLSSVPH 300  
IVVTVMVIT ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLE EPRTHSDKIM 360  
SCVMLPIGAV VMVFGPVMAI TATQDCTHQ EMFYCFPDNF SLTNTSESHV QQTTLSTLN 420  
ISIFQLE

Seq ID NO: 553 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1203

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1 11 21 31 41 51  
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGT TTTCCCTTGT TTTATTGATA 60  
AAAGGAGGGG CCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC 120  
TTTCCAGGAT ATCTGCTCT CTCTGTTCTT CAGTTTTGT ATCCTTTAT AGCAATGATA 180  
AGTTACAGTA TAATAGCTGG AGATACTTGG AGCAAAGTTT TTCAAAGAA CCCAGGAGTT 240  
GATCCTGAAA ACGTGTGTT TGGTCGCCAC TTCATTATG GACTTTCCAC AGTTACCTTT 300  
ACTCTGCCTT TATCCTGTA CCGAAATATA GCAAAGCTG GAAAGGTCTC CCTCATCTCT 360  
ACAGGTTTAA CAGGCTCAT TCTTGAATG GTAATGGCAA GGGCAATTC ACTGGGTCCA 420  
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480

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GGGGTTATGT CTTTTCGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCCTCT 540  
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTTCGTGA 600  
TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660  
GACTTATTGT AAATATTACTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTTGTAT 720  
GGTGTCACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAAGAGA GGTAAATTGCC 780  
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTCCACA TTGTGTAAAC AGTGATGGTC 840  
ATCACTGTAG CCACGCTTGT GTCACTGTCTG ATTGATTGCC TCGGGATAGT TCTAGAAGTC 900  
AATGGTGTGC TCTGTGCAAC TCCCTCAT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
CTGTCTGAAG AACCAAGGAC ACACCTCCAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020  
GGTGTCTGGT TGATGGTTTT TGGATTCTGC ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTCTT CTCTCAGAAA TACCTCAGAG 1140  
TCTCATGTTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200  
TAA

Seq ID NO: 554 Protein sequence  
Protein Accession #: Eos sequence

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MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI 60  
SYNIIAGDTL SKVQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLLIS 120  
TGLTTLILGI VMARAIISLP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180  
EPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFPENYCRND DLVTFGRFCY 240  
GVTVILTYPM ECFVTRVIA NVFPGNLS VFIHVVTVMV ITVATLVSL IDCLGIVLEL 300  
NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVGFV MAITNTQDCT 360  
HGQEMFYCFP DNFLTNTSE SHVQTTQLS TLNISIFQLE

Seq ID NO: 555 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1140

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CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120  
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180  
CCTGAAAACG TGTATTATGG TCGCCACTTC ATTATTGGAC TTTCACAGT TACCTTTACT 240  
CTGCCCTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300  
GGTTTAACAA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360  
ATACCAAAAA CAGAAGACGC TTGGGTATTG GCAAAGCCCA ATGCCATTCA AGCGTCCGGG 420  
GTTATGCTTT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480  
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATT 540  
ATCTGTATAT CTCTGTCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600  
TTATTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660  
GTCACGTGCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720  
GTGTTTTTGT GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780  
ACTGTAGCCA CGCTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840  
GGTGTGCTCT GTGCAACTCC CCTCATTITT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900  
TCTGAAGAAC CAAGGACACA CTCGGATAAG ATTATGTCTT GTGTGATGCT TCCATTGGT 960  
GCTGTGGTGA TGGTTTTTGG ATTCGTCTAT GCTATTACAA ATACTCAAGA CTGCACCCAT 1020  
GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080  
CATGTTACAG AGACACACA ACTTCTACT TTAATATTA GTATCTTCA ACTCGAGTAA

Seq ID NO: 556 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
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MGYQRQEPVI PPQVNKTFGE PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPGVD 60  
PENVFIGRHF IIGLSTVTF LPLSLYRNI KLKVSLLIST GLTTLILGIV MARAISLGP 120  
IPKTEDAWVF AKPNAIQAVG VMSFAFICH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180  
ICIFFATCGY LTFTGFTQGD LFENYCRND LVTFRFCY VTVILTYME CFVTRVIAN 240  
VFFGGNLSV FHVVTVMVI TVATLVSLI DCLGIVLELN GVLCATPLIF FIIPSACYLKL 300  
SEEPRTSDK IMSCVMLPIG AVVMVGFV AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360  
HVQTTQLST LNISIFQLE

Seq ID NO: 557 DNA sequence  
Nucleic Acid Accession #: XM\_057188.1  
Coding sequence: 769..4269

1 11 21 31 41 51  
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CTGCCCTTCC CCAATTCTT TGGTTTTTGC ATCCCCCTCT GCCCTTGGCC TCAGTCAAGT 180  
CTCCCCGTGT TGTCTCTCTC CCCCCGCGCC GACCTCTGCG ACCCCGAGG TCGTGTCCC 240  
TCTGTCCCTT TATCGCGGCC TGGGACCGCG CCTCTCCCG CCTCCGCTT TGGCGTCTCC 300  
AAGACTCCCC GCCCCCCAGA CCTCGCCCCG CCCCAGGCTA GGCTGGAAAG TGGAGGATCC 360  
GGTTTGCTCT GGGCGGGTCT GGAAGCAGAG CCGGCGGAGG GAGCGCGGG CCCTCGGGCT 420  
CGCAGAGGTT CGGGCGGCG CGGAGCATG GTGGTCCGG AGAAGGAGCA GAGCTGGATC 480  
CCCAAGATCT TCAAGAAGAA GACCTGCACG ACGTTCTATG TTGACTCCAC AGATCCGGGG 540  
GATGGGGTCT CGCTCTATG CCCAGGCTGT TCTCAAATCT CTGGGCTCAA GCACTCCTTC 600  
TGCCCTGACC TCCCAAGTGT CTTGGATTGT GCCCAGCGGT CTTGAAGTT TTGCTCAGAA 660  
GAGCAAACCT TCTGGGAAGT AGCTGCAGGT GTTGAAGTA GCTGCAGGG AACTAGGGGA 720

5 TTCAAGGATG GAGCTGAAAT GGGTGAACGG ACAAGATCGG TAAACTGAAT GGAGGATGCC 780  
 TTGGGGGCGAG CCGTGGTGAC CCGTGTGGGAC AGCGATGCAC ACACCACGGA GAAGCCCACC 840  
 GATGCCCTACG GAGAGCTGGA CTTACGCGGG GCCGGCCGCA AGCACAGCAA TTTCCTCCGG 900  
 CTCTCTGACC GAACGGATCC AGCTGCAATT TATAGTCTGG TCACACGCAC ATGGGGCTTC 960  
 CGTGCCCCGA ACCTGGTGGT GTCACTGCTG GGGGATCGG GGGGCCCCGT CCTCCAGACC 1020  
 TGGCTGCAGG ACCTGCTGCG TCGTGGGCTG GTGCGGCTG CCCAGAGCAC AGGAGCCTGG 1080  
 ATTGTCACTG GGGGTCTGCA CACGGGCATC GGGCGGCATG TTGGTGTGGC TGTACGGGAC 1140  
 CATCAGATGG CCAGCACTGG GGGCACCAG GTGGTGGCCA TGGGTGTGGC CCCCTGGGGT 1200  
 10 GTGGTCCGGA ATAGAGACAC CCTCATCAAC CCCAAGGGCT CGTTCCTGCG GAGGTACCGG 1260  
 TGGCGCGGTG ACCCGAGGGA CGGGGTCCAG TTCCCTCTGG ACTACAACTA CTCGGCCTTC 1320  
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 15 CAGGCTCAGC TCCATGTCTT CCTGTGGCTT GGCTCAGGGG GAGCTGCGGA CTGGCTGGGG 1560  
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 GATCGAATCA GGCCTTTCTT TCCCAAAGGG GACCTTGAGG TCCTGCAGGC CCAGGTGGAG 1680  
 AGGATTATGA CCCGGAAGGA GCTCCTGACA GTCTATTCTT CTGAGGATGG GTCTGAGGAA 1740  
 TTTGAGACCA TAGTTTGTAA GGCCTTGTG AAGGCTGTG GAGCTCGGA GGCCTCAGCC 1800  
 20 TACCTGGATG AGGTGCGTTT GGCTGTGGCT TGGAAACCGG TGGACATGCG CCAGAGTGAA 1860  
 CTCTTTCCGG GGGACATFCA ATGGCGGTCC TTCCATCTCG AAGCTTCCTT CATGAGCGCG 1920  
 CTGCTGAATG ACCGGCCTGA GTTCTGTGCG TTGCTCATTT CCCACGGCTT CAGCTTGGGC 1980  
 CACTTCTGTA CCCCGATGGG CCTGGCCCAA CTCTACAGCG CGGCGCCCTC CAACTCGCTC 2040  
 ATCCGCAACC TTTTGGACCA GGCCTCCAC AGCGCAGGCA CCAAGGCCCT AGCCCTAAAA 2100  
 25 GGGGGAGCTG CGGAGCTCGG GCGCCCTGAC GTGGGGCATG TGCTGAGGAT GCTGCTGGGG 2160  
 AAGATGTGGG CGCGAGGTA CCGCTCCGGG GCGCGCTGGG ACCCTCAGCC AGGCCAGGGC 2220  
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 GGCCTCGGGG AGGCCCCCTG GAGCGACCTG CTCTTTGGG CACTGTGTCT GAACAGGGCA 2340  
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 30 TGTTTGCTCG TCCGGGTGAT GGCACGCGTG GAGCCTGACG CTGAGGAGGC AGCACGGAGG 2460  
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 40 TTCTGTGCTG TTTTCTCGCG GGTGCTGCTG GTGGATTTC AGCGCGGCCG GCGCGGCTCC 3060  
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 55 TGCAAGCGAC CCGGAGCGCC CAGCGCGTCC TCCCGGCCCC TOGAGCATT CCGGGTTTAC 3960  
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 60 AAGTGTCTGG AGCGGAGGAT CCAGCAGTGT AGCGCGCTCC TGGGGTGGGT GGGCGAGGCC 4200  
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 65 GCATGCCCCG CTCTCCACG AACCACTCCC AGCCTGGGAG GATCAAGGCC TGGATCCCGG 4500  
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 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 558 Protein sequence  
 Protein Accession #: XP\_057188.1

70 1 11 21 31 41 51  
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 75 AVRHDQMAST GGTQVAVMGV APWGVVRNRD TLINPKGSFP ARYRNRGDPE DGVQFPPLDYN 180  
 YSAFFLVDDG THGCLGGENR FRLRLSEYIS QKKTGVGGTG IDIPVLLLI DGDEKMLTRI 240  
 ENATQAQLPC LLVAGSGGAA DCLAETLEDT LAPGSGGARQ GEARDRIIRF FPKGDLEVLQ 300  
 AQVERIMTRK ELLTVYSSSE GSEEFETIVL KALVKACGSS EASAYLDELRL LAVANNRVDI 360  
 80 AQSELFRGDI QNRSHFLEAS LMDALLNDRP EPVRLLSHIG LSLGHFLTPM RLQAQLYSAAP 420  
 SMSLIRNLDD QASHSAGTKA PALKGGAAEL RPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480  
 PQQGFPGESMY LLSDKATSPF SLDAGLGQAP WSDLLWALL LNRQAQMYF WEMGSNAVSS 540  
 ALGACLLLRV MARLEPDARE AARRKDLAFK FEGMGVDLFG ECRYRSEVRA ARLLLRRCPL 600  
 WGDATCLQLA MQADARAFPA QDGVQSLLTQ KMGDMASTT PIWALVLAF CPPLIYTRLI 660  
 TFRKSEBEPT REELEFDMDS VINGESPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGGRRR 720

LRRWFHFWGA PVTIFMGNV SYLLFLLFS RVLLVDFQPA PGSLLELLY FWAFTLLCEE 780  
LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840  
HLGRTVLICD FMVFTVRLH IPTVVKQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT 900  
EGLLRPRDSF PPSILRRVFF RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPPGAQA 960  
GTCVSOYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQNSDLWY KAQRYRLIRE 1020  
FHSRPALEPP FIVISHLRLR LRQLCRRPRS PQSPPALEH FRVYLSKEAE RKLTLWESVH 1080  
KENFLLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQQCSRVLGW 1140  
VAEALSRSLAL LPPGGPPPPD LPGSKD

Seq ID NO: 559 DNA sequence  
Nucleic Acid Accession #: NM\_006853.1  
Coding sequence: 26..874

1 11 21 31 41 51  
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CATGAGGATT CTGAGATTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180  
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT 240  
CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300  
AGCCCACTGC CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA 360  
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCACCCCG GCTTCAACAA 420  
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATGCCAGT 480  
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540  
CAGCTGCCTC ATTTCGGGCT GGGGCGACAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC 600  
CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAAGC CCTACCCCGG 660  
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAGG ACTCCTGCCA 720  
GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG 780  
CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATGT 840  
GGACTGGATC CAGGAGACGA TGAAGAACA TTAGACTGGA CCCACCCACC ACAGCCCATC 900  
ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCATCTI GTTAATAAGA AACCTTAAGC 960  
CAAGACCTTC TAGCAACATT CTTTGGGCTC CTGGACTAC AGGAGATGCT GTCACTTAAT 1020  
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080  
GACTCTGGGA ATGACAACAC CTGGTTTGTI CTCTGTTGTA TCCCAGCCCC CAAAGACAGC 1140  
TCCTGGCCAT ATATCAAGGT TTCATAAAT ATTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence  
Protein Accession #: NP\_006844.1

1 11 21 31 41 51  
MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60  
AHLCKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHND IMLVKMASPV 120  
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIIE HOKCENAYPG 180  
NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GYVTKVKXYV 240  
DWIQETMKN

Seq ID NO: 561 DNA sequence  
Nucleic Acid Accession #: AY046419.1  
Coding sequence: 1..1743

1 11 21 31 41 51  
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GAGCAGGAAA TGGTGTGTAG CTCCCTCGTC ATTGGAGCCC TCCTTGCCCT ACTCACCGGA 180  
GGGTCTCTGA TAGACAGATA TGAAGAAGG ACAGCAATCA TCTTGTATC CTGCTGTGCT 240  
GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTTCTTAT AGTGGGACGC 300  
ATTGCCATAG GGGTTTCCAT CTCCCTCTCT TCCATGGCCA CTGTGTGTTA CATCGCAGAG 360  
ATTGCTCTCT AACACAGAAG AGGCCCTCTT GTGTCACTGA ATGAGCTGAT GATTGTCAATC 420  
GGCATTCTTT CTGCCATAT TTCAAATTAC GCATTGGCCA ATGTTTTCCT TGGCTGGAAG 480  
TACATGTTTG GTCTTGTGAT TCCTTGGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT 540  
CCTCCAAGCC CTCGTTTCTT GGTGATGAAA GGACAAGAGG GAGCTGCTAG CAAGGTTCTT 600  
GGAAGGTTAA GAGCACTCTC AGATACAACT GAGGAATCA CTGTGATCAA ATCCTCCCTG 660  
AAAGATGAAT ATCAGTACAG TTTTGGGAT CTGTTTGGT CAAAAGACAA CATCGGAGCC 720  
CGAATAATGA TAGGACTAAC ACTAGTATTT TTGTACAAA TCACTGGCCA ACCAAACATA 780  
TTGTTCTATG CATCAACTGT TTTGAAGTCA GTTGGATTTC AAAGCAATGA GGCAGCTAGC 840  
CTCGCTCCA CTGGGTTGG AGTCGTCAAG GTCAATTAGCA CCATCCCTCG CACTCTTCTT 900  
GTAGACCATG TGGGCGACAA AACATCTCCT TGCAATTGGCT CCTCTGTGAT GGCAGCTTGG 960  
TTGGTGACCA TGGGCTAGCT AAATCTCAAC ATCCACATGA ACTTCACCCA TATCTGCAGA 1020  
AGCCACAATT CTATCAACCA GTCTTGGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080  
TCAACCAACA ACAATACTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC 1140  
TCACTCATGC CCTGAGAAA TGATGTGGAT AAGAGAGGGG AGACGACCTC AGCATCCTTG 1200  
CTAAATGCTG GATTAAAGCA CACTGAATAC CAGATAGTCA CAGACCCCTG GGCAGTCCCA 1260  
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CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCCTCAT CTCGTGACA 1440  
TTTTGACTG TAACATGATCT TATTGGCTG CCATGGGTGT GCTTTATATA TACAATCATG 1500  
AGTCTAGCAT CCTGTCTTT TGTGTATTG TTTATACCTG AGACAAAGGG ATGCTCTTTG 1560  
GAACAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACAACAT TGTTTTATG 1620  
AGTCATCACC AAGAAGAAAT AGTGCCAAA CAGCCTCAA AAAGAAAACC CCAGGAGCAG 1680  
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TAA

Seq ID NO: 562 Protein sequence  
Protein Accession #: AAL02327.1

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5      1      11      21      31      41      51
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      GVLIIDRYGRR TAILLSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSISLS SIATCVYIAE 120
      IAPQHRRGLL VSLNELMIVI GILSAYISNY AFANVPHGWK YMFGLVIPLG VLQAIAMYFL 180
      PPSPRELVMK QOEGAASKVL GRRLALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
10     RIMIGLTLVF FVQITGQPNL LFYASTVLKS VGFQSNEMAS LASTGVGVVK VISTIPATLL 300
      VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMFTHICR SHNSINQSLD ESVIYGPNL 360
      STNNITLRDH FKGISHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
      AFLKWLSLAS LLVYVAAFSI GLGPMPLVL SEIFPGGIRG RAMALTSSMN WGINLLISLT 480
15     FLVTVDLIGL PWVCFIYTIM SLASLLEFVM FIPETKGC SL EQISMELAKV NYVKNNICFM 540
      SHHQEELVFK QPKRKPQEQ LLECNLCGR GQSRQLSPET

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Seq ID NO: 563 DNA sequence  
Nucleic Acid Accession #: XM\_059466.1  
Coding sequence: 1..894

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20     1      11      21      31      41      51
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      CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTAOGAGA CCGACCCCGG GCGCCACAAG 120
25     GAGAGCTCGG AGCGCAGCCG CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CCGCTGATG 180
      CCGCTGTGCG ACCTGCGCGT GCGGGACTCG CCCCCTGTGG GCGCGCGGCT GCTCCCGGGC 240
      GGCCCGGGGC GCGCGCACCC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
      GCGGAGTGGG GCGGGCCCTT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
      CTGGGCATCG ACCGGGACAT CGACACCCTC ATCTCGAAG GTATTGCGCA GCGATGCACG 420
30     GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGGGAA ACATTCCTTT TAATTAAACC 480
      AAGACCATAC AGCAGATGA GTGGCACCTG CTTCATTAA AAGAATCAC TGCTGGCTTC 540
      CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
      TGGGAGAGGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
      TGCACCATTT CCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
35     AAGCTAATTT ATAGCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
      GCCTGGTGCA GTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
      ATTAGCCGGA CCAAGATTGC ACAGCTAAG TCTGCAGAG ACTCCACGGT ATGA

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Seq ID NO: 564 Protein sequence  
Protein Accession #: XP\_059466.1

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40     1      11      21      31      41      51
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      PLSHLPLRDS PPLGRRLLPF GPGRADPESW RSLGLGLD AEGRPLPAT YSGLWRKCYF 120
45     LGIDRIDTL ILKGIAQRCT AIKYHFSQPI RLRNIPFNL KTIQDEWHL LHLRRITAGF 180
      LGMVAVALLC GCIVATVSFF WEESLTQHVA GLFLMTGIF CTISLCTYAA SISYDLNRLP 240
      KLIYSLPADV EHYGSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

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Seq ID NO: 565 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3315

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55     1      11      21      31      41      51
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      ACCCGGACCC TGACTCCAG CGGCTCTCGG AGCACAGACT TGCTTTACAG TGAAGCGAC 120
      TTGGTGAATT TATTTCAAG AAATTTTAAG AAACAGAAAT GTGTCTTCTT TACCAAGAT 180
      TCCAGGCCCA CGGAGAATGT GTGCAAGTGT GGCTATGCC AGAGCCAGCA CATGGAAGGC 240
60     ACCCAGATCA ACCAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCTTACC 300
      GAGCCCTTTG GGGATATTCA GTTTGAGACA CTGGGAAGA AAGGGAAGTA TATACGTCTG 360
      TCCTGGGACA CGGACGCGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGAAA 420
      ACACCCAAAC TGGTCATTTC TGTGACCGGG GCGCCCAAGA ACTTGGCCCT GAAGCGCGCG 480
      ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATGCGCGAGT CCAAAGTGTC TTGGATTCTC 540
65     ACGGGAGGCA CCAATTATGG CCTGATGAAG TACATCGGG AGGTGGTGAG AGATAACACC 600
      ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGGCATGGTC 660
      TCCAACCGGG ACACCTCAT CAGGAATTGC GATGCTGAG GCTATTTTT AGCCAGTAC 720
      CTTATGGAG ACTTCACAAG AGATCCAAGT TATATCCTGG ACAACAACCA CACACATTTG 780
      CTGCTCGTGG ACAATGGCTG TCAATGACAT CCCACTGTGG AAGCAAAGCT CCGGAATCAG 840
70     CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
      ATTGTGTGTT TTGCCCAAGG AGGTGGAAAA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
      AAAAAATAAA TTCTTGTGT GGTGGTGAA GGCTCGGGCC AGATCGCTGA TGTGATGCT 1020
      AGCCTGGTGG AGGTGGAGGA TGCCCTGACA TCTTCTGCG TCAAGGAGAA GCTGGTGCG 1080
      TTTTATCCCC GCACGCTGTC CCGGCTCGCT GAGGAGGAGA CTGAGAGTTG GATCAATGG 1140
75     CTCAAAGAAA TTCTCGAATT TCTCACCTA TTAACAGTTA TTAATGGA AGAAGCTGGG 1200
      GATGAAATTG TGAGCAATGC CATCTCTAC GCTCTATACA AAGCCTTCAG CACCAAGTGG 1260
      CAAGACAAGG ATAACTGGAA TGGGCAGCTG AAGCTTCTGC TGGAGTGAA CCAGCTGGAC 1320
      TTAGCCAATG ATGAGATTTT CACCAATGAC CGCCGATGGG AGTCTGCTGA CCTTCAGAA 1380
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80     GGCTTGAAAC TACGGAAGTT TCTCAACCAT GATGCTCTCA CTGAACCTT CTCCAACCA 1500
      TTCAGCACGC TTGTGTACCG GAATCTGCAG ATGCCAAGA ATCTCTATA TGAATGCCCT 1560
      CTCACGTTTG TCTGGAACAT GGTGCGAAG TTCCGAGAG GCTTCCGGA GGAAGACAGA 1620
      AATGGCGGG ACAGATGGA CATAGAATC CACGACGTGT CTCCTATTAC TGGCACCCC 1680
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15  
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TCTGTCTGCT GTTTCAAAAA TGAAGACAAT GAGACTCTGG CATGGGAGGG TGTCAATGAG 3180  
GAAAACTACC TGTCAAGAT CAACACAAAA GCCAACGACA CCTCAGAGGA AATGAGGCAT 3240  
CGATTAGAC AACTGGATAC AAAGCTTAAT GATCTCAAGG GTCTTCTGAA AGAGATTGCT 3300  
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Seq ID NO: 566 Protein sequence  
Protein Accession #: Eos sequence

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40  
45  
50

1 11 21 31 41 51  
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SKATENVCKC GYAQSQHMEG TQINQSEKWN YKHTKEFET DAFGDIQFET LGKKGKYRL 120  
SCDTDAEILY ELLTQHWHLK TPNLVISVTG GAKNPAKPR MRKIFSRILI IAQSKGAWIL 180  
TGGTHYGLMK YIGEVVRDNT ISRSSEENIV AIGIAAWGMV SNRDTLIRNC DAEGYFLAQY 240  
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IVCFAQGGGK ETLKAINTSI KNIKPCVVVE GSGQIADVIA SLVEVEDALT SSAVKEKLV 360  
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Seq ID NO: 567 DNA sequence  
Nucleic Acid Accession #: NM\_006911.1  
Coding sequence: 1..558

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GCCCTATCTG AGAGGCAACC ATCATTACCA GAGCTACAGC AGTATGTACC TGCATTAAG 360  
GATTCCAATC TTAGCTTTGA AGAATTTAAG AAACCTATTG GCAATAGGCA AAGTGAAGCC 420  
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Seq ID NO: 568 Protein sequence  
Protein Accession #: NP\_008842.1

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Seq ID NO: 569 DNA sequence  
Nucleic Acid Accession #: XM\_036453.1



Coding sequence: 1..3978

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Seq ID NO: 570 Protein sequence

Protein Accession #: XP\_036453.1

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10	LDPIQTLQV	VGVVSAVAV	IPWIAIPLVP	LGIIPIFLRR	YFLETSRDVK	RLESTTRSPV	900
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Seq ID NO: 573 DNA sequence  
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 TTTGCCAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180  
 AGAAATCCTA AGTTTGCTTC TGAATTTTTT CCTCATGCGG TAGATGTCAC TCATCATGAA 240  
 GATGCTCTCA CAAAAACAAA TATAATATTT GTTGCTATAC ACAGAGAACA TTATACCTCC 300  
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 55 AGGATAAACC AGTACCAGCA ATCCAATGCT GAATATTGG CTTCATTATT CCCAGATTCT 420  
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 GCCAGCGGCG AGGTTTATAT ATGCAGCAAC AATATTCAAG CGGCACAACA GGTATTGAA 540  
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 ATTGAATATT TACCCTTACG ACTCTTTACT CTCGGAGAG GGCAGTGGT GGTAGCTATA 660  
 60 AGCTTGCCCA CATTTTTTTT CCTTTATTC TTTGTGAGAG ATGTGATTCA TCCATATGCT 720  
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 ATAGTTGCCA TTACTTTGCT CTCCCTAGTA TACCTCGCAG GTCTCTGCG AGCTGCTTAT 840  
 CAACTTTATT ACGGCACCAA GTATAGGAGA TTCCACCTT GGTGGAAAC CTGGTTACAG 900  
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 65 CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTGTGTT TCAACATGCG TTATCAGCAG 1020  
 GTTCATGCAA ATATTGAAA CTCTTGAAT GAGGAAGAAG TTGGAGAAT TGAATGTAT 1080  
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 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTAT TCCAGTCTAC ACTTGGATAT 1200  
 GTCGCTCTGC TCATAAGTAC TTTCCATGTT TTAATTATG GATGGAACAG AGCTTTTGAG 1260  
 70 GAAGAGTACT ACAGATTTTA TACACCAACA AACTTTGTT TGTCTCTGT TTTGCCCTCA 1320  
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Seq ID NO: 574 Protein sequence  
 Protein Accession #: Eos sequence

75  
 1 11 21 31 41 51  
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 80 RINQYFESNA EYLASLPDS LIVKGFNVVS AWALQLGPKD ASRQVYICSN NIQARQVIE 180  
 LARQLNFIPI DLSGLSSARE IENLPLRLFT LWRGPFVVVAI SLATFFFLYS FVRDVIHPYA 240  
 RNQSDFYKI PIBIVNKTLP IVAITLLSLV YLAGLLAAAY QLYGTYKRR FPPWLETWLQ 300  
 CRKQLGLLF PFAMVHVAYS LCLPMRRSER YLFLNMAVQQ VHANIENSWN EEEVWRIEM 360  
 ISFGIMSLGL LSLAVTSIP SVSNALNWRP SFQISTLGY VALLISTFHV LIYGWKRAPE 420  
 EERYRPTTPP NFVLALVLPF IVILDLLQLC RYPD

Seq ID NO: 575 DNA sequence  
Nucleic Acid Accession #: NM\_001873.1  
Coding sequence: 3..1721

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GGTGGCGGAAC TTGCGCGCCC CAGCAGCGCC GCGGGCTAA GCCAGGGGCC GGCAGACAA 240  
AAGAGGCGCG CCGGTAGGA AGGCAGGCC GCGCGGCGG GAGCGCAGCG ATGGCCGGGC 300  
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AGCAGCGTCT TCAGCCTGGT GAACTCAAGG ACTGGTTTGT GGGTCGAAGC AATGCCCAGG 840  
GATAGATCTT GAACCGGACC TTCCAGACC TGGATAGGAT AGTGTACGTG AATGAGAAAG 900  
AAGGTGGTCC AATATACAT CTGTGAAAA ATATGAAGAA AATGTGGAT CAAAACACAA 960  
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CTGCCAATCT CCAATGGAGA GACCTTGTGG CCAATTATCC ATATGATGAG ACGCGGAGTG 1080  
GTAGTGCTCA CGAATACAGC TCCTCCCGAG ATGACGCCAT TTTCCAAAGC TTGGCCCGGG 1140  
CATACTCTTC TTTCACCGCG GCCATGTCTG ACCCCAAATCG GCCACCATGT CGCAAGAATG 1200  
ATGATGACAG CAGCTTTGTA GATGGAACCA CCAACGGTGG TGCTGTGATC AGCGTACCTG 1260  
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GCTGTGAGAA GTTCCCACTT GAAGAGACTC TGAAGACCTA CTGGGAGGAT AACAAAACT 1380  
CCCTCATTAG CTACCTTAG CAGATACACC GAGGAGTTAA AGGATTGTCT CGAGACCTTC 1440  
AAGGTAACCC AATGTGGAAT GCCACCATCT CCGTGGAAAG AATAGACCAC GATGTTACAT 1500  
CCGCAAGGA TGCTGATTAC TGGAGATTGC TTATACCTGG AAACATAAAA CTTACAGCCT 1560  
CAGCTCCAGG CTATCTGSCA ATAACAAGA AAGTGGCAGT TCCTTACAGC CCTGCTGCTG 1620  
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TGGAAATGGT CGAATGATG TCAGAACTT TAAATTTTAA AAAAGGCTTC TAGTTAGCTG 1740  
CTTTAATCT ATCTATATAA TGTAGTATGA TGTAAATGGG TCTTTTTTTT AGATTTTGTG 1800  
CAGTTAATAC TTAACATTGA TTTATTTTTT AATCATTTAA ATATTAATCA ACTTTCCTTA 1860  
AAATAAATAG CCTCTTAGGT AAAAATATAA GAACCTGATA TATTTATTC TCTTATATAG 1920  
TATTCTATTT CCTACCTATA TTACACAAAA AAGTATAGAA AAGATTAAAG TAATTTTGCC 1980  
ATCCTAGGCT TAAATGCAAT ATCTCTGCTA TTATTTACAA TGCAGAAATT TTTGAGTAAT 2040  
TCTAGCTTTC AAAAATAGT GAAGTTCTTT TACTGTAAAT GGTGACAATG TCACATAATG 2100  
AATGCTATTG AAAAGGTTAA CAGATACAGC TCGGAGTTGT GAGCACTCTA CTGCAAGACT 2160  
TAAATAGTTC AGTATAAAT GTGTTTTTTT TCTGTGCTG ACTAATATA AGCATGATCT 2220  
TGTTAATGCA TTTTGTATGG GAAGAAAAGG TACATGTTTA CAAAGAGGTT TTATGAAAAG 2280  
AATAAAAAAT GACTTCTTGC TTGTACATAT AGGAGCAATA CTATTATATT ATGTAGTCCG 2340  
TTAACTACTC TAAAAGTTT AGGGTTTCT CTGTGTTGTA GAGTGGCCCA GAATTGCATT 2400  
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Seq ID NO: 576 Protein sequence  
Protein Accession #: NP\_001864.1

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21  
31  
41  
51  
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EALVSVLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEPKYI GNMHGNEAVG 120  
RELLIFLAQY LQNEYQKQNE TIVNLHSTR IHIMPSLNPD GFKAASQPG ELQDWFVGRS 180  
NAQGDILMRN FPDRLRIYV NEKEGGPNNH LKMKIKIVD QNTKLAPETK AVIHWIMDIP 240  
FVLSANLEGG DLVANYPYDE TRSGSAEYS SSPDDAIFQS LARAYSSFP AMSDPNRPFC 300  
RKNDDSSPV DGTINGGAWY SVPGMDDFN YLSSNCFBIT VELSCSEKFPF EETLKITWED 360  
NKNSLISYLE QIHRGVKGFV RDLQGNPIAN ATISVEGIDH DVTSKDG DY WRLLIPGNYK 420  
LTASAPGYLA ITKVAVPYS PAAGVDFELE SFSEKKEEK EELMEWNKMM SETLNF

Seq ID NO: 577 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..933

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TTCCCTCTGG CCAGCGGCAT CCAATGCATC ATTGGTCGCT TCGCGTGCAA TGGGTTTGAG 180  
GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240  
GCCCCGTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300  
AATAACTGTG AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT 360  
GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTGTGTGATT ACCCCAGCAT CACCTATGCC 420  
ATCATCGGCA GCTCCGTCTT TTTTGTGCTG GTGGTGGCCC TGCTGGCACT GGTCTTGAC 480  
CACCGCGGGA AGCGGAACAA CCTCATGACG CTGCGCGTGC ACCCGCTGCA GCACCTGTG 540  
CTGCTGTCCC GCCTGGTGGT CCTGGACAC CCCCACCACT GCAACGTGAC CTACAACGTC 600  
AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTGGGA AGTAGGCTCC 660  
CCACCTCTCT ACTCCGAGGC CTGTGTGAC CAGAGGCGCT CGTGGTATGA CCTTCCTCCA 720  
CCGCCCTACT CTTCTGACAG GGAATCTCTG AACCAAGCCG ACCTGCCCCC CTACCGCTCC 780  
CGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGCAAGCA GCAGCCTCCT GAGCGTGGAA 840  
GACACCAAGC ACAGCCCGGG GCAGCCTGCG CCCCAGGAGG GCATGCTGA GCCCAGGAGC 900

TCTGAGCCCC GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence  
 Protein Accession #: Bos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MCSNGRCIPG AWQCDGLPDC FDKSDEKECP RAKSKCGPTF PPCASGIHCI IGRFRCNGFE 60
DCPDGSDDEEN CTANPLLCST ARYHCKNGLC IDKSFICDQO NNCQDNDSEE SCESSQEPGS 120
GQVFTVTSNQ LVYYPSTIYA IIGSSVIFVL VALLALVLH HQRKRNNLMT LPVHRLQHPV 180
LLSLVLVDH PHHCNVTYV NNGIQYVASQ AEQNASEVGS PPSYSEALLD QRPAYDLPP 240
PPYSSDTESL NQADLPPYRS RSGSANSASS QAASSLLSVE DTSHSPQPG PQEGTAEPDR 300
SEPSQGTTEE

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Seq ID NO: 579 DNA sequence  
 Nucleic Acid Accession #: AF179274.1  
 Coding sequence: 1..1125

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TGGCTGCTGC TGGTGGCCGT CATGCTACTC ATCGTAGCCC GCCCGGTGAA GCTCGCTGCT 120
TTCCCTACCT CCTTAAGTGA CTGCCAAACG CCCACCGGCT GGAATTGCTC TGGTTATGAT 180
GACAGAGAAA ATGATCTCTT CCTCTGTGAC ACCAACACCT GTAAATTGTA TGGGGAATGT 240
TTAAGAATTG GAGACACTGT GACTTGCCTC TGTCAGTTCA AGTGCAACAA TGACTATGTG 300
CCTGTGTGTG GCTCCAATGG GGAGAGCTAC CAGAATGAGT GTTACCTGCG ACAGGCTGCA 360
TGCAACACAG AGAGTGAGAT ACTTGTGGTG TCAGAAGGAT CATGTGCCAC AGATGCAGGA 420
TCAGGATCTG GAGATGGAGT CCATGAAGGC TCTGGAGAAA CTAGTCAAAA GGAGACATCC 480
ACCTGTGATA TTTGCCAGTT TGGTGCAGAA TGTGACGAAG ATGCCGAGGA TGTCTGGTGT 540
GTGTGTAATA TTGACTGTTC TCAACCAAC TCAATCCCC TCTGCGCTTC TGATGGGAAA 600
TCTTATGATA ATGATGCCA AATCAAGAA GCATCGTGTC AGAAACAGGA GAAAATTGAA 660
GTCATGTCTT TGGTGTGATG TCAAGATAAC ACAACTACAA CTACTAAGTC TGAAGATGGG 720
CATTATGCAA GAACAGATTA TGCAGAGAAT GCTAACAAAT TAGAAGAAAG TGCCAGAGAA 780
CACCATATAC CTGTGCGGGA ACATTACAAT GGCTTCTGCA TGCAATGGGA GTGTGAGCAT 840
TCTATCAATA TGCAGGAGCC ATCTTGCAGG TGTGATGCTG GTTATACITG ACAACACTGT 900
GAAAAAAGG ACTACAGTGT TCTATACGTT GTTCCCGGTC CTGTACGATT TCAGTATGTC 960
TTAATCGCAG CTGTGATTGG AACAAATCAG ATTGCTGTCA TCTGTGTGGT GGTCTCTCTG 1020
ATCACAAAGG AATGCCCCAG AAGCAACAGA ATTACAGAC AGAAGCAAAA TACAGGGCAC 1080
TACAGTTCAG ACAATACAAC AAGAGCGTCC ACGAGGTTAA TCTGA

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Seq ID NO: 580 Protein sequence  
 Protein Accession #: NP\_057276.2

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DRENDLFLCD TMTCKFDGEC LRIGDVTVCV CQFKCNNDYV PFCGNSGESY QNECYLRQAA 120
CKQQSEILV SEGSCATDAG SGSGDVHEG SGETSQKETS TCDICQFAE CDEDAEDVWC 180
VCNIDCSQTN FNPLCASDGK SYDNACQIKE ASCQKQEKIE VMSLGRQDN TTTTTSKSEDG 240
HYARTDYAEN ANKLEESARE HHIPCEPHYN GFOMHGKCEH SINMQEPSCR CDAGYTQGH 300
EKKDYSLVY VPGPVRFPYV LIAAVIGTIQ IAVICVVVLC ITRKCFRPNR IHQKQNTGH 360
YSSDNTTRAS TRLI

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Seq ID NO: 581 DNA sequence  
 Nucleic Acid Accession #: S78203.1  
 Coding sequence: 1..2190

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TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCCTGTATT TCCTGCACTG GAATGAAGAT 240
ACCTCCACAT CTATATACCA TGCCTTCAGC AGCCTCTGTT ATTTTACTCC CATCTGGGA 300
GCAGCCATTG CTGACTGTGT GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCCTTGGTG 360
TATGTGCTTG GCCATGTGAT CAAGTCCTTG GGTGCCCTTAC CAATACTGGG AGGACAAGTG 420
GTACACACAG TCCTATCATT GATCGGCTTG AGTCTAATAG CTTTGGGGAC AGGAGGCATC 480
AAACCCGTGT TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAAAACATG AGAGGAACGG 540
ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATT 600
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TTTGGAGTTC CAGGACTGCT CATGGTAATT GCATTTGTTG TGTTTGCAAT GGGGAAGCAAA 720
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TTTGCTATT CCAATGTTT CAAGAACCGT TCTGGAGACA TTCCAAAGCG ACAGCACTGG 840
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CGGACACAGA TGCAAGTTCT AAATCCCTTT CTGTTCTTAA TCTTCATCCC GTTGTGTGAC 1080
TTTGTCAATT ATGCTCTGTT CTCCAAGTGT GGAATTAAT TCTCATCACT TAGGAAATG 1140
GCTGTTGGTA TGATCTAGC GTGCTGGCA TTTGCACTG CGGCAGCTGT AGAGATAAAA 1200
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5 ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGTT 1560  
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 TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC 1800  
 ATTCACGCCA ACAAAATGTC CATTGCGTGG CAGTACCAC AATATGCCCT GGTACAGCT 1860  
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 10 CTGTGTGTGG CACAGTTCAG TGGCCTGGTA CAGTGGGCGG AATTCATTTT GTTTCTCTGC 2040  
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Seq ID NO: 582 Protein sequence  
 Protein Accession #: AAB34388.1

1 11 21 31 41 51  
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 YVLGHVIKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QFEKHAHER 180  
 TRYFSVFYLS INAGSLISTF ITPMLRGDVQ CFGEDCYALA FGVPGLLMVI ALVVFAFGSK 240  
 IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKQHW LDWAAEKYPK QLIMDVKALT 300  
 25 RVLFYLIPLP MFWALLDQGG SRWTLQAIRN NRNLGFFVLQ PDQMQLVNPFL LVLFIFPLFD 360  
 FVIYRLVSKC GINFFSLRKM AVGMILACLA FAVAAAVEIK INEMAPAQSG POEVFLQVLN 420  
 LADDEVKVTY VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDFHFLKY HNLSLYTEHS 480  
 VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540  
 EDYVSAYRT VQRGEYPAHV CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQANKIED 600  
 IPANKMSIAW QLPQYALVTA GEVMFSVTGL EFSYSQAPSS MKSVLQAAWL LTIAGVNIIV 660  
 30 LVVAQPSGLV QWAEFLFSC LLLVICLIFS IMGYIYVPVK TEDMRGPADK HIPHIQNMNI 720  
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Seq ID NO: 583 DNA sequence  
 Nucleic Acid Accession #: NM\_032642.1  
 Coding sequence: 184..1263

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 ACCATGCCCA GCCTGTCTGT GCTGTTCACG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT 240  
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 50 ACCTGCGGCT GCAGCGGAC GCGCGGCGCC AAGGACCTGC CCGCGGACTG GCTGTGGGGC 660  
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 70 GGAAACGCTC CTTCCTTAAA ATGAGAAGTC CAAGGTCAAT TCTGGCCAG TGACCAACAGA 1860  
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 GGTTCACTAG CTCTACCTG AAGAGGAAAG GGGGCCATTT GACCTGACAT GTCAGGAAAG 1980  
 CCCTAAACTG AATGTTTGGC CTTGGGCTGC AGAAGCCAGG GTGCAATGAC AGGCTCGTG 2040  
 GACGTTATAC TGTCTTCCCC CACCCCGGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100  
 75 CTCCACCGAG GGAGGCTTCA CAAACACAG GACGCTGCAA CGGCTCAGGC TGGCGGGCCC 2160  
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Seq ID NO: 584 Protein sequence  
 Protein Accession #: NP\_116031.1

1 11 21 31 41 51  
 80 MPSLLLLFTA ALLSSWAQLL TDANSWWSLA LNPVQRPEMF IIGAQPVCQSQ LPGLSPGQRK 60  
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SAAGVVNAIS RACREGELST CGCSRTARPK DLPRDMLWGG CGDNVEYGYR FAKEFVDARE 180  
 REKNFAKGSE EQGRVLMNLIQ NNEAGRRVAV KMADVACKCH GVSQSGSLKT CWLQLAEPK 240  
 VGDRLEKEYD SAAANRVTRK GRLELVNSRF TQPTPEDLVY VDSPDYCLR NESTGSLGTQ 300  
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Seq ID NO: 585 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1479

1 11 21 31 41 51  
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 TCCAACCCCG TGGTCTGCAC GCAGCCCAA TCCCATCCG GGACAGTGTG CACCTCAAAG 240  
 ACTAAGAAAG CACTGTGCAT CACCTTGACC CTGGGGACCT TCCTCGTGGG AGCTGCGCTG 300  
 GCCGCTGGCC TACTCTGGAA GTTCATGGGC AGCAAGTGCT CCACTCTGG GATAGAGTGC 360  
 GACTCTCAG GTACCTGCAT CAACCCCTT AACTGGTGTG ATGGCGTGTG ACACCTGCCC 420  
 GGCGGGGAGG AGGAGAATCG GTGTGTTCCG CTCTACGGAC CAAACTTCAT CCTTCAGGTG 480  
 TACTCATCTC AGAGGAAGTC CTGGCACCTT GTGTGCCAAG ACGACTGGAA CGAGAACTAC 540  
 GGGCGGGCGG CTGCAAGGGA CATGGGCTAT AAGAATAATT TTTACTCTAG CCAAGGAATA 600  
 GTGGATGACA GCGGATCCAC CAGCTTTATG AAAGTGAACA CAAGTGCCGG CAATGTCGAT 660  
 ATCTATAAAA AACTGTACCA CAGTGATGCC GTTCTTCAA AAGCAGTGGT TTCTTTACGC 720  
 TGTATAGCCT GCGGGGTCAA CTGAACTCA AGCCGCCAGA GCAGGATCGT GGGCGGCGAG 780  
 AGCGGCTCCG CGGGGGGCTG GCCCTGGCAG GTCAAGCTGC ACGTCCAGAA CGTCCACGTG 840  
 TGCGGAGGCT CCATCATCAC CCCCGAGTGG ATCGTGACAG CCGCCCACTG CGTGGAAAAA 900  
 CCTCTTAAAC ATCCATGGCA TTGGACGGCA TTTGCGGGGA TTTTGAGACA ATCTTTTCATG 960  
 TTCTATGAGG CGGATACCA AGTAGAAAAA GTGATTTCTC ATCCAAATTA TGACTCCAAG 1020  
 ACCAAGAACA ATGACATTGC GCTGATGAAG CTGCAGAAC CTCTGACTTT CAACGACCTA 1080  
 GTGAACACAG TGTGTCTGCG CAACCCAGGC ATGATGCTGC AGCCAGAACA GCTCTGCTGG 1140  
 ATTTCCGGGT GGGGGGCCAC CGAGGAGAAA GGAAGACCT CAGAAGTGTG GAACGCTGCC 1200  
 AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGTCTATGA CAACCTGATC 1260  
 ACACAGACCA TGATCTGTGC CGGCTTCCTG CAGGGGAACG TCGATTCTTG CCAGGGTGAC 1320  
 AGTGGAGGGC CTCTGCTCAC TTCGAAGAAC AATATCTGGT GGCTGATAGG GGATACAAGC 1380  
 TGGGGTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGGTATTC 1440  
 ACGACTGGA TTTATCGACA AATGAGGGCA GACGGCTAA

Seq ID NO: 586 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
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 MALNSGPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTA 60  
 SNPVVCTQPK SPFGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLMKFMG SKCSNSGIEC 120  
 DSSGTACNPS NWCODVSHCP GGEDENRCVR LYGNPFIQV YSSQRKSWHP VCQDDWENY 180  
 GRAACRDMGY KNFYSQGI VDSGGTSFM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240  
 CIACGVNLNS SRQSRIVGGE SALPGAHPWQ VSLHVQNVHV CGSGIITPEW IVTAAHCVEK 300  
 PLNNFHWHTA FAGILRQSFY FYGAGYQVEK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360  
 VKFVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNL 420  
 TPAMICAGFL QGNVDSQCGD SGGPLVTSKN NIWNLIGDTS WSGCAKAYR PGVYGVNVMVF 480  
 TDWIYRQMR A DG

Seq ID NO: 587 DNA sequence  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57..1535

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 CGGAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCGAC TGTCTACGAG GTGCATCCGG 180  
 CTCAGTACTA CCGCTCCCCC GTGCCCCAGT ACGCCCGAG GGTCTGAGC CAGGCTTCCA 240  
 ACCCCGTGCT CTGCACGCG CCCAAATCCC CATCGGGGAC AGTGTGCACC TCAAGACTA 300  
 AGAAGACAT GTGCATCACC TTGACCTGCG GGAACCTTCT CGTGGGAGCT GCGCTGGCGG 360  
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGTCTCAA CTCTGGGATA GAGTGCAGCT 420  
 CCTCAGTAC CTGCATCAAC CCTCTAACT GGTGTGATGG CGTGTACAC TGCCCGCGCG 480  
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 CATCTCAGAG GAAGTCTGCG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 GGGCGGCTG CAGGGACATG GGCATATAAGA ATAAITTTTA CTCTAGCCAA GGAATAGTGG 660  
 ATGACACGCG ATCCACGAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720  
 ATAAAAAAT GTACCAAGT GATGCTGTGT CTTCAAAAGC AGTGGTTTCT TTAGCGTGT 780  
 TAGCTCCGGG GGTCACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GTGAGAGCG 840  
 CGCTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCAGCT CCAGAACGTC CACGTGTGCG 900  
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960  
 TTAACAATCC ATGGCATTGG ACGGCATTTC CGGGGATTTT GAGACAATCT TTCATGTTCT 1020  
 ATGGAGCCGG ATACCAAGTA CAAAAGTGA TTTCTCATCC AAATATGAC TCCAAGACCA 1080  
 AGAACATGA CATTCGCTGC ATGAAGCTGC AGAAGCTCT GACTTTCAC GACCTAGTGA 1140  
 AACCAGTGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200  
 CGGGGTGGGG GGCACACGAG GAGAAAGGGA AGACCTCAGA AGTGTCTGAC GCTGCCAAGG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAA CTGATCACAC 1320  
 CAGCCATGAT CTGTGCGGCG TTCTGTCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG 1380  
 GAGGCGCTCT GGTCACTTCG AACAAACAATA TCTGTGGGCT GATAGGGGAT ACAAGCTGGG 1440  
 GTTCTGCGTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTACGG 1500  
 ACTGGATTTA TCGACAAATG AAGGCAACAG GCTAATCCAC ATGGTCTTGG TCCTTGACGT 1560

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CGTTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCGG TGCAATGATT ACTCTTAGAG 1620
ATGATTCAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680
TGCCATACATG TGCAGGCTGC AGTGGCTCCC CTGCCAGGCC TGCTCTCCCT AACCCCTTGT 1740
CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800
GTTGGAGGCT GCCCCCATTT AGATCTTCCT GCTGAGTCTT TCCAGGGGC CAATTTTGA 1860
TGAGCATGGA GCTGTCACTT CTCAGCTGCT GAGTGACTTG AGATGAAAA GGAGAGACAT 1920
GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGGTAGTGT 1980
TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
GATGGTGGCC AGAAATAAAG GGACCAAGCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100
AAGGGGAACA GAACATTTT TGTCTTATG GGGTGAGAAT ATAGACAGTG CCTTGGTGTG 2160
GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
CATTGGGTGG GGCTCTCTGG AGGGAGACTC AGCCTTCTCT CTCATCTCTC CTGACCCCTG 2280
TCCTAGCACC CTGAGAGATG AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
ATGTCCGCCT CTTCAGGCCT GATAGTCATT GAAATTTAG GTCCATGGGG GAAATCAAGG 2400
ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
CTGAGTTCAA AGCCATCTT

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Seq ID NO: 588 Protein sequence  
Protein Accession #: NP\_005647.1

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1 11 21 31 41 51
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SNFVVCTQPK SPSGTVCSTK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
DSSGTCINPS NWCDDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VQDDWNENY 180
GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240
CLACGVNLNS SRQSRIVGGE SALPGANFWQ VSLHVQNVHV CGSSIITPEW IVTAAHCVKE 300
PLNNPFWHTA FAGILRQSFM FYGAGYQVOK VISHFNYSK TKNNIDIALMK LQKPLTFNDL 360
VKPVLCLNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLETQRC NSRYVYDNL 420
TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIWMLIGDTS WSGGCAKAYR PGVYGNVMVF 480
TDWIYRQMK NG

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Seq ID NO: 589 DNA sequence  
Nucleic Acid Accession #: NM\_001935.1  
Coding sequence: 1..2301

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AAAACCTTACA CTCTAACTGA TTACTTAAAA AATACTTATA GACTGAAGTT ATACTCCTTA 180
AGATGGATTT CAGATCATGA ATATCTCTAC AAACAAGAAA ATAATATCTT GGTATTCAAT 240
GCTGAATATG GAACAGCTC AGTTTCTTGG GAGAACAGTA CATTGTATGA GTTTGGACAT 300
TCTATCAATG ATTATTCAT ATCTCTGAT GGGCAGTTTA TTCTCTTGA ATACAACATC 360
GTGAAGCAAT GGAGGCATTC CTACACAGCT TCATATGACA TTTATGATT AAATAAAGG 420
CAGCTGATTA CAGAAGAGAG GATTCCAAC AACAACAGT GGGTCACATG GTCACCAAGT 480
GGTCAATAAT TGGCATATGT TTGGAACAA GACATTATG TTAATAATGA ACCAAATTTA 540
CCAAGTTACA GAATCACATG GACGGGAAA GAAGATATAA TATATAATGG AATAACTGAC 600
TGGGTTTATG AAGAGGAAGT CTTCAGTGCC TACTCTGCTC TGTGGTGGTC TCCAAACGGC 660
ACTTTTTTAG CATATGCCCA ATTTAACGAC ACAGAAGTCC CACTTATTGA ATACTCTTC 720
TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAAGGCAGGA 780
GCTGTGAATC CAACTGTAAA GTTCTTGTG GTAAATACAG ACTCTCTCAG CTCAGTCACC 840
AATGCAACTT CCATACAAAT CACTGCTCCT GCTTCTATGT TGATAGGGGA TCACTACTTG 900
TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTTCTTTC AGTGGCTCAG GAGGATTTCAG 960
AACTATTCCG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACTGCTTA 1020
GTGGCACGGC AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCCTTCA 1080
GAACCTCATT TTACCTTGA TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT 1140
TACAGACACA TTTGCTATTT CCRAATAGAT AAAAAAGACT GCACATTAT TACAAAAGGC 1200
ACCTGGGAAG TCATCGGAT AGAAGCTCTA ACCAGTGATT ATCTATACTA CATTAGTAAT 1260
GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCAACCTAG TGACTATACA 1320
AAAGTGACAT GCCTCAGTTG TGAGCTGAAT CCGGAAAGGT GTCAGTACTA TTCGTGTCTA 1380
TTCAGTAAAG AGGCGAAGTA TTATCAGCTG AGATGTTCCG GTCCCTGGTCT GCCCCTCTAT 1440
ACTCTACACA GCAGCGTGAA TGATAAAGGG CTGAGAGTCC TGGAGAGCAA TTCAGCTTGT 1500
GATAAAATGC TGCAGAAATG CCAGATGCCC TCCAAAAAAC TGGACTTCAT TATTTTGAAT 1560
GAAACAAAT TTTGGTATCA GATGATCTTG CCTCTCATT TTGATAAATC CAAGAAATAT 1620
CCTCTACTAT TAGATGTGTA TGCAGGCCCA TGTAGTCAAA AAGCAGACAC TGTCTTCAGA 1680
CTGAACCTGG CCACCTACCT TGCAAGCACA GAAACATTA TAGTAGCTAG CTTTGTATGG 1740
AGAGGAAGTG GTTACCAAGG AGATAAGATC ATGCATGCAA TCAACAGAAG ACTGGGAACA 1800
TTTGAAGTTG AAGATCAAT TGAAGCAGCC AGACAATTTT CAAAATGGG ATTGTGGAC 1860
AACAAACGAA TTGCAATTTG GGGCTGGTCA TATGGAGGT AOGTAACTC AATGGTCTGT 1920
GGATCGGGAA GTGGCGTGT CAAGTGTGGA ATAGCGGTG CGCCTGTATC CCGTGGGAG 1980
TACTATGACT CAGTGTACAC AGAAGCTTAC ATGGGTCTCC CAATCCAGA AGACAACCTT 2040
GACCATTACA GAATTTCAAC AGTCATGAGC AGAGCTGAAG ATTTTAAACA AGTTGAGTAC 2100
CTCCTTATTC ATGGAACAGC AGATGATAAC GTTCACTTTC AGCAGTCAGC TCAGATCTCC 2160
AAAGCCCTGG TCGATGTTGG AGTGGATTTC CAGGCAATGT GGTATACTGA TGAAGACCAT 2220
GGAATAGCTA GCAGCACAGC ACACCAACAT ATATATACCC ACATGAGCCA CTTCAATAAA 2280
CAATGTTTCT CTTTACCTTA G

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Seq ID NO: 590 Protein sequence  
Protein Accession #: NP\_001926.1

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1 11 21 31 41 51
MKTPWKILLG LIGAAALVTI ITVPVLLNK GTDDATADSR KTYTLIDYLK NTYRLKLYSL 60

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RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQFILLEINY 120  
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 PSYRITWTGK EDIYXNGITD WYEEVFSFA YSALMWSPNG TFLAYAQFND TEVPLIEYSF 240  
 YSDESLQYPK TVRVPYPKAG AVNPTVKPFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300  
 CDVTNATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGVVGRFRPS 360  
 EPHFTLDGNS FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYIYN 420  
 EYKMPGGGRN LYKIQLSDYT KVTCLSCELN PERCQYYSVS FSKEAKYQQL RCSGPGPLPLY 480  
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDIFIILN ETKFWYQMKI PPHFDKSKKY 540  
 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RGSQYQGDKI MHAINRRLGT 600  
 FEVEDQIEAA RQFSKMGFVD NKRIAIWNS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660  
 YYDSVYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720  
 KALVDVGVDG QAMWYDDEH GIASSTAHOH IYTHMSHFIF QCFSLP

Seq ID NO: 591 DNA sequence  
 Nucleic Acid Accession #: NM\_016077.1  
 Coding sequence: 128..667

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Seq ID NO: 592 Protein sequence  
 Protein Accession #: NP\_057161.1

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Seq ID NO: 593 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1896

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 GCGGATGCGC GCGCAGCGCC GCGCCCGGGG CCGCGGGAACA CCACCCGGTT TGGGTCTGGG 180  
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Seq ID NO: 594 Protein sequence  
 Protein Accession #: FGENESH predicted

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KKTRKYDIIT TPAERVEMAP LNEEDEDED STVFDIKYRV SLPAALRRQL PGQTLTLLVP 180  
VPPPFILID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240  
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STLGLDVFCC AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPLLS 420  
THFVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480  
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAAGHEPV KRGPSSQLTR HTCPGWGITH 540  
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Seq ID NO: 595 DNA sequence  
Nucleic Acid Accession #: NM\_021614.1  
Coding sequence: 1..1740

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25 GGAGGAGGTG GCGGCGCGTC CTCCCCTCTC GCAGCCGCTG CGCGCCCGCC CGCTGTTTCG 180  
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CACGCGAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360  
CTGGGCCACC GCGCGCGCCT GTTCGAAAAG CGCAAGCGCG TCAGCGACTA CGCGCTCATC 420  
30 TTCCGCGATG TCGGCATCGT GGTCTATGTC ATCGAGACCG AGCTGTCGTG GGGCGCCTAC 480  
GACAAGCGGT CGCTGTATTCT CTTAGCTCTG AATAGCCTTA TCAGTCTCTC CAGCATCATC 540  
CTGCTCGGTC TGATCATCGT GTACCAGCC AGGAAATAC AGTTGTTTCT GGTGGACAAT 600  
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CTTGCTTCT CTATGCCCC ATCCACAACC ACCGCTGATG TGATATTTAT TTTATCTATA 780  
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45 AAAAGATAG ATCATGCAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTCT 1380  
CAATTAAGT GTGTAAAAAT GGAGCAGAGG AAATCTGAATG ACCAAGCAAA CACTTGGTG 1440  
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Seq ID NO: 596 Protein sequence  
Protein Accession #: NP\_067627.1

55 1 11 21 31 41 51  
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70 NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVIOMEQR KLNDQANTLV 480  
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Seq ID NO: 598 Protein sequence  
 Protein Accession #: NP\_057113.1

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 IVENSILAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISQEP FLLVTYLMQY 300  
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25 Seq ID NO: 599 DNA sequence  
 Nucleic Acid Accession #: NM\_000793.2  
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 Protein Accession #: NP\_000784.2

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 75 CATGCAGTGC TTCACTCTCA TTAAGACCAT GATGATCCTC TCAATTTGCT TCATCTTTCT 180  
 GTGTGGTGA GGCCTGTGAG CAGTGGGCAT CTGGGTGTC ATCGATGGGG CATCCTTTCT 240  
 GAAGATCTTC GGGCCACTGT CGTCCAGTGC CATGCAGTTT GTCAACGTGG GCTACTTCTT 300  
 CATCGCAGCC GCGGTGTGAG TCTTTGCTCT TGGTTTCTG GGTGCTATG GTGCTAAGAC 360  
 TGAGAGCAAG TGTGCCCTCG TGACGTTCTT CTTCACTCTC CTCTCATCT TCATTGCTGA 420  
 80 GGTTCGAGCT GCTGTGGTGC CCTTGGTGTG CACCACAATG GCTGAGCACT TCCTGACGTT 480  
 CCTGTGTAGT CTGCGCATCA AGAAAGATTA TGGTTCACG GAAGACTTCA CTCAGTGTG 540  
 GAACCCACC ATGAAAGGGC TCAAGTGTG TGGCTTCACC AACTATACGG ATTTTGAGGA 600  
 CTCACCTTAC TTCAAAGAGA ACAGTGCTCT TCCCTCATTC TGTGCAATG ACAACGTCAC 660  
 CAACACAGCC AATGAAACCT GCACCAAGCA AAGGCTCAC GACCAAAAAG TAGAGGGTTG 720  
 CTTCAATCAG CTTTGTATG ACATCCGAAC TAATGCACTC ACCGTGGGTG GTGTGGCAGC 780

5 TGGAAATTGGG GGCCTCGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT 840  
 ACAATAAGTC CACTTCTGCC TCTGCCACTA CTGCTGCCAC ATGGGAACCTG TGAAGAGGCA 900  
 CCCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACAAATGTCA CTGGGGCCAG 960  
 AATGGACCTG CCCTTTCTGC TCCAGACTTG GGGCTAGATA GGGACCACTC CTTTATAGGCG 1020  
 ATGCCTGACT TTCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080  
 GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAACC CTTGATATGC CCCTAGGCC 1140  
 TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200  
 AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC 1260  
 TGTACAATG TTAATAAA

Seq ID NO: 604 Protein sequence  
 Protein Accession #: NP\_005718.1

15 1 11 21 31 41 51  
 MQCPSFIKTM MILFNLLIFL CGAALLAVGI WVSIDGASPL KIFGPLSSSA MQFVNVGYFL 60  
 IAAGVVVFAL GFLGCTGAKT ESKCALVTFE FILLIFIAE VAAAVVALVY TMAEHFLL 120  
 LVVPAIKDXY GSGEDFTQVW NITMGLKCC GFNTYDFED SPYFKNSAF PPFCCNDNV 180  
 20 NTANETCTEQ KAHDQKVEGC FNQLLYDIRT NAVTVGGVAA GIGGLELAAM IVSMYLYCNL 240  
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Seq ID NO: 605 DNA sequence  
 Nucleic Acid Accession #: NM\_000729.2  
 Coding sequence:

25 1 11 21 31 41 51  
 GGCTCAGCTG CCGGGCTGCT CCGGTTGGAA ACGCCAAGCC AGCTGCCGTC CTAATCCAAA 60  
 AGCCATGAAC AGCGGGGTGT GCCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120  
 30 GAGCAGCCGG GTGCTCCCGG CAGATCCCGG GGGCTCCGGG CTGCAGCGGG CAGAGGAGGC 180  
 GCGCCGTAGG CAGCTGAGGG TATCGCAGAG AACCGATGGC GAGTCCCGAG CGCACCTGGG 240  
 CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CTTCTGGGAC GAATGTCCAT 300  
 CGTTAAGAAC CTGCAGAAC TGGACCCGAG CCACAGGATA AGTGACCGGG ACTACATGGG 360  
 CTGGATGGAT TTGGGCGTGC GCAGTGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420  
 35 GCGCCATCA GCGCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA 480  
 TCACACTCAT AACTCATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540  
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACAGCT CACCAGAAGT 600  
 TGTCAAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTGTG 660  
 40 TATGCTATTA AAGTGATTTC ATTCGTCC

Seq ID NO: 606 Protein sequence  
 Protein Accession #: NP\_000720.1

45 1 11 21 31 41 51  
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRQLRVSRQT DGESEHLGA 60  
 LLARYIQQAR KAPSGRMSIV KNLQNLDPFH RISDRDYMGW MDFGRRSAP EYEPS

50 Seq ID NO: 607 DNA sequence  
 Nucleic Acid Accession #: NM\_001423.1  
 Coding sequence: 219..692

55 1 11 21 31 41 51  
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 CAGGGCTGCT GCCAGCACCT GCCACTCAGA GCGCCTCTGT CGCTGGGACC CTTGAGAACT 180  
 CTCTTTGCTC ACAAGTTACC AAAAAAATAA GAGCCAACAT GTTGGTATTG CTGGCTGGTA 240  
 60 TCTTTGTGGT CCACATCGCT ACTGTTATTA TGCTATTGTT TAGCACCAAT GCCAATGTCT 300  
 GGTGTGTTTC CAATACGGTA GATGCATCAG TAGGTCTTTG GAAAACTGT ACCAATCATTA 360  
 GCTGCAGTGA CAGCCTGTCA TATGCCAGTG AAGATGCCCT CAGACAGTG CAGGCCTTCA 420  
 TGATTCTCTC TATCATCTTC TGTGTCTTTC CCCTCCTGGT CTTCTGTGTC CAGCTCTTCA 480  
 CCATGGAGAA GGGAAACCGG TTCTTCTCT CAGGGGCCAC CACACTGGTG TGCTGGCTGT 540  
 GCATTCTTGT GGGGGTGTCC ATCTACACTA GTCATATGCG GAATCGTGAT GGAACGCACT 600  
 65 ATCACCACGG CTATTCTTAC ATCCTGGGCT GGATCTGCTT CTGCTTCAGC TTCTCATCTG 660  
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 GGTGGGGAGG AGGAAGCCGT TGAATCTGGG AGGGAAGTGG AGGTCTCTGT ACAGGAAAAA 780  
 COGAGATAGG GGAGGGGGGA GGGGGAAGCA AAGGGGGGAG GTCAATCCC AACCAATTAC 840  
 70 TGAGGGGATT CTCTACTGCC AAGCCCTGTC CCTGGGGAGA AAGTAGTTGG CTAGTACTTT 900  
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 75 TCTGACCCAA AGCAAAACAT CACATTCCAG TCTGAAGTGC CTACTGGGGG GCTTTGGGCT 1200  
 GTGAGCCATT GTCCCTCTTT GGAACAGATA TTTAGCTCTG TGGAAATCAG GTACAAAATG 1260  
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 CTTTTCACAA TGGAAACCT GGGGGATGGT CAGAGCCAG TCGAGACCTC ACACAGGCT 1380  
 GTCCCTCATG GAGACCTCAT GCCATGGTCT TTGCTAGGCC TCTTGCTGAA AGCCAAGGCA 1440  
 80 GCTCTTCTGG AGTTTCTCTA AAGTCACTAG TGAACAATTC GGTGGTAAAA GTACCAACA 1500  
 AACTATGGGA TCCAGGGGGC AGTCTTGCAA CAGTGCCATG TTAGGGTTAT GTTTTATGGA 1560  
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 TCAATGTAGC ACAATCCTAT TACTCTTCTT CTAACATTTT TGAGGAAGTT TTGTCTAATT 1680  
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5 GGAAGCTGAT TAAACACAC ATAAACCAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860  
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 GCATTCCAG GAAATACGA AATCCCATG AGATAAATAA AATATAGGT GATGGGCAGA 1980  
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 TAAGCAGCA TTGCTTTGCC CTGGAGCAGC TATTTAAGC CATCTCAGAT TCTGTCTAAA 2160  
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 TGAGACATCT TGCCTACTTT TCTTTATTAG CTTTCTCCTC ATCCATTCT TTTATACCTT 2280  
 TCCTTTTTGG GGAATGTGTA TGCCATGATT TTTGGTATTT ATGTAAAGG ATTATTACTA 2340  
 ATTCTATTTC TCTATGTTTA TTCTAGTTAA GGAATGTGT AGGGCAAGCC ACCAAATTAC 2400  
 CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAAACTGTGG GAAGATGAAC TTTGTCTATA 2460  
 TGATTTTATT ATCAGATGAT TATAGAAGGC TGTCTTAGTG CAAAAACAT ACTTACATTT 2520  
 CAGACATATC CAAAGGGAAT ACTCACATT TGTTAAGAAG TTGAACTATG ACTGGAGTAA 2580  
 ACCATGTATT CCCTTATCTT TTAATTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTGC 2640  
 ATTACTCTGG TGGATTGTTC TAGTACTGTA TTGGGCTTCT TCGTTAATAG ATTATTTTAT 2700  
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 TTCTGATCC CTTCAAAAA AAAAAA

20 Seq ID NO: 608 Protein sequence  
 Protein Accession #: NP\_001414.1

25 1 11 21 31 41 51  
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 LKTVQAFMIL SIIFCVIALV VFVQLFTME KGNRPFLSGA TTLVWCILIL VGVSIYTSY 120  
 ANRDGTQYHH GYSYILGWIC FCFSTIIGVL YLVLRKK

30 Seq ID NO: 609 DNA sequence  
 Nucleic Acid Accession #: NM\_004961.2  
 Coding sequence: 55..1575

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 CCTCAGACTG AATCAAGAA TGAAGCCTCT TCCCGTGATG TTGTCTATGG CCCCAGCCC 180  
 CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTGAGAC TGAGACTGGG 240  
 AGCAGAGTTG GCAAACTGCC AGAAGCCTCT CGCATCTGA ACACATCTCT GAGTAATTAT 300  
 GACCACAAAC TGCGCCCTGG CATTGGAGAG AAGCCCACTG TGGTCACTGT TGAGATCGCC 360  
 GTCAACAGCC TTGGTCTCTC CTCTATCCTA GACATGGAAT ACACCATGTA CATCATCTTC 420  
 TCCAGACCTT GGTACGAGCA AGCCTCTGT TACAACGACA CCTTGAGTTC TCTGTCTCTG 480  
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 GTGTTGTACA CAATTAGGAT GACCATTGAT GCCGGATGCT CACTCCACAT GCTCAGATT 660  
 CCAATGGATT TCTCATCTTG CCTCTATCT TTCTTAGCT TTTCTTATCC TGAGAAATGAG 720  
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 TTCCAGTTTG ATTTTACAGG AGTGAGCAAC AAAACTGAAA TAATCAACAC CCCAGTTGGT 840  
 GACTTCATGT TCAATACGAT TTTCTTCAAT GTGAGCAGGC GGTTTGGCTA TGTGTCTTT 900  
 CAAACTATG TCCCTTCTTC CGTGACCAGC ATGCTCTCTC GGGTTTCCIT TTGGATCAAG 960  
 ACAGAGTCTG CTCCAGCCCG GACCTCTCTA GGGATCACCT CTGTTCTGAC CATGACCAGC 1020  
 TTGGGCACTT TTCTCTGTAA GAATTTCCCG CGTGTCTCTC ATATCACAGC CTGGATTTC 1080  
 TATATGCCCA TCTGCTTGT CTCTGCTTC TGCGCTCTGT TGGAGTTTGC TGTGCTCAAC 1140  
 TTCTGATCT ACACACAGAC AAAAGCCCAT GCTTCTCTTA AACTCCGCA TCCTCGTATC 1200  
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 GAAGCTTTTG TGTGCCAGAT TGTCAACACT GAGGGAAGTG ATGGAGAGGA GCGCCCGTCT 1320  
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 TACTCGAGAG TTGTTTCTCC AGTGACTTTC TTCTTCTCA ATGTCTCTA CTGGCTTGT 1560  
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 AGTTTTCTCT GCCCATTTCC CAAACAGAA GCTTGCAGAG GGTTTGTCTT TGTGCCCT 1740  
 CTCCTCTACC TGGCCCATTC ACTGAGTCTT CTCAGCAGAC CATTCAAAT TATTAATAAA 1800  
 TGGGCCACCT CCCTCTCTCT CAAGGAGCAT CCGTGATGCT CAGTTTCAA AACCAAGCC 1860  
 ACTTAGTGAT CAGCTCCCTA AAACCATGCC TAAGTACAGG CGGATTAGCT ATCTTCCAAC 1920  
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 CTTTGGCCCC AGTTCTGGCC TCAGCCTCAA AGTGCAACGA CTAGTTGCTT GCCTATACCT 2040  
 GGCACCTCAT TAAGATGCTG GGCAGCAGTA TAACAGGAGG AAGAGATCCC TCTCCTTTGG 2100  
 TCAGATTATT ATGTTCTCAG TTCTCTCTCC CTGCTACCCC TTTCTCTGCA GATAGATAGA 2160  
 CACTGGCAAT ATCCCTTTAG GAAGAGGGGG GGGCAGCAAG AGAGCCTATT TGGGACAGCA 2220  
 TTCTCTCTC TCTGCTGCTG TGACATCTCC CTCTCCTTGC TGGCTCCATC TTTGCTCTGC 2280  
 ACTACCAATT CAATGCCCTT CATCCAATGG GTATCTATTT TTGTGTGTGA TTATAGTAAC 2340  
 TACTCCCTGC TTTATAAGCC ACCCTCTTCC TTCTCTTTGA CCGCTGTGAC TCTTTCTGTA 2400  
 ACTTTCCAG TGACTTCCC TAGCCCTGAC CCAGGCACTA GGCCTTGGT ACTTCTCTGG 2460  
 GCCAGAAAC TAAGAAACT CGCTTTGCA ACAGGCATTA CTGCCATTG ATTGGTGGCC 2520  
 ACCAGGGCA CACTGTGCGA GTTCTATCAC TTGCTTGACC CTGGAGCCCA TAAACAGTC 2580  
 CACTGTATA CCGGGGGCAC TCTAACATC ACAATCAATC AATCAAATTC CCTTAAATTT 2640  
 GTATGGCAT GGAACCTTTG CAAAGCACTT TTGACAAGTT GTGTCTGATT GGAGCTTCAT 2700  
 GATAGCCTTG TGACATCTTT AGGGCAGGAT TCTATCCCC ATTTGTCAGA TGAACCCCT 2760  
 GAGTCACAGA TTTCTGTGGG ACTGTGGATC TCACTGGAAG CTATCCAAGA GCCACTGTG 2820  
 ACCTTCTAGA CCACATGATA GGGCTAGACA GCTCAGTTCA CCAATGATTCT CTCTGTCTAC 2880  
 CTCTGCTGGC ACACAGTGG CAAGGCCAGC AATGGGAGCC TCTCTTAGC TCAATTTCTG 2940  
 GGCTGAGGT GCTCAGACTG CCCCAGAT CAAATCTCTC CTGGCTGTAG TAACCCAGTG 3000  
 GAATGAATTT GGACATGCC CAATGCTCT ATATGCTAAG TGAATCTGT GTCTGTAAT 3060

TGTTGGGGGG TGGATAGGGT GGGGTCTCCA TCTACTTTTT GTCCACATCA TCTGAAATGG 3120  
GGAAATATGT AAATAAATAT ATCAGCAAAG CAAAAGAAA AAAAAAAA

5 Seq ID NO: 610 Protein sequence  
Protein Accession #: NP\_004952.1

	1	11	21	31	41	51	
10	MLSKVLPLVLL	GILLILQSRV	EGPQTESKNE	ASSRDVVYGP	QPQPLENQLL	SEETKSTETE	60
	TGSRVKGKLE	ASRIILNTLS	NYDHKLRLPGI	GEKPTVVIVE	IAVNSLGLPLS	ILDMEYTIID	120
	IFSQTWYDER	LCYNDTFESL	VLNGNVVSQL	WIPDTFFRNS	KRTHHEITM	PNQMVRIYKD	180
	GKVLTYTIRM	IDAGCSLHML	RFPMDSHSCP	LSFSSFSYPE	NEMIYKWNF	KLEINEKNSW	240
	KLFOFDFTGV	SNKTEIITTP	VGDFMVTIF	FNVSRRFGYV	AFQNVVPSSV	TTMLSNVSEF	300
15	IKTESAPART	SLGITSVLTM	TTLGTFSRKN	FPRVSITAL	DFYIAICFVF	CFCALLEPAV	360
	LNFLIYNQTK	AHASPRLRHP	RINSRAHART	RARSACARQ	HQEAFCQIV	TTGSDGEER	420
	PSCSAQQPPS	PGSPGPRSL	CSKLACCEWC	KRFKIFYCMV	PDCEGSTWQQ	GRLCIHVYRL	480
	DNYSRVVFPV	TFFFFNVLVW	LVCLNL				

20 Seq ID NO: 611 DNA sequence  
Nucleic Acid Accession #: NM\_021984.1  
Coding sequence: 572..1753

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	CAGAGAAGTG	CTCAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAT	GACCACAGCG	180
	GTGTAAGAA	AGCCAAATCA	AGGACCGGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
	CACTGCCTCC	CAGCAAAGGC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TCGAGGGACC	300
30	TCAGACTGAA	TCAAAGAATG	AAGCCTCTTC	CCGTGATGTT	GTCTATGGCC	CCAGCCCCA	360
	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCTCTA	GTAATTATGA	480
	CCACAAACTG	CGCCTTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTTG	AGATCTCCGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCTTAGA	CATGGAATAC	ACCATGACAA	TCATCTTCTC	600
35	CCAGACCTGG	TACGACGAAC	GCCTCTGTTA	CAACGACACC	TTTGAGTCTC	TGTTCTGAA	660
	TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
	CCACGAGCAT	GAGATCACC	TGCCCAACCA	GATGGTCCGC	ATCTACAAGG	ATGGCAAGGT	780
	GTGTATACCA	ATTAGCATGA	CCATTGATGC	CGGATGCTCA	CTCCACATGC	TCAGATTCTC	840
40	AATGGATTCT	CATCTTGCC	CTCTATCTTT	CTCTAGCTTT	TCCTATCTTG	AGAATGAGAT	900
	GATCTACAAG	TGGGAAAATT	TCAAGCTTGA	AATCAATGAG	AAGAAGCTCT	GGAAGCTCTT	960
	CCAGTTGGAT	TTTACAGGAG	TGAGCAACAA	AAGTGAATA	ATCACAACCC	CAGTTGGTGA	1020
	CTTCTATGTC	ATGACGATT	TCTTCAATGT	GAGCAGCGG	TTTGGCTATG	TTCCTTTTCA	1080
	AAACTATGTC	CCTTCTCCG	TGACCAAGAT	GCTCTCTGG	GTTCCTTTT	GGATCAAGAC	1140
45	AGAGTCTGCT	CCAGCCCGGA	CCTCTCTAGG	GATCACTCT	GTTCGACCA	TGACCAAGTT	1200
	GGGCACTTTT	TCTCTGAAGA	ATTTCCTGCG	TGTCTCTCT	ATCAGAGCCT	TGGATTCTTA	1260
	TATGCGCATC	TGCTTGTGCT	TCTGCTTCTG	CGCTCTGTTG	GAGTTTGCTG	TGCTCAACTT	1320
	CCTGATCTAC	AACACAGCAA	AAGCCCATGC	TTCTCTCTAA	CTCCGCCATC	CTCGTATCAA	1380
	TAGCCGTGCC	CTTCTTCCGA	CCCGTGACAG	TTCCCGAGCC	TGTGCCCGCC	AACATCAGGA	1440
	AGCTTTTGTG	TGCCAGATTG	TCACCACTGA	GGGAAGTGAT	GGAGAGGAGC	GCCCGTCTTG	1500
50	CTCAGCCGAG	CAGCCCTCTA	GCCCAAGTAG	CCCTGAGGGT	CCCGCCAGCC	CTCTGTCCAA	1560
	GCTGGCCTGC	TGTGAGTGGT	GCAAGCGTTT	TAAGAAGTAC	TTCTGCAATG	TCCCGAGATT	1620
	TGAGGGCAGT	ACCTGCGCAG	AGGCCCGCCT	CTGCATCCAT	GTCTACCGCC	TGGATAACTA	1680
	CTCGAGATGT	GTTTTCCGAG	TGACTTTCTT	CTTCTTCAAT	GTGCTCTACT	GGCTTGTTTG	1740
	CCTTAATCTG	TAGTATCCAG	CTGGTACCCT	GTGGGGCAAC	CTCTCCAGTT	CCCCAGGAGG	1800
55	TCCAAAGCCC	TTGCCAAGGG	AGTTGGGGGA	AAGCAGCAGC	AGCAGCAGGA	GCGACTAGAG	1860
	TTTTTCTGTC	CCCATTCCCC	AAACAGAAAG	TTGCAGAGGG	TTTGCTTTTG	CTGCCCTCTT	1920
	CCCTCACTGC	GCCCATCTAC	TGAGTTTCTT	CAGCAGACCA	TTTCAAAATTA	TTAATAAATG	1980
	GGCCCACTCC	CTCTTCTTCA	AGGAGCATCC	GTGATGCTCA	GTGTTCAAAA	CCACAGCCAC	2040
60	TTAGTGATCA	GCTCCCTAAA	ACCATGCCTA	AGTACAGCGG	GATTAGCTAT	CTTCCAACAA	2100
	TGCTGACCA	CAGACAATTA	CTGCATTTT	CCAGAAGCCC	ACTATTGCC	TTGCACTGCT	2160
	TTCCGCCCAG	TTCTGGCCTC	AGCCTCAAAG	TGCACCGACT	AGTTGCTTGC	CTATACCTGG	2220
	CACCTCATT	AGATGCTGGG	CAGCAGTATA	ACAGGAGGAA	GAGATCCCTC	TCCTTTGGTC	2280
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	CTGGCATTAT	CCCTTTAGGA	AGAGGGGGGG	GCAGCAAGAG	AGCCTATTTG	GGACAGCATT	2400
65	CCTCTCTCTC	TGCTGCTGTG	ACATCTCCCT	CTCCTTGCTG	GCTCCATCTT	TGCTCTGCAC	2460
	TACCAATTCA	ATGCCCTTCA	TCCAATGGGT	ATCTATTTTT	GTGTGTGATT	ATAGTAACCTA	2520
	CTCCCTGCTT	TATATGCCAC	CCTCTCTCCT	CTCTTGACCC	CCTGTGACTC	TTTCTGTAA	2580
	TTTCCAGTGT	ACTTCCCTCA	GCCCTGACCC	AGGCACTAGG	CCTTGGTGAC	TTCTGGGGGC	2640
70	CAAGAACTA	AGGAACTCG	GCTTTGCAAC	AGGCATTACT	CGCCTATTAT	TGGTGCCAC	2700
	CCAGGGCACA	CTGTGAGAGT	TCTATCACTT	GCTTGACCCC	TGGACCCATA	AACCACTCCA	2760
	CTGTTATACC	CGGGGCATC	TAAACATCAC	AATCAATCAA	TCAAATTCCT	TTAAATTTGT	2820
	ATGGCATCTG	AATTTGGGCA	AAGCACTTTT	GACAAGTTGT	GTCTGATTGG	AGCTTCATGA	2880
	TAGCCTTTGT	ACATCTTAG	GGCAGGATT	TTATCCCAT	TTTGAGATG	AAAAACCTGA	2940
	GTACAGATT	TCTGTGGGAC	TGTGGATCTC	ACTGGAAGCT	ATCCAGAGC	CCACTGTAC	3000
75	CTTCTGAC	ACATGATAGG	GCTAGACAGC	TCAGTTACCC	ATGATTCTCT	TCTGTCACT	3060
	CTGCTGGCAC	ACCACTGGCA	AGGCCAGAA	TGGCGACCTC	TCCTTAGCTC	AATTTCTGGG	3120
	CCTGAGGTGC	TCAGACTGCC	CCCAAGATCA	AATCTCTCCT	GGCTGTAGTA	ACCCAGTGG	3180
	ATGAATTGG	ACATGCCCCA	ATGCTTCTAT	ATGCTAAGTG	AAATCTGTGT	CTGTAATTGG	3240
80	TGCGGGGGTG	GATAGGGTGG	GGTCTCCATC	TACTTTTGT	CACCATCATC	TGAAATGGGG	3300
	AAATATGTAA	ATAAATATAT	CAGCAAAGC				

Seq ID NO: 612 Protein sequence  
Protein Accession #: NP\_068819.1



1 11 21 31 41 51  
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5 MVRKYDKGV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWFNFLE 120  
INEKNSWKLQ QLDFTGVSNK TEIITTPVGD FMVTIIFPNV SRREGVYVAFQ NYVPSSVTIM 180  
LSWVSWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IAICFVFCPC 240  
ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300  
GSDGEERPSC SAQPPSPSGS PEGPRSLCSK LACCWCKRF KKYFCMVDFC BGSTWQQARL 360  
10 CHIVYRLDNY SRVVPVTF FNVLYWLVLC LNL

Seq ID NO: 613 DNA sequence  
Nucleic Acid Accession #: NM\_021987.1  
Coding sequence: 572..1657

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20 CAGAGAAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGOG 180  
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CACTGCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300  
TCAGACTGAA TCAGAAGATG AAGCCTCTTC CCGTGATGTT GTCTATGGCC CCCAGCCCCA 360  
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420  
CAGAGTTGGC AAATGCTCCG AAGCCTCTCG CATCTGAAC ACTATCTCGA GTAATTATGA 480  
25 CCACAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTTG AGATCTCCGT 540  
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35 CTCTGTCTG ACCATGACCA GGTGGGCAC CTTTCTGCT AAGAAATTTCC CGCTGTCTC 1140  
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70 GTGAAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGGTCTCC ATCTACTTTT 3180  
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Seq ID NO: 614 Protein sequence  
Protein Accession #: NP\_068822.1

75 1 11 21 31 41 51  
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80 VMTIIFPNVR RFGYVAFQNY VPSSVTMLLS WVSFWIKTES APARTSLGIT SVLTMITLGT 180  
FSRKNFPRVS YITALDFYIA ICFVFCFAL LEFAVLNFI YNQTKAHASP KLRHPRINSR 240  
AHARTRARSR ACARQHQEAF VCQIVITEGS DGEERPSCSA QPPSPSGSPE GPRSLCSKLA 300  
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Seq ID NO: 615 DNA sequence  
Nucleic Acid Accession #: NM\_021990.1  
Coding sequence: 1309..2490

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20    AAATGCCCTT TCAATTTTAC GTGTAACATT CTTTAAAAAT CTAGGTCTTG GTTTTGTGA 780
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25    TCTAGGGTCG AGGGACCTCA GACTGAATCA AAGAATGAAG CCTCTCCCG TGATGTTGTC 1080
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Seq ID NO: 616 Protein sequence  
Protein Accession #: NP\_068830.1

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INEKNSWKLQ OFDFTGVSNK TELIITPVGD FMVMTIFENV SRRFGYVAFQ NYVPSSVTIM 180
LSNVSWIKT ESAPARTSLG ITSVLMTTL GTPSRKNPFR VSYITALDFY IAI CFVFCFC 240

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Seq ID NO: 617 DNA sequence  
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Coding sequence: 26..952

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30 TTATTATTAT TTAATTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140  
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Seq ID NO: 618 Protein sequence  
Protein Accession #: NP\_004855.1

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40 EDLLTFLRAN QSNEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLEPEASRL 120  
HRALFRLSPT ASRSMDVTRP LRRQLSLARP QAPALHLRLS PFPQSQDQLL AESSSARFQL 180  
ELHLRPQAA RRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC 240  
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Seq ID NO: 619 DNA sequence  
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Seq ID NO: 620 Protein sequence  
 Protein Accession #: NP\_003970.1

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 KLVRGRKPLS LLVLGLLAVG FSLVQDVIAI EYIVLTNRT NVNVFSELSA PRNEDFVLL 180  
 LTVVLFLMAL TFLMSSFTFC GSFTGWKRHG AHYLTMLLS IAIWVANITL LMLPDFDRRW 240  
 DDTILSALA ANGVNLLAY VSPFVLLTK QRNPMDYFVE DAFCKPQLVK KSYGVENRAY 300  
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Seq ID NO: 621 DNA sequence  
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 Coding sequence: 48..851

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Seq ID NO: 622 Protein sequence  
 Protein Accession #: NP\_002414.1

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Seq ID NO: 623 DNA sequence  
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 CTGTGTTGGT GGTGGCAGCC CACAATGTTT ATCCTGTGAC CCGAGGAATT ATGTCTCAG 300  
 TGCCCTGTGA TCCAAACAGC CAGCCGCAAG TCCACTAGT TCTTGGGAAC CCACCTAGTT 360  
 TGGTGTGCAA TGTGAATGGG CAGCCTGTGC AGAAAGCTCT GAAAGAAGGC AAAACCTTGG 420  
 GGGCCATCCA GATCATCATT GGCCTGGCTC ACATCGCCT CGGCTCCATC ATGGGGAOAG 480  
 TTCTCGTAGG GGAATACCTG TCTATTTCAT TCTACGGAGG CTTTCCCTTC TGGGGAGGCT 540  
 TGTGTTTAT CATTTACGGA TCTCTCTCG TGGCAGAGA AAATCAGCCA TATTCTTATT 600  
 GCCTGCTGTC TGGCAGTTTG GGCCTGAACA TCGTCAGTGC AATCTGCTCT GCAGTTGGAG 660  
 TCATACTCTT CATCACAGAT CTAAGTATTC CCCACCCATA TGCTTACCCC GACTATTATC 720  
 CTACAGTCCA GGTGTGAAC CCTGGAATGG CGATTCTGG CGTCTGCTG GTCTTCTGCC 780  
 TCTTGGAGTT TGGCATCGCA TCGGCATCTT CCCACTTTGG CTGCCAGTTG GTCTGCTGTC 840  
 AATCAAGCAA TGTGAGTGT ATCTATCCAA ACATCTATGC AGCAAAACCA GTGATCACCC 900  
 CAGAACCGGT GACCTCACCA CCAAGTTATT CCAAGTATG CCAAGCAAT AAGTAAGGCT 960  
 ACAGATTCTG GAAGCATCTT TCACTGGGAG CAAAAGAAGT CCTCTCCCTT TTCTGGGCTT 1020  
 CCATAACCCA GTGCTTCTCT GTTCTGACAG CTGAGGAAC GTCTCTCCCA CTGTTTGTAC 1080  
 TCTCACCTTC ATTCTTCAAT TCAGTCTAGG AAACCATGCT GTTCTCTAT CAAGAAGAAG 1140  
 ACAGAGATT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGCACATG CATCAGACA 1200  
 TATGTGGGCA TCCAGCTCTT GGGCCCTTGG CACACACACA TTGCTGTGCT CTGCTGCATG 1260

TGAGCTTGTG GGTAGAGGA ACAAATATCT AGACATTCAA TCTTCACTCT TTCAATTGTG 1320  
CATTCTATTA ATAAATAGAT ACTGAGCATT CAAAAA AAAAAA

5 Seq ID NO: 624 Protein sequence  
Protein Accession #: NP\_113645.1

1 11 21 31 41 51  
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPNSQ PQVHLVPGNP PSLVSNVNGQ 60  
10 PVQKALKEGK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFPFW GGLWFIISGS 120  
LSVAAENQPY SYCLLSGSLG LNIIVSAICSA VGVILFITDL SIPHPYAYPD YYPYAWGVNP 180  
GMAISGVLLV FCLLEFGIAC ASSHFGCQLV CQSSNVSVI YPNIYAANPV ITPEVTSPP 240  
SYSSEIQANK

15 Seq ID NO: 625 DNA sequence  
Nucleic Acid Accession #: NM\_005221.3  
Coding sequence: 1..870

1 11 21 31 41 51  
20 ATGACAGGAG TGTITGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60  
TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACITT GCCCGAGTCT 120  
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCAGCG CTACTGCTCT 180  
25 CCTACTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG 240  
AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300  
TACCACAGT ACGGGGGGCG CTACACCGCG GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360  
GAAGTAGCCG AGCCCGAGGT GAGAAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC 420  
AGGACTATTT ATCTCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480  
30 TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCTCGC TGGGATTGAC ACAACACAG 540  
GTGAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AACCGGGGAG 600  
ATGCCCCCGG AGCAGAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC CCGCAGTCT 660  
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCAACC TCATGCCAC 720  
CCTCGACCT CCAACCACTC CCAGCGTCC AGCTACCTGG AGAACTCTGC ATCTGGTAC 780  
35 ACAAGTGACG CAGCTCAAT CAATCCCAC CTGCCGCCG CCGGCTCCTT ACAGCACCG 840  
CTGGCGCTGG CCTCCGGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence  
Protein Accession #: NP\_005212.1

40 1 11 21 31 41 51  
MTGVFDRVP SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSYYSF TGGAPHGYCS 60  
PTSASYGKAL NPYQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120  
45 EVTEPEVRMV NGPKPKVRKP RTIYSSPOLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180  
VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHHPAH 240  
PPTSNSQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLV

50 Seq ID NO: 627 DNA sequence  
Nucleic Acid Accession #: NM\_014420  
Coding sequence: 118..792

1 11 21 31 41 51  
55 GCACGAGAGA CGACGTGCTG AGCTGCCAGC TTAGTGGAAG CTCTGCTCTG GGTGGAGAGC 60  
AGCCTCGCTT TGGTGACGCA CAGTGCTGGG ACCCTCCAGG AGCCCCGGA TTGAAGGATG 120  
GTGGCGGCGG TCCTGCTGGG GCTGAGCTGG CTCTGCTCTC CCTGCGGAGC TCTGGTCTCG 180  
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCAATGGG CCGGAAGGG CTCACAGTGC 240  
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGGA TGAGAAGCGC 300  
60 TTCTGTGCTA CATGCTGTGG GTTGGGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360  
GGGACACTCT GTGTGAACGA TGTTTGTACT ACGATGGAAG ATGCAACCCC AATATTAGAA 420  
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA CCCAGTCCAG 480  
GAAACCAAC CCAAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540  
GGAGAAAGTT GTCTGAGAAC TTTTGAAGTGT GGCCCTGGAC TTTGCTGTGC TCGTCAITTT 600  
65 TGGACGAAAA TTTGTAAGCC AGTCTCTTTG GAGGGACAGG TCTGCTCCAG AAGAGGGCAT 660  
AAAGACACTG CTCAGCTCC AGAAATCTTC CAGCGTTGCG ACTGTGGCCC TGGACTACTG 720  
TGTGAAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780  
GAAAAGCTAT AAATATTTC AATAAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840  
A

70 Seq ID NO: 628 Protein sequence  
Protein Accession #: NP\_055235

1 11 21 31 41 51  
75 MVAALLGLS WLCSPILGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCLQPRDEK 60  
PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TIMEDATPIL ERQLDEQDGT HAEGTGHPV 120  
QENQPKRKPS IKKSQGRKGQ EGESCLRTFD CGPGLCCARH FWTKICKPVL LEGQVCSRRG 180  
HSDTAQPEI FQRCDGGL LCRSGLTSNR QHARLRCQK IEKL

80 Seq ID NO: 629 DNA sequence  
Nucleic Acid Accession #: NM\_002448.1  
Coding sequence: 241..1134

1 11 21 31 41 51

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GCGCGAGTGC TCCCGGGAAC TCTGCCTGCG CGGCGGCAGC GACCGGAGGC CAGGCCAGGC 60
ACGCCCGGAGC TGGCCTGCTG GGGAGGGGCG GGAGGCGGCG GCGGAGGGT CCGCCCGGCC 120
AGGCCCGGGG CCTTCGCGAGA GGC CGGCGCGC GCTCCAGACC CGCCCGGAGC CCATGCCCGG 180
CGGCTGGCCA GTGCTGCGGC AGAAGGGGGG GCGCGGCTCT GCATGGCCCC GGCTGCTGAC 240
ATGACTTCTT TCCCACTCGG TGTCAAAGTG GAGGACTCCG CCTTCGGCAA GCCGCGGGGG 300
GGAGCGCGGG GCCAGGCCCG CAGCGCCGCG GCGGCCACGG CAGCCGCCAT GGGCGCGGAC 360
GAGGAGGGGG CCAAGCCCAA AGTGTCCCT TCGCTCCTGC CCTTCAGCGT GGAGGCGCTC 420
ATGGCCGACC ACAGGAAGCC GGGGGCCAA GAGAGCGCCC TGGCGCCCTC CGAGGCGCTG 480
CAGGCGCGGG GTGGCTCGGC CGAGCCACTG GCGTCCCGC CGGGGTGCTG GGGAGCCCCG 540
GACGCGCCCT CTTCGCGCGG GCGGCTCGGC CATTCTCGG TGGGGGGACT CCTCAAGCTG 600
CCAGAAGATG CGCTCGTCAA AGCCGAGAGC CCGAGAAAG CCGAGAGGAC CCGTGGATG 660
CAGAGCCCCC GCTTCTCCCC GCGCGCGGCC AGCGGCTGA GCCCCACG CTGCACTCTC 720
CGCAAAACAC AGACGAACCG TAAGCCGCGG ACGCCCTTCA CCACCGCGCA GCTGCTGGCG 780
CTGGAGCGCA AGTTCGCGCA GAAGCAGTAC CTGTCCATCG CCGAGCGCGC GGAGTTCTCC 840
AGCTCGCCCT TCTCGCTGAG CAGCAGGTG AAGATATGGT TCCAGAACCG CCGCGCCAA 900
GCAAGAGAC TACAAGAGCG AGAGCTGGAG AAGCTGAAGA TGGCCGCCAA GCCCATGCTG 960
CCACCGCGCT CCTTCGCGCT CTCTTCCCT CTGCGCGGCC CGCAGCTGT AGCGCGCGG 1020
GGGGGTGCTT CGCTCTAGCG TGCTCTGCGC CCTTCCAGC GCGCGCGCT GCTGTGGCG 1080
CCCGTGGGAC TCTACAGCGC CCATGTGGGC TACAGCATGT ACCACCTGAC ATAGAGGGTC 1140
CAGGTCCCCC ACCTGTGGGC CAGCGGATTC CTCCAGCCCT GGTGCTGTAC CCGGACGCTG 1200
CTCCCTGCT CGSCACGCGC AGCCGCTTC CCTTAAACC TCACATGCT CAGTTTTCAC 1260
CTCTTGTCT CTTGAGTTCA CTCTCGAAG TCTGATCCCT GCCAAAAGT GGCTGGAAGA 1320
GTCCCTTAGT ACTCTTCTAG CATTAGATC TACACTCTCG AGTTAAAGAT GGGGAACTG 1380
AGGGCAGAGA GGTAAACAGA TTTATCTAGG GTCCCCAGCA GAATTGACAG TTGAACAGAG 1440
CTAGAGGCCA TGCTCTCTGC ATAGCTTTTC CCTGTCTGTA CACCAGGCAA GAAAAGCGCA 1500
GAGAAATCGG TGCTGACGAA TTTTGAAAT GAGAACAAAT TCAAAAAA AAAAAA 1560
AAAAAAGAAA GAAAAGAGAA AAAAAAGACT AGCCAGCCAG GAAGATGAAT CCTAGCTTCT 1620
TCCATTGGAA AATTAAAGAC AAGTTCAACA ACAAACATT TGCTCTGGG GGCAGGGA 1680
ACACAGATGT GTTGCAAAAG TAGGTTGAAG GGA

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Seq ID NO: 630 Protein sequence  
Protein Accession #: NP\_002439.1

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1 11 21 31 41 51
MTSLPLGVKV EDSAFGKPG AGAGQAPSAA AATAAMGAD EBGAKPKVSP SLLPFSVEAL 60
MADHRKPGAK ESALAPSEGV QAAGGSAQPL GVPPGSLGAP DAPSSPRPLG HFSVGLLKL 120
PEDALVKAES PEKPERTPMW QSPRFPSPPA RRLSPACTL RKHKTNRKPR TPFTTAQLLA 180
LERKFRQKY LSIAERAEFS SLSLSTETQV KIWFQNRRAK AKRLQEAELE KLMMAAKPML 240
PPAALGLSFP LGGPAAVAAA AGASLYGASG PFQRAALEVA PVGLYARVG YSMYHLT

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Seq ID NO: 631 DNA sequence  
Nucleic Acid Accession #: NM\_002557.1  
Coding sequence: 13..2049

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1 11 21 31 41 51
CAGACCATG AGATGTGGAA GCTGTTGCTG TGGGTGGGCG TGTTCTTGT GCTGAAACAC 60
CAGCATGGT CTGCCCCATA ACTCGTGTGT TATTTCACCA ACTGGGCACA CAGTCGGCCA 120
GGCCCTGCTT CGATCTTGCC CCATGACCTG GACCCCTTTC TCTGCACCCA CCTGATATT 180
GCCTTTGCTT CAATGAACAA CAATCAGATT GTTGCTAAGG ATCTCCAGGA TGAGAAAAAT 240
CTCTACCCAG AGTTCAACAA ACTAAGGAG AGGAACAGAG AGCTGAAAC ACTACTGTCC 300
ATCGGCGGGT GGAACCTTGG CACCTCAAGA TTCACCACTA TGTGTCCAC ATTTGCCAAC 360
CGTGAAGAAT TTATGTCTTC AGTTATATCC CTCTGAGGA CACATGACTT TGATGTCTCT 420
GACCTTTCTT TCTTATATCC TGGACTAAGA GGCAGCCCCA TGATGACCG GTGGACTTTT 480
CTCTCTTAA TTGAAGAGCT CCGTGTGCC TTCCGGAAGG AGGCACTGCT CACCATGCGC 540
COGAGGCTGC TGCTGTCTGC TGCTGTCTCT GGGGTCCAC ACATGTTCA AACATCTAT 600
GATGTGCGCT TTCTAGGAAG ACTCTGGAT TTCATCAATG TCTGTCTTA TGACTTACAT 660
GGAAGTTGGG AAAGGTTTAC AGGACATAAT AGCCCCCTCT TCTCTGCTC TGAAGACCCC 720
AAATCTTGG CATATGCTAT GAATTATTGG AGAAAGCTTG GGGCACCCCTC AGAGAAGCTC 780
ATCATGGGGA TCCCCACCTA TGGACGTACC TTTCGCTCC TCAAAGCCTC TAAGAATGGG 840
TTGACGGCCA GAGCGATCGG ACCAGCATCT CCAGGGAAGT ACACCAAGCA AGAAGGCTTC 900
TTGGCTTATT TTGAGATTGT TTCTTTGTC TGGGAGCGA AGAAGCACTG GATTGATTAC 960
CAGTATGTCC CGTATGCCAA CRAAGGGGAA GAGTGGGTTG GCTATGACAA TGCCATCAGC 1020
TTCAATTACA AGGCATGGTT TATAAGGCGA GAGCATTTG GGGGGGCCAT GGTGTGGACA 1080
TTGGACATGG ATGACGTGAG GGGCACTTTC TGTGGCACTG GCCCTTTCCC CCTTGTCTAC 1140
GTATTGAATG ATATCTGTGT GCGGCTGAG TTCAGTTCAA CTCTTTTACC ACAATTTTGG 1200
CTGTCACTG CTGTGAATTC TTCAGCACT GACCTGAAA GGCTGGCTGT GACCACGGCA 1260
TGGACCACTG ATAGTAAGAT TTTGCCCTCA GGAGGAGAGG CTGGGGTCACT TGAGATCCAC 1320
GGAAAGTGG CATAATATGAC TATAACCCCT AGAGGTACAA CTGTGACCCC TACAAAGGAA 1380
ACTGTATCCC TTGGAAGACA CACTGTAGCT CTAGGAGAGA AGACTGAGAT CACTGGGGCA 1440
ATGACCATGA CTTCGTGTGG TCATCAGTCC ATGACCCCTG GAGAGAAGGC CCTGACCCCT 1500
GTGGGTCTAT AATCTGTGAC CACTGGACAG AAGACCTGGA CCTCTGTGG TTATCAGTCT 1560
GTGACCCCTG GGGAAAGAC CCTGACCCCT GTGGGTCTAT AGTCTGTGAC CCCTGTGAGT 1620
CATCAGTCTG GAGCCCTGAG AGGAACGACT ATGACCCCTG TCCATTTTCA GACTGAGACC 1680
CTTAGACAGA ATACAGTGGC CCTAGAAAGG AAGGCTGTGG CCGGTGAAA GGTGACTGTC 1740
CCCTCCAGAA ACATCTCAGT CACCCCTGAA GGCAGACTA TGCCCTTAAG AGGGGAGAA 1800
TTGACTTCTG AGGTGGGCAC TCACCCAGG ATGGGTAACT TGGGTCTTCA GATGGAAGCT 1860
GAAAACAGGA TGATGCTGTG CTCCAGCCCC GTCATCCAGC TCCCGGAACA AACTCTCTTA 1920
GCTTTTGACA ACCGCTTTGT TCCCATCTAT GGAAACCATT CCTCTGTCAA CTCAGTAACC 1980
CCTCAACAGA GTCTCTTTCT TCTAAAAA GAAATCCAG AAAACTCTGC TGTGGATGAA 2040
GAAGCCTAAG CCCCTCTGGT GTCAAGAAC AGGGAAACCT CTGTCTTTT CTCTAAGTG 2100
ACATGTTGGA AGCCTTCTCA TCCCGGGGCA AAGCAGGCAT CAAAACAGA ATAGGCCAAT 2160

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CTCTTTTCCA TTAATAAAC TGTAACACA AGAACCCA

Seq ID NO: 632 Protein sequence  
 Protein Accession #: NP\_002548.1

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1	11	21	31	41	51				
MWKL	LLVVL	LVKHH	DGA	AHKL	VCYFTN	WAHSRPGPAS ILPHDLDPFL CTHLIFAFAS 60			
MNNQ	IVAIKD	LQDEK	ILYPE	FNKL	KERNRE	LKTL	LSIGGW	NFGTSRFTTM	LSTFANREKF 120
IASV	ISLLRT	HD	FDGLDLFF	LYPGL	RGS	SPM	HDRWT	FLFLI	EELLFAFRKE ALLTMRPRL 180
LSAA	VSQVPH	IVQTS	YDVRF	LGRLL	DFINV	LSYDL	HGSWE	RFTGHNSPLF	SLPEDPKSSA 240
YAMN	YWRKLG	APSEK	LIMGI	PTYGR	TFRLL	KASKN	GLQAR	AIGPASPGKY	TKQEGFLAYF 300
EICS	FVWGAK	KHWID	YQYVP	YANKG	KEWVG	YDNAI	SFSYK	AWFIRREHFG	GAMVWTLDM 360
DVRG	TPCGTG	PFPLV	VYVIND	ILVRA	EFSST	SLPQF	WLSSA	VNSSSTDPER	LAVTTAWTTD 420
SKIL	PPGGEA	GVTEI	HGKCE	NMTIT	PRGTT	VTPKT	ETVSL	GKHTVALGEK	TEITGAMTMT 480
SVGH	QSMTPG	EKALT	FPVGHQ	SVTTG	QKTLT	SVGYQ	SVTPG	EKTLTPVGHQ	SVTPVSHQSV 540
SPGG	TMTTPV	HFQTE	TLRQN	TVAPR	RKAVA	REKVT	VPSPRN	ISVTPBGGTM	PLRGENLTSE 600
VGTH	PRMGNL	GLQME	AEENRM	MLSSS	FPVIQL	PEQT	PLAFDN	RFVPIYGNHS	SVNSVTPQTS 660
PLSL	KKKEIPE	NSA	VDDEA						

Seq ID NO: 633 DNA sequence  
 Nucleic Acid Accession #: NM\_003885.1  
 Coding sequence: 98..1021

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1	11	21	31	41	51					
AAAC	TCAGAA	TTTT	CGCGGG	CTCG	TGAGC	GGTTT	TATCC	CTCC	GGCGCG	CAGGCTGGGC 60
GCAG	GGGGCG	AGCC	CCCCGCC	CGGC	CGCGCAG	CAGCA	CCCATG	GGCA	CGGTGC	TGTCCCTGTC 120
TCCC	AGCTAC	CGGA	AGGCCA	CGCT	GTTTGA	GGAT	GGCGCG	GCCAC	CGTGG	GCCACTATAC 180
GGCC	GTACAG	AACAG	CAAGA	ACGCC	AAGGA	CAAGA	ACCTG	AAGCG	CCACT	CCATCATCTC 240
CGTG	CTGCCT	TGGA	AGAGAA	TCTG	GCCGT	GTCCG	CCCAAG	AAGA	AAGACT	CCAAGAAGGT 300
GCAG	CCTAAC	AGCAG	CTACC	AGA	CAACAT	CACGC	ACCTC	AACA	ATGAGA	ACCTGAAGAA 360
GTCT	GTCTCG	TGCG	CCAACC	TGT	CCACAT	CGCCC	AGCCC	CCACC	GGCCC	AGCCGCTGTC 420
ACCC	CCGCC	AGCC	AGCTCT	CGGG	TCCCA	GACCG	GGGGC	TCCT	CCTCAG	TCAAGAAAGC 480
CCCT	CACCTT	GCCG	TCACCT	CCGC	AGGGAC	GCCCA	AAACGG	GTCA	TCGTCC	AGGCGTCCAC 540
CAGT	GAGCTG	CTTG	CTGCC	TGGG	TGAGTT	TCTC	TGCCGC	CGTG	CTTACC	GCCTGAAGCA 600
CCTG	TCCCCC	ACGGA	ACCCG	TGCT	CTGGCT	GCGC	AGCGTG	GACCG	CTCGC	TGCTTCTGCA 660
GGGT	GGGCAG	GACCA	GGGCT	TCAT	CACGCC	GGCCA	ACGTG	GTCT	TCTCT	ACATGCTCTG 720
CAGG	GATGTT	ATCT	CCTCCG	AGGT	GGGCTC	GGAT	CACGAG	CTCC	AGGCG	TCCTGCTGAC 780
ATGC	CTGTAC	CTCT	CCTACT	CCTA	CATGGG	CAAC	GAGATC	TCCT	ACCCGC	TCAAGCCCTT 840
CCTG	TGGGAG	AGCT	GCAAGG	AGGC	CTTTTG	GGAC	CGTTGC	CTCT	CTGTCA	TCAACCTCAT 900
GAGC	TCAAG	ATGCT	GCAAGA	TAAAT	GCCGA	CCCA	CACATAC	TTCA	CACAGG	TCTTCTCCGA 960
CCTG	AAGAAC	GAGAG	CGGCC	AGGAG	GACAA	GAAG	CGGCTC	CTCT	TAGGCC	TGGATCGGTG 1020
AGCA	CTGTAG	CCTG	CGTCAT	GGCT	CAAGGA	TTCA	ATGCAT	TTTA	AAGAAT	TTATTATTAA 1080
ATCA	GTTTTTG	TGTAC	G							

Seq ID NO: 634 Protein sequence  
 Protein Accession #: NP\_003876.1

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1	11	21	31	41	51						
MGTV	LSLSPS	YRKAT	LPEDG	AATV	GHYTAV	QNSKN	AKDKN	LKRHS	IIISVL	PWKRI	VAVSA 60
KKNS	KKVQP	NSSY	QNNITH	LNNEN	LKKS	L	SCAN	LSTFAQ	PPPA	QPPAPP	ASQLSGSQTG 120
GSSS	VKKAPH	PAVTS	AGTPK	RVIV	QASTSE	LLRCL	GFEFLC	RRCY	RLKHL	PTDP	VLWLRS 180
VDRS	LLQLGW	QDQG	FITPAN	VVFL	YMLCRD	VISSE	VGS	DELQ	AVLLTCL	YLSY	SYMGNE 240
ISYP	LKFLV	ESCKE	AFWDR	CLSV	INLMSS	KMLQ	INADPH	YFTQ	VPSDLK	NESQ	QEDKKR 300
LLGL	DLR										

TABLE 79A:

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
15	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
	443646	AI085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
20	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AI910275	Hs.350470	trifol factor 1 (breast cancer, estroge	Seq ID No. C10 & C226
	411789	AF245505	Hs.72157	Adican	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
25	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
30	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
35	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C23 & C238
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
40	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
45	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
50	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
55	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
	408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
60	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	Seq ID No. C48 & C263
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazarus	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
65	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
70	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
	416965	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.54795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
75	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
80	421563	NM_005433	Hs.105806	granulysin	Seq ID No. C68 & C283
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-tRNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287



5	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	A1393742	Hs.199057	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
10	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
	431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
	426484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85952	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	Seq ID No. C106 & C321
	440559	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AI015709	Hs.172089	PORIMIN Pro-oncosis receptor inducing me	Seq ID No. C120 & C335
50	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16352	pyrimidineric receptor P2Y, G-protein c	Seq ID No. C125 & C340
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plaxin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
60	432874	W94322	Hs.279551	melanoma inhibitory activity	Seq ID No. C131 & C346
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
65	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
70	432596	AJ224741	Hs.278461	matritin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
75	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	Seq ID No. C146 & C361
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gaslin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C156 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	Seq ID No. C160 & C375
	436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179557	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
15	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197366	smoothed (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW97938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AI732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
55	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.37796	EphB6	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

## 65 TABLE 79B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

## 70

Pkey CAT Number Accession  
414991 1785135\_1 D78831 C17858 D78863

## 75 TABLE 79C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

## 80

Pkey Ref Strand NL\_position

5

404682	9797231	Minus	40977-41150
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence  
Nucleic Acid Accession #: NM\_005814  
Coding sequence: 345..1304

	1	11	21	31	41	51	
5	CTACCCCTTT	GTGAGCAGTC	TAGGACTTTG	TACACCTGTT	AAGTAGGGAG	AAGGCAGGGG	60
10	AGGTGGCTGG	TTTAAGGGGA	ACTTGAGGGA	AGTAGGGAAG	ACTCTCTTTG	GGACCTTTGG	120
	AGTAGGTGAC	ACATGAGCCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACCAGAC	AGCTCAGACC	TGCTGGAGG	300
15	CTGCCAGTGA	CAGGTTAGGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAAGATGT	360
	GGCCTGTGTT	GTGGACACTC	TGTGCAGTCA	GGGTGACCGT	CGATGCCATC	TCTGTGGAAA	420
	CTCGCGAGGA	CGTTCTTCGG	GCTTCGCAGG	GAAAGAGTGT	CACCCCTGCC	TGCACCTACC	480
	ACACTTCCAC	CTCCAGTCGA	GAGGGACTTA	TTCAATGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGAAAGGGT	GGTCATCTGG	CGTTTTCAA	ACAAAACTA	CATCCATGGT	GAGCTTTATA	600
20	AGAATCGCGT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCCTCCATC	ACCATTGATC	660
	AGCTGACCAT	GGCTGACAA	GGCAGCTACG	AGTGTTCGTG	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	CAAGTACAGT	GTCCGCTGTG	TGGTCTCTGT	GCCACCTCC	AAACCAAGAT	780
	CGCGCATCGA	GGGAGAGACC	ATAATTGGGA	ACAACATCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCACC	AACCCCTCAG	TACAGCTGGA	AGAGGTACAA	CATCCTGAAT	CAGGAGCAGC	900
25	CCCTGGCCCA	GCCAGCCTCA	GGTCAGCCTG	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
	CGGGTTACTA	CATCTGTACC	TCCAGCAATG	AGGAGGGGAC	GCAGTTCTGC	AACATCACGG	1020
	TGGCCGTGAG	ATTCCTCTCC	ATGAACGTGG	CCCTGTATGT	GGGCATCGCG	GTGGGCGTGG	1080
	TGTCAGCCCT	CATTATCATT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGACG	1140
	ACAACACTGA	AGACAAGGAG	GATGCAAGGC	CGAACCGGGA	AGCCTATGAT	GAGCCACCCG	1200
30	AGCAGCTAAG	AGAACCTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAAGAAGAGC	1260
	AGAGGAGCAC	TGGGCGTGAA	TCCCGGAGCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGCGGAG	GAAGGGTTAG	GGGTTTATTC	TCCGCTTCC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCCAG	ACATTGATGG	GGACATTCTC	TCCCCAGTGT	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
35	ACTGTCTGTT	GAAGTAACCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCTG	GCCCTCACTC	1560
	AAGACCAGGC	TGCAGCCTCC	ACTTCCCTCG	TAGTTGGCAG	GAGCTCCTGG	AAGCACAGCG	1620
	CTGAGCATGG	GGCGCTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCAGC	CTTGGGGGGT	1680
	GGGGCTGTCT	CTGCTCACCT	GTGTGCCAG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
	CACTCCACAC	ATCTTCTTTG	AATGAATGAA	AGAATAAGTG	AGTATGCTTG	GGCCCTGCAT	1800
40	TGGCTGGGCC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
	TCCAAACCTC	CTTGGGAAGG	CCACCTCCCA	CTCCTGCTGC	ACAGGCCCTG	GGGAGCTTTT	1920
	GGCCACACAC	TTCCTCATCT	TGCCGTGCAA	TATCGTACCT	GTCCCTCCAG	GCCCATCTCA	1980
	AATCACAAGG	ATTCTCTCTA	CCCTATCCCTA	ATTGTCCACA	TACGTGGAAA	CAATCCTGTT	2040
	ACTCTGTCCC	AGCTCCAATC	ATGGGCCACA	AGGCACATC	TTCTGAGCGA	GTGCTCTCAC	2100
45	TGTATTAGAG	CGCCAGCTCC	TTGGGGCAGG	GCCTGGGCCT	CATGGCTTTT	GCTTTCCCTG	2160
	AAGCCCTAGT	AGCTGGCGCC	CATCCTAGTG	GGCATTAAAG	CTTAATTGGG	GAAACTGCTT	2220
	TGATTGGTTG	TGCCCTCCCT	TCTCTGGTCT	CCTTGAGATG	ATCGTAGACA	CAGGGATGAT	2280
	TCCCAACCAA	ACCCAGTAT	TCATTCACTG	AGTTAAACAC	GAATTGATTT	AAAGTGAACA	2340
	CACACACAGG	AGCTGCTCTG	CAGATGGTCT	GAGTTCTTGT	GTCCCTGGTA	TTCTCTCCCA	2400
50	GGCCAGAATA	ATTGGCATGT	CTCCTCAACC	CACATGGGGT	TCTCTGTTGT	TCTGCTATCC	2460
	CGATACCTCA	GCCTTGGCCC	TGCCAGAGCC	ATTGGGGCTC	TGGTTTCTGT	GTGGGGCTGT	2520
	CTGCTGGCCC	TCCCAAGAGC	TCCTTCTGTT	TGTCGAGCAT	TTCTTCTACT	CTTGAGAGCT	2580
	CAGGAGGCTG	TAGGGCTGCT	TAGGTCTCAT	GGACCAAGTG	CTGGTCTCAC	CCAACTGCAG	2640
	TTTACTATGT	CTATCTTTTC	TGGATGATCA	GAAAAATAAT	TCCATAAATC	TATTGTCTAC	2700
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Seq ID NO: C2 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3150

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65	CGCCGACCCC	CGCTSSGTGC	GCTGCTGTTG	CTGCTSSGTG	CGCCGCCACC	CAGGGTCCGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTAA	CGGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTC	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTGG	ACAGCAAAGG	CTCTCGGCTC	360
70	CTGGAGTCTC	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
	TGGTTCGGGG	CAACAGTTCC	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600
	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAGT	GCGAGTTTCA	CCAAGACTGG	CGGTGTGGTT	660
75	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCTGCCAC	TCAGGAGCAG	720
	ATTGCAGAA	CTTATTACCC	CGAGTACCTG	ATCAACCTGG	TTCAAGGGCA	GCTGCAGACT	780
	CGCCAGGCCA	GTTCATCTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCAAGTGGT	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
	GGCTATGTCA	CATACCTTAA	TGGCTCAGAC	ATTGATCCCC	TCTACAACCT	CTCAGGGGAA	960
80	CAGATGGCCT	CCTACTTTGG	CTATGCAGTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
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	GAGGTGGGCA	GGGTCTACGT	CTACCTGCAG	CACCCAGCCG	GCATAGAGCC	CAGCCGCCAC	1140
	CTTACCTCTA	CTGGCCATGA	TGAGTTTGGC	CGATTGGGCA	GCTCCTTGAC	CCCCCTGGGG	1200
	GACCTGCAGC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCTTTGG	TGGGGAGAGC	1260
	CAGCAGGGAG	TAGTGTTTGT	ATTTCCTGGG	GGCCAGGAG	GGCTGGGCTC	TAAGCCTTCC	1320

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 15 GCTGAGTACT CTGAGCTCGT CAGACACCCA GGGAACTTCT CCAGCTGAG CTGTGACTAC 2160  
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Seq ID NO: C3 DNA Sequence

Nucleic Acid Accession #: NM\_002421.2

Coding sequence: 1..1410

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CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
TACTACAACC	TGAAGAATGA	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCAGTGT	180
GTTGAAAAAT	TGAAGCAAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAAGT	240
GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCCTGATGT	GGCTCAGTTT	300
GTCTCTACTG	AGGGGAACCC	TCGCTGGGAG	CAAAACATC	TGACCTACAG	GATTGAAAT	360
TACACGCCAG	ATTGCGCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACCT	420
TGGAGTAATG	TCACACCTCT	GACATTCAAC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AATCTCCTT	TTGATGGAAC	TGGAGGAAAT	540
CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
GAAAGGTGGA	CCAGCAATTT	CAGAGAGTAC	AACCTTACATC	GTGTTGCGGC	TCATGAACTC	660
GGCCATTCTC	TTGACTCTCT	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
ACCTTCACTG	TTGAGTTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
GGACGTTCCC	AAAATCCTGT	CCAGCCCATC	GGCCACAAA	CCCCAAAAGC	ATGTGACAGT	840
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GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATAGCACA	TGACTTTTCT	1260
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Seq ID NO: C4 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1410

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TACTACAACC	TGAAGAATGA	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCAGTGT	180
GTTGAAAAAT	TGAAGCAAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAAGT	240
GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCCTGATGT	GGCTCAGTTT	300
GTCTCTACTG	AGGGGAACCC	TCGCTGGGAG	CAAAACATC	TGACCTACAG	GATTGAAAT	360
TACACGCCAG	ATTGCGCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACCT	420
TGGAGTAATG	TCACACCTCT	GACATTCAAC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
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CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
GAAAGGTGGA	CCACAATTT	CAGAGAGTAC	AACCTTACATC	GTGTTGCGGC	TCATGAACTC	660
GGCCATTCTC	TTGACTCTCT	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
ACCTTCACTG	TTGAGTTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
GGACGTTCCC	AAAATCCTGT	CCAGCCCATC	GGCCACAAA	CCCCAAAAGC	ATGTGACAGT	840
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AATAGCTGGT TCAACTGCAG GAAAAATTAG 1410
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Seq ID NO: C5 DNA Sequence  
Nucleic Acid Accession #: NM\_014331.2  
Coding sequence: 1..1506

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	GTCAATGACA	ATTTCAGGG	GGTGTGCGAG	AATGTGAGGT	TGTCTTTTGG	AACCACACCA	780
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10	AAGGACTTGC	AAGCCATCTG	CGGCATCTCC	TGTGATGAGC	TGTCCAGCAT	GGTCTCGGAA	960
	CTCAGGGGCC	TGGCCACCAT	TGTGACCAAG	CTGCAGGACA	GCATCCGCAA	AGTGACTGAA	1020
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	CAGTACAGAA	ATAACAGGGA	ATGAGCTGTT	GATAGCTGCA	CTGAGTGTCA	CTGTGAGAAC	1140
	TCAGTTACCA	TCTGCAAAAA	GGTGTCTCTG	CCCATCATGC	CCTGCTCCAA	TGCCACAGTT	1200
15	CCTGATGGAG	AATGCTGTCC	TGGCTGTTGG	CCCAGGAGCT	CTGCGGAGCA	TGGCTGTCTT	1260
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	CACATTACAG	AGTGTGACAA	AAGATTAAAA	CAGGATGGTG	GCTGGAGCCA	CTGTCCCCCG	1440
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	ATCCAGTGCA	CAGATGTTGA	TGAGTGCAAA	GAAGTGCCTG	ATGCCCTGCT	CAACCAACAAT	1920
	GGAGGAGCAC	GGTGTGAGAC	CACGGACCCC	GGCTACAACT	GCCTGCCCTG	CCCCCAACGC	1980
	TTCACCGGCT	CACAGCCCTT	CGGCCAGGGT	GTGGAACATG	CCACGGCCAA	CAACACAGGTG	2040
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30	AACTACCTGG	GCCACTATAG	GCACCCCATG	TACCGCTGGG	AGTGCAAGCC	TGGCTACGCT	2160
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	ACTGATATGG	ATGGGGTTGG	AGATCAGTGT	GACAATTGCC	CCTTGGAAAC	CAATCCGGAT	2640
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45	CCTCTGGACC	CCAAAGGGAC	ATCCCAAAAT	GACCTTAAC	GGGTTGTACG	CCATCAGGGT	3060
	AAAGAACTCG	TCCAGACTGT	CAACTGTGAT	CCTGGACTCG	CTGTAGGTGA	TGATGAGTTT	3120
	AATGCTGTGG	ACTTCAGTGG	CACCTTCTTC	ATCAACACCG	AAAGGGACGA	TGACTATGCT	3180
	GGATTGTGCT	TTGGCTACCA	GTCCAGCAGC	CGCTTTTATG	TTGTGATGTG	GAAGCAAGTC	3240
	ACCCAGTCTT	ACTGGGACAC	CAACCCACCG	AGGGCTCAGG	GATACCTCGG	CCTTTCTGTG	3300
50	AAAGTTGTAA	ACTCCACCA	AGGGCTTGGC	GAGCACCTGC	GGAAACGCGT	TGGGCACACA	3360
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	GTGATGTATG	AAGGGAAGAA	AATCATGGCT	GACTCAGGAC	CCATCTATGA	TAAAACTTAT	3540
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55	AAATACGAAT	GTAGAGATCC	CTAATCATCA	AATGTTTGAT	TGAAAGACTG	ATCATAAACC	3660
	AATGCTGTGA	TGACACCTTC	TGGAACATAT	GGCTTGAGAA	AAACCCACAG	ATCACTTCTC	3720
	CTTGGCTTCC	TCTTTTCTTG	TGCTTGCAAT	AGTGTGGACT	CCTAGAACGT	GCGACCTGCC	3780
	TCAGAAAAAT	GCACTTTTCA	AAAAAGAGCT	CATCAGCAAT	CAGCCTCCAA	TGAATAAGAC	3840
	ATCTTCCAA	CATATAAACA	ATTGCTTTGG	TTTCTCTTTG	AAAAAGCATC	TACTTGTCTT	3900
60	AGTTGGGAAG	GTGCCCATTC	CACCTCTGCT	TTGTACAGAA	GCAGGGTGCT	ATTGTGAGGC	3960
	CATCTCT						3967

Seq ID NO: C7 DNA Sequence

Nucleic Acid Accession #: NM\_002192

Coding sequence: 86..1366

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70	AATCAACA	ACTTTTGTCTG	CCAGGATGCC	CTTGCTTTGG	CTGAGAGGAT	TTCTGTGGC	120
	AAGTTGCTGG	ATTATAGTGA	GGAGTTCCCC	CACCCACAGG	TCCGAGGGGC	ACAGCGGGC	180
	CCCCACTGT	CCGTCTGTGG	CGCTGGCCGC	CCTCCCAAAG	GATGTACCCA	ACTCTCAGCC	240
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75	GGGCAAGTTC	GGGGAGAAGC	GGTATGTGGA	GATAGAGGAT	GACATTGGAA	GGAGGGCAGA	420
	AATGAATGAA	CTTATGGAGC	AGACCTCGGA	GATCATCAGC	TTTGCAGAGT	CAGGAACAGC	480
	CAGGAAGACG	CTGCACCTTC	AGATTTCCAA	GGAAGGCAGT	GACCTGTGCA	TGGTGGAGCG	540
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	CATCCGCTCT	TTCCAGCAGC	AGAAGCACCC	GCAGGGCAGC	TTGGACACAG	GGGAAGAGGC	660
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	CGCTCGGAAG	AGCACCTGCG	ATGCTCTCCC	TGCTCTCAGC	AGCATCCAGC	GGTGTGCTGA	780
	CCAGGGCAAG	AGCTCCCTCG	ACGTTCCGAT	TGCCTGTGAG	CAGTGCCAGG	AGAGTGGCGC	840
	CAGCTTGGTT	CTCTCTGGCA	AGAAGAAGAA	GAAAGAAGAG	GAGGGGGGAG	GGAAAAAGAA	900
	GGCGGAGGTT	GAAGGTGGGG	CAGGAGCAGA	TGAGGAAAAG	GAGCAGTGC	ACAGACCTTT	960
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Seq ID NO: C8 DNA Sequence  
Nucleic Acid Accession #: NM\_00095.1  
Coding sequence: 26..2299

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Seq ID NO: C9 DNA Sequence  
Nucleic Acid Accession #: XM\_057014  
Coding sequence: 143..874

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Seq ID NO: C10 DNA Sequence  
Nucleic Acid Accession #: NM\_003225  
Coding sequence: 41..295

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GCCCTCCAG TGTCGAAATA AGGGCTGCTG TTGCGACGAC ACCGTTCGTG GGGTCCCTCG 240
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TCTGCAGGGA TCTGCTCTGA TCCTGAGCGG GTGCCGTCCC CAGCACGGTG ATTAGTCCCA 360
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Seq ID NO: C11 DNA Sequence  
Nucleic Acid Accession #: NM\_015419.1  
Coding sequence: 1..8487

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AATTGCGGGT TTAATAGCAT ACAGGCCCTG TCAGAAACCT CATTTGCAGG ACTGACCAAG 240
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Coding sequence: none

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AAGCCCAGCA GCCCGGGGCG GATGCTCTCC GGCGGCTGCG CTCGCGAGCG CGGCCGCGCG 60
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AGCCCTGCCC CAGTGCCTGG CACCTGCCCC TGCCAGCGAG GAAGCCCCCG GGCCTGCCAG 240
CAGCCTCAGG CCTCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300
CCGACAGAAG AGGTTGCTGC TTTTGGCGCG GCGCTGGGAG AAGACGAGAC TCACCTACAG 360
GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
CTAAAGGTTA TGGAGCGATG TGAGCCCACT CACCTTACT GAGGTGCACG AGGGCCGTGC 480
TGACATCATG ATCGACTTGC CCAGGTACTG GCATGGGAC GACCTGCGT TTGATGGGCC 540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGSGG ATGTCCACTT 600
CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCGAGGC ACAGACCTGC TGCAGGTGGC 660
AGCCCATGAA TTTGGCCAGC TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGGCT 780
TCAACACAGA TATGCCAGC CTGGCCAC TGTCACCTCC AGGACCCAG CCTGGGGCCC 840
CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC 900

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5 CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960  
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 TCGCCACTGG CAGGAGCTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080  
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 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCCACCC 1260  
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 10 CCTTACTTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGTCTCGT 1440  
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 15 AGCGACTGTC TCAGACTGGG CAGGAGGCTT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740  
 GGGACCCGCT ATCAGGTGCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800  
 GTAGCACCAT GGCAGGACTG GGGAACTGG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860  
 TCCTTCCAGG GCTTGGCTCT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920  
 TGAGCACTG GGCCTGAGGG CAGGGCCACT TCTGAGGTG AGGTCTTGTG AGGTGCCTGC 1980  
 20 ATCTGTCTGC CTCTGAGGCT ACAATCTTGG AATCTGTGTC TCCAGATCC AGGCCAAAA 2040  
 GTTCACATG AATGGGGAG GGTATTCTT CATGCAGSAG ACCCCAGGCC CTGGAGGCTG 2100  
 CAACATACCT CAATCTGTG CCAGGCCGGA TCCTCTGAA GCCCTTTTCG CAGCACTGTG 2160  
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25 Seq ID NO: C16 DNA Sequence  
 Nucleic Acid Accession #: NM\_024022  
 Coding sequence: 202..1563

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 35 AGAGGTCTCG AATAGTCTAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGGG CCTGTATGAT TTGAAAATAA GTCTGTGTGC ACCAGATGCA 300  
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATGTGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCT CTATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 40 GAGTCTCTCG ATTGCAAGAG CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGTG TGCTGTGGCC CACTGGGTT TCCCAAGCTA TGTGAGTCA 660  
 GATAAECTCA GAGTGTGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 45 TGTGCTCTGC GCCAGTGTGT TACCTTGCA TGCACAGCCT GTGTCTAG AGGGGGCTAG 840  
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 CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTGTATC CTCGCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCCAC 1080  
 50 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGCT GSCCGGGCCA 1140  
 CTCAGTTTCA ATGAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTTCCC 1200  
 GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGG TGACGCTTCC 1260  
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 ACCCGTGTCA CCTCTTCTC GACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560  
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 TCCCTTGGAC TCCGCTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTT 1680  
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 GCAGTGGGGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860  
 CCTCAGCTTC CCCAGTAGCT GGGACCAAG GTGCCCGCCA CCACACCCAA CTAATTTTTG 1920  
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 65 CAAATGATGT GCCTGCTTCA GCCTCCCAAC GTGCTGGGAT TACAGGCATG GGCCACCAAG 2040  
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 70 AACCCACCTT TTCTACTTCC AAGACTTATT TTCAATGTG GGGAGGTTAA TCTAGGAATG 2340  
 ACTCGTTTAA GGCCTATTTT CATGATTCT TTGTAGCATT TGGTGTGTA CGTATTATTG 2400  
 TCCTTTGATT CCAATAATA TGTTCCTTC CCTCAAAAAA AAAAAAAA 2460  
 AAAAA 2465

75 Seq ID NO: C17 DNA Sequence  
 Nucleic Acid Accession #: NM\_003220  
 Coding sequence: 63..1376

80 1 11 21 31 41 51  
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 GCACACGCAA CGGACCGGCA CGGTTGCCCG AGCTGGGCAC TGTAGGTCAA TCTCCCTACA 180  
 CGAGCGCCCC GCGCTGTCTC CACACCCCCA ATGCGGACTT CCAGCCCCCA TACTTCCCCC 240  
 CACCCCTACCA GCCTATCTAC CCCCAGTCGC AAGATCCTTA CTCCACGTC AACGACCCCT 300

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GGCAGAGCCA GGAGTCTGGG CTCCTGCACA CGCACCAGGG GCTGCCTCAC CAGCTGTGG 420
GCCTGGATCC TCGCAGGAG TACAGGCGCG ACAGGAGCCT CTGCAACGGC CCACACGGCG 480
TCAGCTCAGG ACTCGGAGAC CTCTCGATCC ACTCCTTACC TCACGCCATC GAGGAGGTCC 540
CGCATGTAGA AGACCCGGGT ATTAACATCC CAGATCAAAC TGTAAATTAAG AAAGGCCCG 600
TGTCCTGTGC CAAGTCCAAC AGCAATGCCG TCTCCGCCAT CCTATTAAAC AAGGACAAAC 660
TCTTGGGCGG CGTGGTGAAC CCCAACGAAG TCTTCTGTTC AGTTCGGGT CGCCTCTCGC 720
TCCTCAGCTC CACCTCGAAG TACAAGGTCA CGGTGGCGGA AGTCAGCGG CGGCTCTCAC 780
CACCCGAGTG TCTCAACGCG TCGCTGCTGG GCGAGGTGCT CCGGAGGCG AAGCTAATAA 840
ATGGAGGAAG ATCTTTAAGA GAAAACTGG ACAAATAGG ATTAATCTG CCTGCAGGGA 900
GACGTAAAGC TGCCAACGTT ACCCTGTCTA CATCACTAGT AGAGGGAGAA GCTGTCCACC 960
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TTCTCAACCG ACAACATTCC GATCCCAATG AGCAAGTGAC AAGAAAAAC ATGCTCCTGG 1080
CTACAAAAAC GATATGCAAA GAGTTCACCG ACCTGCTGGC TCAGGACCGA TCTCCCTGG 1140
GGAACCTACG GCCCAACCCC ATCCTGGAGC CCGGCATCCA GAGTGTCTG ACCCACTTCA 1200
ACCTCATCTC CCACGGCTTC GGCAGCCCCG CGGTGTGTGC CGCGGTCAAG GCCCTGCAGA 1260
ACTATCTCAC CGAGGCCCTC AAGGCCATGG ACAAATGTA CTCAGCAAC AACCCCAACA 1320
GCCACAGGGA CAACAACGCC AAAAGCAGTG ACAAAGAGGA GAAGCAGAGA AAGTGAGGCT 1380
CTCCTCCCGC CCGGCCCTC CCACGCCCTA CCAGCCCCC GCGGCCAC CCTCCGGCGG 1440
GTGACAGCTC CCGGATCAGC AACCTTCTCT GCTGTGCTA CTGCTGCTG TGTGCGCGC 1500
GCCGCCCGCG CGCTGCCCTT TGGTCCCCC CGAGTCTCCG GGAAGTCCCT CTGACTGTG 1560
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TGTGCCCCG GAATTC

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Seq ID NO: C18 DNA Sequence  
Nucleic Acid Accession #: NM\_002988  
Coding sequence: 71..340

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1 11 21 31 41 51
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GCCAGCATC ATGAAGGGCC TTGCAGCTGC CCTCTTGTCT CTGCTCTGCA CCATGGCCCT 120
CTGCTCCTGT GCACAGTTTG GTACCAACAA AGAGCTCTGC TGCTCTGTCT ATACCTCTCTG 180
GCAGATTCCA CAAAGTTTCA TAGTTGACTA TTCTGAAACC AGCCCCAGT GCCCAAGCC 240
AGGTGTCTAT CTCTTAACCA AGAGAGGCGG GCAGATCTGT GCTGACCCA ATAAGAAAGT 300
GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCTGA GGGGCTGGA AGCTGCCAGG 360
GCCAGTGAAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420
CCACCCCTGA GGGCCCTCT TCTAAGAGTC CCATCTGCTA TGCCACAGCA CATTAACTAA 480
CTTTAATCTT AGTTTATGCA TCTATTTC TTTGAAATT GATTCTATT GTTGAGCTGC 540
ATTATGAAT TAGTATTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTTCCCT 600
TTCCCTTCAA CTCTTGTGAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTCTCAG 660
CAGACATTGT GCCATATGTA TCAAATGACA AATCTTTATT GAATGGTTT GCTCAGCACC 720
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AAAAAAAAA AAAAAAAAAA AAA

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Seq ID NO: C19 DNA Sequence  
Nucleic Acid Accession #: NM\_004063  
Coding sequence: 121..2619

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75  
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1 11 21 31 41 51
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ATGATACTTC AGGCCCATCT TCACTCCCTG TGTCTTCTTA TGCTTTATT GGCAACTGGA 180
TATGGCCAAG AGGGGAAGTT TAGTGGACCC CTGAAACCCA TGACATTTTC TATTATGAA 240
GGCCAAGAAC CGAGTCAAAT TATATTCCAG TTAAAGGCCA ATCCTCCTGC TGTGACTTTT 300
GAACCTAAGT GGGAGACAGA CAACATATTT GTGATAGAAC GGGAGGGACT TCTGTATTAC 360
AACAGACGCT TGGACAGGGA AACAGATCT ACTCACAATC TCCAGGTTGC AGCCCTGGAC 420
GCTAATGGAA TTATAGTGA GGGTCCAGTC CCTATCACCA TAGAAGTGAA GGACATCAAC 480
GACAAATGAC CCAGTCTTCT CCACTCAAAG TACGAAGGCT CAGTAAGGCA GAACCTCTGC 540
CCAGGAAGC CCTTCTTGTA TGTCAATGCC ACAGACCTGG ATGATCCGGC CACTCCCAAT 600
GGCCAGCTT ATTACAGAT TGTATCCAG CTTCCTCATG TCAACAATGT CATGTACTTT 660
CAGATCAACA ACAAACCGG AGCCATCTCT CTTACCCGAG AGGGATCTCA GGAATTGAAT 720
CCTGCTAAGA ATCCTTCTTA TAATCTGGTG ATCTCAGTGA AGGACATGGG AGGCCAGAGT 780
GAGAATTCCT TCAGTGATAC CACATCTGTG GATATCATAG TGACAGAGAA TATTGGAAA 840
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CAGGTGCGGT GGAATGATCC CGGTGCACAA TATTCCTTAG TTGACAAAGA GAAGCTGCCA 960
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TCATATCCGC TGGAAATTC TGTAAAGTT AAAGATATTA ATGATAATCC ACCTACATGT 1140
CCGTACACAG TAACCGTATT TGAGGTCCAG GAGAATGAAC GACTGGGTAA CAGTATCGGG 1200
ACCTTTACTG CACATGACAG GGATGAAGAA AATACTGCCA ACAGTTTCT AAACACAGG 1260
ATTGTGAGC AAACCTCCAA ACTTCCCATG GATGGACTCT TCCTAATCCA AACCTATGCT 1320
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ACGATAGAGG TGTCTGACAA AGATTTCAG ACCCTTGTG TGTGCAAAAT CAACGTATT 1440
GATATCAATG ATCAGATCCC CATCTTGAA AATCAGATT ATGGAACCT GACTCTTGCT 1500
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TTTGTGTGTA AGTACAATGC AAGTTCTTTT GCCAAGTTCA CGCTTATTGT GACAGATGTG 1800
AATGAAGCAC CTCAATTTTC CCAACAGCTA TTCCAAGCGA AAGTCAGTGA GGATGTAGCT 1860
ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGGTCTGGA CATAAGCTAT 1920
TCACTGAGGG GAGACACAA AGGTGGCTT AAAATTGACC ACGTGACTGG TGAGATCTTT 1980

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	AGTGTGGCTC	CATTGGACAG	AGAAGCCGGA	AGTCCATATC	GGGTACAAGT	GGTGGCCACA	2040
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	AATGACAACC	CTCCCAGGCT	AGCCAAGGAC	TACACGGGCT	TGTTCTTCTG	CCATCCCCTC	2160
5	AGTGACCTG	GAAGTCTCAT	TTTCGAGGCT	ACTGATGATG	ATCAGCACTT	ATTTCCGGGT	2220
	CCCCATTTTA	CATTTTCCCT	CGGCAGTGGG	AGCTTACAAA	ACGACTGGGA	AGTTTCCAAA	2280
	ATCAATGGTA	CTCATGCCCG	ACTGTCTACC	AGGCACACAG	AGTTTGAGGA	GAGGGAGTAT	2340
	GTCGTCTTGA	TCCGCATCAA	TGATGGGGGT	CGGCCACCCT	TGGAAGGCAT	TGTTTCTTTA	2400
	CCAGTTACAT	TCTGCAGTTG	TGTGGAAGGA	AGTTGTTTCC	GGCCAGCAGG	TCACCAGACT	2460
10	GGGATACCA	CTGTGGGCAT	GGCAGTTGGT	ATACTGCTGA	CCACCCTTCT	GGTGATTGGT	2520
	ATAATTTTGA	CAGTGTGTGT	TATCCGCATA	AAGAAGGATA	AAGGCAAGA	TAATGTTGAA	2580
	AGTGCTCAAG	CATCTGAAGT	CAAACCTCTG	AGAAGCTGAA	TTTGAAAAGG	AATGTTTGAA	2640
	TTTATATAGC	AAGTGCTATT	TCAGCAACAA	CCATCTCATC	CTATTACTTT	TCATCTAAAG	2700
	TGCATTATAA	TTTTTTAAAC	AGATATTCCC	TCTGTCTCTT	TAATATTGTC	TAAATATTTC	2760
15	TTTTTTGAGG	TGGAGTCTTG	CTCTGTGCGC	CAGGCTGGAG	TACAGTGGTG	TGATCCAGC	2820
	TCACTGCAAC	CTCCGCTCC	TGGGTTTACA	TGATTTCTCT	GCCTCAGCTT	CCTAAGTAGC	2880
	TGGGTTTACA	GGCACCCACC	ACCATGCCCA	GCTAATTTTT	GTATTTTTTA	TAGAGACGGG	2940
	GTTCGCCAT	TGCGCCAGGC	TGGTCTTGAA	CTCCTGACGT	CAAGTGATCT	GCCTGCCCTG	3000
	GTCTCCCAAT	ACAGGCATGA	ACCACTGCAC	CCACTACTTT	AGATATTTC	TGTGCTATAG	3060
20	ACATTAGAGA	GATTTTTCAT	TTTTCCATGA	CATTTTCTCT	CTCTGCAAA	GGCTTAGCTA	3120
	CTGTGTTTT	TCCCTTTTGG	GGCAAGACAG	ACTCATTAAA	TATTCGTAC	ATTTTCTCT	3180
	TATCAAGGAG	ATATCTCAGT	GTGTCTCAT	AGAACTGCCT	GGATTCCATT	TATGTTTTTT	3240
	CTGATTCCAT	CCTGTGTCCT	CTTCATCCTT	GACTCCCTTG	GTATTTCACT	GAATTTCAAA	3300
	CATTGTTCAG	AGAAGAAAA	CGTGAGGACT	CAGGAAAAAT	AAATAAATA	AAGAACAGCC	3360
25	TTTTCCCTTA	GATTTTAAAC	AAATGTTTCT	GTGTCAITAA	CCATCTTTAA	TCAATGTGAC	3420
	ATGTTGCTCT	TGCGCTGAAA	TTCTTCAACT	TGGAAATGAC	ACAGACCCAC	AGAAGGTGTT	3480
	CAAAACAAC	CTACTCTGCA	AACCTTGGTA	AAGGAACCA	TCAGCTGGCC	AGATTTCTCT	3540
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	GGTTATTATA	TATTTAATCAT	GTGGAAGAAA	ACAAGACATG	AAAAGAGTGG	TGACAAATCA	3660
30	AGAATAAACA	CTGGTTGTAG	TCAGTTTGT	TTGTTAA			3697

Seq ID NO: C20 DNA Sequence  
 Nucleic Acid Accession #: NM\_004443  
 Coding sequence: 28..3024

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	CCCGCGCGCT	GGCGGGCGCT	GGAAAGAGAC	CTCATGGACA	CAAAATGGGT	AACATCTGAG	180
	TGTGGCTGGA	CATCTCATCC	AGAAAGTGGG	TGGGAAGAGG	TGAGTGCTTA	CGATGAGGCC	240
	ATGAATCCCA	TCCGCACATA	CCAGGTGTGT	AATGTGCGCG	AGTCAAGCCA	GAACAACCTG	300
	CTTCGCACGG	GGTTCATCTG	GGCGCGGGAT	GTGCAGCGGG	TCTACGTGGA	GCTCAAGTTC	360
45	ACTGTGCGTG	ACTGCAACAG	CATCCCAAC	ATCCCGGCT	CCTGCAAGGA	GACCTTCAAC	420
	CTCTCTACT	ACGAGGCTGA	CAGCGATGTG	GCCTCAGCCT	CCTCCCGCTT	CTGGATGGAG	480
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	ACCTGCTGCG	TCAATTGCTC	TGGCACCTGC	ATCCCTAACG	CGGTGGAGGT	GTCGGTGCCA	780
	CTCAAGCTCT	ACTGCAAGCG	OGATGGGGAG	TGGATGGTGC	CTGTGGGTGC	CTGCACCTGT	840
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55	TCCCGAGCGG	CACGAGCTCG	CACCTGCCAC	AATAACTTCT	ACCGTGCGAG	CTCGGACTCT	1020
	GGCGGAGCTG	CCTGTACCA	CGTGCCATCT	CCACCCGAG	GTGTGATCTC	CAATGTGAAT	1080
	GAAACCTCAC	TGATCTCGA	GTGGAGTGAG	CCCCGGGACC	TGGGTGGCGG	GGATGACCTC	1140
	CTGTACAATG	TCATCTGCAA	GAAGTGCCAT	GGGGCTGGAG	GGGCCTCAGC	CTGCTCACGC	1200
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	GAGTACACGG	AGAAGCTGCA	GCAGTACATT	GCTCCTGGAA	TGAAGGTTTA	TATTGACCTT	1860
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	TGCGTCAAGA	TGAGGAGGAT	GATCGGAGCT	GGGGAATTTG	GGGAAGTGTG	CGGTGGTGA	1980
	CTGAACACAG	CTGGCGCGCG	AGAGGTGTTT	GTGGCCATCA	AGACGCTGAA	GGTGGGCTAC	2040
	ACCGAGAGGC	AGCGCGCGGA	CTTCCTAAGC	GAGGCCCTCA	TCATGGGTCA	GTTTGATCAC	2100
	CCCAATATAA	TCCGGTCTGA	GGGCGTGGTC	ACCAAAAGTC	GGCCAGTTAT	GATCCTCACT	2160
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	TACACCAAGT	CCCTGGGCGG	GAAGATCCCC	ATCCGCTGGA	CTGCCCCAGA	GGCCATAGCC	2460
80	TATCGAAGT	TGACTTCTGC	TAGTATGTGC	TGGAGCTACG	GAATTGTGAT	GTGGGAGGTC	2520
	ATGAGCTATG	GAGAGGAGCC	CTACTGGGAC	ATGAGCAACC	AGGATGTGAT	CAATGCCGTG	2580
	GAGCAGGATT	CTGGCGTGGC	ACCACCCATG	GACTGTCCCA	CAGCACTGCA	CCAGCTCATG	2640
	CTGGACTGCT	GGGTGCGGGA	CCGGAACCTC	AGGCCCAAT	TCTCCAGAT	TGTCAATACC	2700
	CTGGACAAGC	TCATCCGCAA	TGCTGCCAGC	CTCAAGGTCA	TTGCCAGCGC	TCAGTCTGGC	2760
	ATGTACAGC	CCCTCTCTGA	CCGCAAGGTC	CCAGATTACA	CAACCTTCA	GACAGTTGGT	2820



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GATTGGCTGG ATGCCATCAA GATGGGGCGG TACAAGGAGA GCTTCGTGAG TGGGGGTTT 2880
GCATCTTTTG ACCTGTGTGG CCAGATGACG GCAGAAGACC TGCTCGGTAT TGGGGTCACC 2940
CTGGCCGGCC ACCAGAAGAA GATCCTGAGC AGTATCCAGG ACATGCGGCT GCAGATGAAC 3000
CAGACGCTGC CTGTGCAGGT CTGACACCGG CTCCCACGGG GACCTTGAGG ACOGTGCAGG 3060
GATGCCAAGC AGCCGCTGG ACTTTCGGAC TCTTGGACTT TTGGATGCCT GGCCTTAGGC 3120
TGTGGCCCAAG AAGCTGGAAG TTTGGGAAAG GCCCAAGCTG GGACTTCTCC AGGCCTGTGT 3180
TCCCTCCCCA GGAAGTGC GC CCAAACTC TTCAATTGA AGATGGATTA GGAGAGGGGG 3240
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TAAGCCGGGG TTCCACAGGG CCCAGCCCTG GCAGGGGTCT GGCCCCCAG GTAGGCGGAG 3420
AGCAGTCCCT CCCTCAGGAA CTGGAGGAGG GGACTCCAGG AATGGGAAA TGTGACACCA 3480
CCATCTGAA GGCAGCTTGC ACCTCCAGTT TGCACAGGGA TTTGTCTGG GGGCTGAGGG 3540
CCCTGTCCCC ACCCCCGCCC TTGGTGTCTGT CATAAAAGGG CAGGCAGGGG CAGGCTGAGG 3600
AGTTGCCCTT TGCCCCCAG AGACTGACTC TCAGAGCCAG AGATGGGATG TGTGAGTGTG 3660
TGTGTGTGTG TGTGCGCGCG CGCGCGCGTG TGTGTGTGCA CGCACTGGCC TGCACAGAGA 3720
GCATGGGTGA GCGTGTAAAA GCTTGGCCCT GTGCCCTACA ATGGGGCCAG CTGGGCCGAC 3780
AGCAGAATAA AGGCAATAAG ATGAA 3805

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Seq ID NO: C21 DNA Sequence  
Nucleic Acid Accession #: NM\_001804  
Coding sequence: 82..879

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1 11 21 31 41 51
AGGTGAGCGG TTGCTGCTCG TCGGGGCGGC CGGCAGCGGC GGCTCCAGGG CCCAGCATGC 60
GCGGGGGACC CCGCGGCCAC CATGTATGTG GGCTATGTGC TGGACAAGGA TTCGCCCGTG 120
TACCCCGGCC CAGCCAGGCC AGCCAGCCTC GGCTTGGGCC CGGCAAACTA CGGCCCCCGG 180
GCCCGGCCCC CGCGGCCCCC GCAGTACCCC GACTTCTCCA GCTACTCTCA CGTGGAGCOG 240
GCCCGCGGCC CCGCGACGCG CTGGGGGGCG CCTTCCCTG CGCCCAAGGA CGACTGGGCC 300
GCCGCTTACG GCCCGGCCCG CGCGGCCCTT CGCGCCAGCC CAGCTTCGCT GGCATTGCGG 360
CCCCCTCCAG ACTTTAGCCC GGTGCGCGCG CCCCCTGGGC CGGCCCCGGG CTTCTGGCG 420
CAGCCCCCTG GGGGCCCGGG CACACCGTCC TGSCCCGGAG CGCAGAGGCC GAGGCCCTAC 480
GAGTGGATGC GGGCGACGCT GCGGCCCGGA GCGGCGGTG GCAGCGSTA GACTCGGACC 540
AAGGACAAGT ACCCGTGGT CTACACCGAC CACCAACGCC TGGAGCTGGA GAAGGAGTTT 600
CATTACAGCC GTTACATCAC AATCCGCGCG AATCAGAGC TGGCTGCCAA TCTGGGCTC 660
ACTGAACGGC AGGTGAAGAT CTGGTTCCAA AACCGCGGG CAAAGGAGCG CAAAGTGAAC 720
AAGAAGAAAC AGCAGCAGCA ACAGCCCCCA CAGCGCCGA TGGCCACGA CATCAGGCC 780
ACCCACGCCG GGCATCCCT GGGGGGCTG TGTCCAGCA ACACAGCCT CTTGGCCACC 840
TCCTCTCCAA TGCTGTGAA AGAGGAGTTT CTGCCATAGC CCCATGCCCA GCCTGTGCGC 900
CGGGGACCTG GGGGATACGG GTGCTGGGAG TGTGCTCCT GTGGGCCAG GAGGTCTGGT 960
CGAGTCTCA GCCCTGACCT TCTGGGACAT GGTGGACAGT CACCTATCCA CCTCTGCAT 1020
CCCCTTGGCC CATTTGTGTG AGTAAGCCTG TTGGATAAAG ACCTTCCAGC TCCTGTGTTT 1080
TAGACCTCTG GGGGATAAAG GAGTCCAGGG TGGATGATCT CAATCTCCG TGGGATCTC 1140
AAGCCCAAAA TGGTTGGGG AGGGGCCTAG ACAAGGCTCC AGGCCCAACC TCCTCTCCA 1200
TACGTTAGAG GTTGCAGCTG GAGGCCCTGT TGGGACCACT ACTGATCTG GAGAAAAGGG 1260
ATGAGAGCTG AAAAGATGGA ATGCTTGCA AGCATGACCT GAGGAGGGAG GAACGTGCTC 1320
AACTCACACC TGCTCTTCT GCAGCCTCAC CTCTACCTGC CCCATCATA AGGGCACTGA 1380
GCCCTTCCCA GGGGTGATAC TAAGCACAAA GCCCATAGCA CTGGGCTCTG ATGGCTGCTC 1440
CACTGGGTTA CAGAATCACA GCCCTCATGA TCAATCTCAG TGAGGGCTCT GGAATTGAGG 1500
GGAGGCGCTG GAGGAGGAGA AGGGGGCAGA GTCTTCCCTA CCAGGTTTCT ACACCCCGC 1560
CAGGCTGCCC ATCAGGCCCC AGGGAGCCCC CAGAGGACTT TATTGAGACC AAGCAGAGCT 1620
CACAGCTGGA CAGGTGTTGT ATATAGAGTG GAATCTCTTG GATGCAGCTT CAAGATAAA 1680
TTTTCTTCT CTTTTCAAA 1699

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Seq ID NO: C22 DNA Sequence  
Nucleic Acid Accession #: NM\_021978  
Coding sequence: 36..2603

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1 11 21 31 41 51
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TGAATGGCTT GGAGGAAGGC GTGAGTTCC TGCCAGTCAA CAACGTCAA AAGGTGAAA 180
AGCATGGCCC GGGCGCTGG GTGGTGTGCG CAGCCGTGCT GATCGGCTC CTCTTGTCT 240
TGCTGGGGAT CGGCTTCTG GTGTGGCATT TGCAGTACCG GGAAGTGGCT GTCCAGAAGG 300
TCTTCAATGG CTACATGAGG ATCACAATG AGAATTTGT GATGCTTAC GAGAATCCA 360
ACTCCACTGA GTTTGTAAGC CTGGCCAGCA AGGTGAAGGA CGCGCTGAAG CTGCTGTACA 420
GCGGAGTCCC ATTCTTGGC CCTTACCACA AGGAGTCCGG TGTGAGGCC TTCAGGAGG 480
GCAGGCTCAT CGCCTACTAC TGCTCTGAGT TCAGCATCCC GCAGCACCTG GTGGAGGAGG 540
CGAGGCGGCT CATGGCCGAG GAGCGGTAG TCATGCTGCC CCGCGGGGCG CGCTCCCTGA 600
AGTCTTTGT GGTCACTCA GTGGTGGCTT TCCCACGGA CTCCAAAACA GTACAGAGGA 660
CCAGGACCAA CAGCTGCAGC TTTGGCTGCG ACCCGCGGG TGTGGAGCTG ATGCCCTTCA 720
CCAGCGCCGG CTTCCCTGAC AGCCCTTACC CGCTCATGCG CGCTGCCAG TGGGCCCTGC 780
GGGGGAGCGC CGACTCAGTG CTGAGCCTCA CCTTCCGAG CTTTACCTT GGTCTCTGCG 840
ACGAGCGGCT CATGGCCGAG GTGACGTTGT ACAACACCTT GAGCCCCATG GAGCCCCACG 900
CCCTGGTCCA GTTGTGTGGC ACCTACCTTC CCTCTACAA CCTGACCTTC CACTCTCTCC 960
AGAACGTCTT GCTCATACA CTGATAACCA ACATGAGCG GCGGCATCCC GGTCTTGGAG 1020
CCACTTCTT CCAGCTGCTT AGGATGAGCA GCTGTGGAGG CGCTTACGT AAGGCCAGG 1080
GGACATTCAA GCGCCCTTAC TACCCAGGCC ACTACCCACC CAACATTGAC TGACATGGA 1140
ACATTGAGGT CAGCAACAA CAGCATGTGA AGGTGCGCTT CAAATTTCTT TACCTGCTGG 1200
AGCCCGGGCT GCTCGCGGGC ACCTGCCCCA AGGACTACGT GGAGATCAAT GGGGAGAAAT 1260
ACTGCGGAGA GAGGTCCAGG TTGCTGCTCA CCAGCAACAG CAACAAGATC ACAGTTCGCT 1320
TCCACTCAGA TCAGTCTTAC ACCGACACCG CCTTCTTAGC TGAATACCTC TCCTACGACT 1380

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ACGCCGGCCA CCAGTTACAG TGCAAGAAAC AGTTCTGCAA GCCCCTCTTC TGGGTCTGCG 1560
ACAGTGTGAA CGACTGCGGA GACAACAGCG ACGAGCAGGG GTGCAGTTGT CCGGCCAGAG 1620
CCTTCAGGTG TTCCAATGGG AAGTGCCTCT CGAAAGCCA GCAGTGCAAT GGGAGGAGCG 1680
ACTGTGGGGA CGGGTCCGAC GAGGCTCTCT GCCCAAGGT GAACGTCGTC ACTTGTACCA 1740
AACACACCTA CCGCTGCCCTC AATGGGCTCT GCTTGAGCAA GGGCAACCTT GAGTGTGAGC 1800
GGAAAGAGGA CTGTAGCGAC GGCTCAGATG AGAAGGACTG CGACTGTGGG CTGCGGTCTAT 1860
TCACGAGACA GTTGGGTGTT GTTGGGGGCA CGGATGCGGA TGAGGGCGAG TGGCCCTGGC 1920
AGGTAAAGCT GCATGCTCTG GCCCAGGGCC ACATCTGCGG TGCTTCCCTC ATCTCTCCCA 1980
ACTGGTGGT CTCTGCCGCA CACTGCTACA TCGATGACAG AGGATTGAGG TACTCAGACC 2040
CCACGCACTG CACCGCCCTT CTGGGCTTGC ACGACAGAG CCAGCGCAGC GCCCCTGGGG 2100
TGCAGGAGCG CAGGCTCAAG CGCATCATCT CCCACCCCTT CTTCATGAC TTCACCTTCG 2160
ACATATGACAT CGCGCTGCTG GAGCTGGAGA AACCGGCAGA GTACAGCTCC ATGGTGGCGC 2220
CCATCTGCCT GCCGACGCC TCCATGTCT TCCCTGCCGG CAAGGCCATC TGGGTCAAGC 2280
GCTGGGGACA CACCCAGTAT GGAGGCACTG GCGCGCTGAT CCTGCAAAAG GGTGAGATCC 2340
GGCTCATCAA CCAGACCACC TGCGAGAAC TCCTGCCGCA GCAGATCAGC CCGCGCATGA 2400
TGTGCGTGGG CTTCCTCAGC GCGCGCTGGG ACTCCTGCCA GGGTGATTCC GGGGGACCCC 2460
TGTCCAGCGT GGAGGCGGAT GGGCGGATCT TCCAGGCGGG TGTGGTGAGC TGGGGAGAGC 2520
GCTGCGCTCA GAGGAACAAG CCAGGCGTGT ACACAAGGCT CCCTCTGTTT CGGGACTGGA 2580
TCAAAGAGAA CACTGGGGTA TAGGGGCCGG GGCACCCCAA ATGTGTACAC CTGCGGGGGC 2640
ACCCATCGTC CACCCGAGTG TGCAACGCTG CAGGCTGGAG ACTGGACCGC TGACTGCACC 2700
AGCGCCGCCA GAACATACAC TGTGAACCTA ATCTCCAGGG CTCCAAATCT GCCTAGAAAA 2760
CCTCTCGCTT CCTCAGCCTC CAAAGTGGAG CTGGGAGGTA GAAGGGGAGG AACTGGTGG 2820
TTCTACTGAC CCAACTGGGG GCAAAAGTTT GAAGACACAG CCTCCCGCAG CAGCCCAAG 2880
CTGGGCCGAG GCGCGTTTGT GTATATCTGC CTCCCTGTCT TGTAAAGAGC AGCGGGAACG 2940
GAGCTTCGGA GCCTCTCTAG TGAAGGTGGT GGGGCTGGCG GATCTGGGCT GTGGGGCCCT 3000
TGGGCCACGC TCTTAGGAGG GCCCAGGCTC GGAGGACCCT GGAACACAGA CGGCTCTGAG 3060
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AACATTTTAT TTCTTTTAA AAAAAAAA 3149

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Seq ID NO: C23 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2268

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AGCGTGGGGA AAGGAGGCTT TGAAGGTCC AAGCACTTTG CCATCAGAGT CTGTGACGCT 240
CTGGACATCA GCCCGAGAGG GGTGAGAGTG GAGCAGTTCC AGTTGAGTTC CACTCCTCAT 300
CTGGAATTCC CCTTGAATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
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AAGTCCAGAG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
TTTGTGTGGG GGGTCAGGTT TCCAGGTGGG GAGGAGCTGC ATGCACTGCG CAGCGAGCCT 600
AGAGGGCAGC ACGTGTCTGT GGCTGAGCAG GTGGAGGATG CCACCAACCG CCTCTTCAGC 660
ACCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGAGTTTGG CTGGCAATGC CCCATGCTGG 780
AGAGGATCCG GCGGACCCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
AGAGTGTTC TAAACCCACC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900
TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAA GACTGGACGG CTACCAAGTGC 960
CTCTGCCCCG TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC 1020
AGGTCGAGC TCCTCTTCTC GCTGGACAGC TCTGCGGCA CCACTCTGGA CGGCTTCTCT 1080
CGGGCCAAAG TCTTCTGTGA GCGGTTTGTG CCGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
CGAGTGGGTG TGGCCACATA CAGCAGGAGG CTGCTGGTGG CGGTGCGCTG GGGGGAGTAC 1200
CAGGATGTGC CTGACCTGCT GTGAGCCTC GATGGCATT CTCTCCGTGG TGGCCCCACC 1260
CTGACGGGCA GTGCCTTGGC GCAGGCGGCA GAGCGTGGCT TCGGGAGGCG CACCAGGACA 1320
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GTTGCGGGCC CAGCGCTGCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCACT 1440
GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGACGCC CAAAGCATGT GATGGTCTAC 1500
TCGGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
CAGCGGCCAG GGTGCGGAGC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CAOCTCTGCC 1620
TCAGTAGGGC CCGAGAAATT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
TTTGAGGTGA ACCCTGAGCT GACACAGTGC GGCTGCTGGG TGTATGGCAG CCAGGTGCAG 1740
ACTGCTTTCG GGCTGGACAC CAAACCCACC CCGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA 1920
GGCGGAGAG GCGCAGAGGA TGCAGCGGTT CTGCCCCA AGCTGAGGAA CAATGGCATC 1980
TCTGTCTTGG TCGTGGGCGT GGGGCTGTCT CTAAGTGAGG GTCTGCGGAG GCTTGCAAGT 2040
CCCGGGGATT CCGTATCCA CGTGGCAGCT TACGCGACCC TCGGTTACCA CCAGGACGTC 2100
CTCATTGAGT GGCTGTGGG AGAAGCCAA GCGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
TGCAATGAAT AGGGCAGCTG CGTCTGAGC AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
GGCTGGGAGG GCGCCCACTG CGAGAACCGA TTCTTGAGAC GCGCCCTGA 2268

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Seq ID NO: C24 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2424

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CTGGACATCA GCCCGAGAGG GGTTCAGAGT GGAGCATTCC AGTTCAGTTC CACTCCTCAT 300
CTGGAATTCC CTTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACCTTGCTC TGAATACCT TCTGCACAGA 420
GGGTTGCTCG GAGGCAGAAA TGCTTCTGTG CCCAGATCC TCATCATCGT CACTGATGGG 480
AAGTCCACAG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
AGAGGGCAGC ACGTCTGTTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTTCTCAGC 660
ACCTTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
CCCTGTGAGC ACAGCAACGT GGAGATGGTC CGGGAGTTGG CTGGCAATGC CCCATGCTGG 780
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AGAGTGTTCC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCTGTGAC 900
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CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCTGTG GGGGGAGTAC 1200
CAGGATGTGC CTGATCTGGT CTGGAGCCTC GATGGCAATC CCTTCGTGG TGGCCCCACC 1260
CTGACGGGCA GTGCCCTTGG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACGAGGACA 1320
GGCAGGAGC GCGCAGAGCT AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
GAGGCGGTGC GGGCAGAGCT GAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
TCGGATCCCT AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
CAGCGGCCAG GGTGCGGAGC ACAAGCCCTG GACCTGTGCT TCATGTTGGA CACCTCTGCC 1620
TCAGTAGGGC CCGGAATTTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
TTTAGAGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
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GCCCTCTACC TAGGTGGGTG GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
GTGATGACCG TCCAGAGGGG TGCCCGGCTC GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920
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TCTGTCTTGG TCGTGGGCTG GGGCCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
CCCCGGGATT CCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGAGCTG 2100
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TGCAATGAAT AGGGCAGCTG CGTCTGCGA AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
GGCTGGGAGG GCGGCACTG CGAGAACCGT GAGTGAAGCT CTTGCTCTGT ATGTGTGAGC 2280
CAGGATGGA TTCTTGAGAC GCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340
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AATGTCTGTG CCCCAGGTCC TTAG 2424

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Seq ID NO: C25 DNA Sequence  
Nucleic Acid Accession #: XM\_097386.3  
Coding sequence: 142..795

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TCCCGTGCAC CAGGGTCTGC AGCAGCCACT GGGGCCCTGC TGCTGCTGCT ATCTGGCGGC 240
CTTGAACCCC TGGGGCCCCC GTGCACCTGC CCACTCGGA GCGTGGGAG GGGCCGTGCA 300
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CGAGGCTGGG TCCCGGCCCA GGAGAAGGAA GTGCTGAAG GCACTGGCCA TGCTGGCGGT 540
GGAAATGGGA GCGGTTGCA GAGGCTCTAT GGGGCCCGGT CCGTGATACT CGGCAGGAAG 600
CGGTGCTGCG AGAGGCTCCT CCCTGCCTCA GGTGGCCCGG TTCAACCCCA GCGTGCCTCA 660
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CAGCACCCCC CCTATGCGAG ACTGGGAGGG GGTGCGGCAG TCCCTCAGC CAGCAGGACC 780
CTGATGGGT TCTAGTTTAC TTGGGACCGT GGGGCCCTGC TGCGTACTGA GTGGGTGCC 840
CACAGTCAAG GCCAACGGGG GCTCCCCCTG CTCTGAGATG TTGGGAGAAA GCGGCTTCT 900
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TCTTATCATG TTTTACCCAC CTGTCCCTT TTTTCCCCAA TTGTGCTTTT GCATTTTTTT 1080
CCTTGGCAAA TGTAACTCA GCCTTTTATT CATGAOGTGT GAAATTTTCA TTTCTCTGGA 1140
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AACTTAAAAA AATTTTAAAA AAACATAAAA CTACTCTCTA CCTTGGCTG GCGCCAGCCT 1260
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GTATTAAAG GAAAAAA 1337

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Seq ID NO: C26 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 95..2128

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CACACTGAGA GTATCTGAGG ACCTTCATGT TGGAGGAGTG ATGCTCAAGT TAGTAGAACA 240
GATCAATATA TCCCAAGACT GGTGAGACTT TGCTCTTTGG TGGGAACAGA AGCAITGCTG 300
GCTTCTGAAA ACCCACTGGA CCTTGGACAA ATATGGGGTC CAGGCAGATG CAAAGCTTCT 360
CTTACCCCTC CAGCATAAAA TGCTGCGCCT TCGTCTGCGG AATTTGAAGA TGGTGAAGTT 420
GCGAGTCAGC TTCTCAGCTG TGGTTTTTAA AGCTGTCACT GATATCTGCA AAATCTGAAA 480

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 TATATATGAC CCCATCAATG GAACACCAGC ATCATCCACC ATGACTTGGT TCAGTGACAG 720  
 CCCTTTGACG GAACAAAAC TGCAGATCCT CGCATTGAGC CAACCCCCC AGTCCCCAGA 780  
 AGCACTTGCG GATATGTACC AGCCTCGGTC TCTGGTTGAT AAAGCCAAGC TCAATGCAGG 840  
 TTGGCTAGAC TCCTCAGGCT CCCTTATGGA ACAAGGCATC CAAGAGGATG AGCAGCTGCT 900  
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 AAACCAACTC TATGAGCAAG CCAGGTGGGC CATTCCTTA GAAGAAATTG ATTGCACAGA 1020  
 GGAAGAAATG TTGATCTTTG CAGCTCTACA GTACCACATT AGCAAACTGT CGTTGCTGTC 1080  
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 TTTGGAAGTA ACCCTAGAAG GTGAAAAGC GGACAGCCTT TTGGAGGACA TTAAGTATAT 1200  
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 GTTGGCATCG AAGGGCAAAA CCATGGCAGA CAGCTCTAC CAGCCAGAGG TCCTCAACAT 1560  
 CCTTTCATT CTGAGGATGA AAAACAGGAA CTCTGCATCT CAGGTGGCTT CCAAGTCTGA 1620  
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Seq ID NO: C27 Protein Sequence  
Protein Accession #: NP\_005161.1

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Seq ID NO: C28 DNA Sequence  
Nucleic Acid Accession #: NM\_017763  
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Protein Accession #: NP\_004280.2

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	PDSDSLSLSD	SSHNNTSVIK	SNSSHSVCDE	GAIGYCTDHE	SSSHDLLEGA	VGGYYPEPSK	180
75	LCHLDQSDSD	PHGDLTFQHV	FHNHTYHLQP	TAPESTSEPF	PWPGKSQKIR	SRYLEDTRDN	240
	LSRDEQRAKA	LHIFPVSDEI	VGMPVDSFNS	MLSRYYLTDL	QVSLIRDIRR	RGNKVAQN	300
	CKRRGLDIL	NLEDDVCNLQ	AKKETLKREQ	AQCNAKINIM	KQKLHDLVHD	IFSRRLDDQG	360
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80 Seq ID NO: C30 DNA Sequence  
Nucleic Acid Accession #: NM\_004442  
Coding sequence: 19..2982

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 35 GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCCACTGC AGGTGCTGGA CTCGGCCACA 360  
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 AGGCAGATGG GCTACAGCAG CAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480  
 GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATCGG GAACTCAAGT 540  
 GGGCCCTGTC TCTCAGGCTC CTGCTCTCC CTGACTGTC TTGCTGTGG GAAGAGCCTG 600  
 40 AAGACCCCCC GTGTGGTGGG TGGGAGGAGG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660  
 AGCATCCAGT ACGACAAACA GCAGCTGTGT GGAGGGAGCA TCCTGGAGCC CCACTGGGTC 720  
 CTCAGCATGG CCGCTGCTT CAGGAAACAT ACCGATGTGT TCACTGGAA GGTGCGGGCA 780  
 GGCTCAGACA AACTGGGCGA CTTOCCATCC CTGGCTGTGG CCAAGATCAT CATATTGAA 840  
 TTCAACCCCA TGATACCCAA AGACAATGAC ATGCGCCTCA TGAAGCTGCA GTTCCCACTC 900  
 45 ACTTTCTCAG GACACAGTCA GCGCATCTGT CTGCTCTCT TTGATGAGGA GCTCACTCCA 960  
 GCCACCCAC TCTGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020  
 GACATACATG TGCAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080  
 GGTACCAGG GGGAACTCAC CGAGAAGATG ATGTGTGCGG GCATCCCGGA AGGGGCTGTG 1140  
 GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200  
 50 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260  
 AAGGTCTCAG CTAATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA 1314

Seq ID NO: C34 DNA Sequence  
 Nucleic Acid Accession #: NM\_003045.1  
 Coding sequence: 148..2037

55 1 11 21 31 41 51  
 CGATCCTGCC GGAGCCCGGC CGCGCCCGGC TTGGATTCTG AAACCTTCTT TGTATCCCTC 60  
 CTGAGACATC TTGTCTGCAA GATCGAGGCT GTCTCTGTTG GAGAAGGTGG TGAGGCTTCC 120  
 60 CGTCATATTC CAGCTCTGAA CAGCAACATG GGTGCGAAAG TCCTGCTCAA CATTTGGCAG 180  
 CAGATGCTGC GCGCGAAGGT GGTGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240  
 CTGAACACTT TTGATCTGGT GGCCTTCGGG GTGGGCGACA CACTGGGTGC TGGTGTCTAC 300  
 GTCCTGGCTG GAGCTGTGGC CCGTGAGAAAT GCAGGCCCCG CCATTGTCTT CTCCTTCTCT 360  
 65 ATGCGTGGCG TGGCCTCAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420  
 CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTACCGG TTGGAGAGCT CTGGGCCCTT 480  
 ATCAACCGCT GGAACCTAAT CCTCTCTAC ATCATCGGTA CTTCAGCGT AGCGAGGGCC 540  
 TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC 600  
 ATGACTCTGA ACGCCCCCGG CGTCTGGGCT GAAACCCCGC ACATATTGCG AGTGATCATA 660  
 70 ATTCTATCTT TGACAGGACT TTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA 720  
 ATATTCACTT GTATTAAAGT CCTGGTCTCT GGCTTCATAA TGGTGTGAGG ATTTGTGAAA 780  
 GGATCGGTTA AAACTGGCA GCTCACGGAG GAGGATTTTG GGAACACATC AGGCGGCTCT 840  
 TGTTTGAACA ATGACACAAA AGAAGGGAAG CCGGTTGTTG GTGGATTCAT GCCCTTCGGG 900  
 TTCTCTGGTG TCCTGTGCGG GGCAGGAGCT TGCTTCTATG CCTTCGTGGG CTTTGAAGTC 960  
 75 ATCGCCACCA TGGCTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCGGT GGGGATGCTG 1020  
 GCGTCCCTCT TGATCTGCTT CATCGCTTAC TTTGGGGTGT CGGCTGCGCT CAGCTCATG 1080  
 ATGCCCTACT TCTGCTCTGA CAATAACAGC CCGCTGCCCC ACGCTTTTAA GCACGTGGGC 1140  
 TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC CGCCAGTCTT 1200  
 CTAGGTTCCA TGTTTCCCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260  
 80 TTTAAATCTT TAGCCAAAGT CAATGATAGG ACCAAAACAC CAATAATGCG CACATTAGCC 1320  
 TCGGGTGGCG TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380  
 ATGTCTACTG GCACTCTCCT GCCTTACTCG TTGGTGGCTG CTTGTGTGTT GGTCTTACGG 1440  
 TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500  
 CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560  
 CGAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAAA ACATGGAGCC TTCCAAAATC 1620



5 TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680  
 ATTGTGACCG TGCTTGGAGG GGAGGCTCTC ACCAAAGGGG CGCTGTGGGC AGTCTTCTG 1740  
 CTCGAGGGT CTGCGCTCTC CTGTGCGCTG GTCAAGGGGC TCATCTGGAG CGAGCCCGAG 1800  
 AGCAAGACCA AGCTCTCAT TAAGGTTCCC TTCCTGCCAG TGCTCCCAT CCTGAGCATC 1860  
 TTCTGTAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTGTCTGTG 1920  
 TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCAGC CGAGGAGGCG 1980  
 TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAGTG CAAGTGACGC 2040  
 ACAGCCCGCG CCCCAGGAGG TGGCAGCAGC CCGAGGGGAC GCCCCAGAG GACCGGGAGG 2100  
 CACCCACACC TCCCACACG TGCAACAGAA ACCACCTGGC TCCACACCT CACTGCA 2157

Seq ID NO: C35 DNA Sequence  
 Nucleic Acid Accession #: NM\_002776.1  
 Coding sequence: 82..912

15 1 11 21 31 41 51  
 ACCAGCGGCA GACCACAGGC AGGGCAGAGG CAGCTCTGGG TCCCTCTCCCT CCTTCTATC 60  
 GGCGACTCCC AGATCCTGGC CATGAGAGCT CCGACCTCC ACCTCTCCGC CGCTCTGGC 120  
 20 GCGCGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGCG 180  
 GCGCTGTCTC CCAAAACGCA CAGCGCTTG GACCCGGAAG CCTATGGGCG CCGTGTGCGG 240  
 CGCGGCTGCG AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGGCGGGT 300  
 GTCTTGGTGG ACCAGAGTTG GGTGCTGACG GCGCGCACT GCGGAAACAA GCCACTGTGG 360  
 GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG AGCAGCTCCG CCGGACGACT 420  
 CGCTCTGTGG TCCATCCCAA GTACCAACAG GGCTCAGGCC CCATCTGGCC AAGGCGAAGC 480  
 25 GATGAGCAGC ATCTCATGTT GCTAAGCTG GCCAGGCCG TAGTGGCGGG GCCCGCGTCT 540  
 CCGGCGCTTC AGCTTCCCTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTGTCTGGC 600  
 TGGGCGACCA CGCGCGCCCG GAGAGTGAAG TACAACAAGG GCCTGACCTG CTCAGCATC 660  
 ACTATCCTGA GCCTAAAGA GTGTGAGGTC TTCTACCTCG GCGTGGTTCAC CAACAACATG 720  
 ATATGTGCTG GACTCGACCG GGGCCAGGAC CCTTGGCAGA GTGACTCTGG AGGCCCCCTG 780  
 30 GTCTGTGACG AGACCTCCA AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC 840  
 CAGCATCCAG CTGTCTACAC CCAGATCTGC AATATCATGT CCTGGATCAA TAAAGTCATA 900  
 CGCTCCAATC GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CCTGCTGATC 960  
 CAGATGCCCA GAGGCTCCAT CGTCCATCCT CTTCCTCCCC AGTCGGCTGA ACTCTCCCTT 1020  
 TGTCTGCACT GTTCAAACTT CTGCCGCCCT CCACACTCTT AAACATCTCC CCTCTCACT 1080  
 35 CATTCGCCCA CCTATCCCA TTCTCTGCC TACTGAAAG TGAATGCGAG GAAGTGGTGG 1140  
 CAAAGGTTTA TTCAGAGAA GCCAGGAAGC CGTCTATCAC CCAGCTCTG AGAGCAGTTA 1200  
 CTGGGCTCAC CCAACCTGAC TTCTCTGCC ACTCCCGCT GTGTGACTTT GGGCAAGCCA 1260  
 AGTGCCTCTC CTGAACCTCA GTTCTCTCAT CTGCAAAATG GGAACAATGA CGTGCTTACC 1320  
 40 TCTTAGACAT GTTGTGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATT 1380  
 GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTCTGACT AAAGTTTACC TGTGTGCTG 1440  
 AAAAAAAAAA AAAA 1454

Seq ID NO: C36 DNA Sequence  
 Nucleic Acid Accession #: XM\_095088  
 Coding sequence: 1..4074

45 1 11 21 31 41 51  
 ATGACCGGGG CCGGACAGC CGAGCGGGG CGCGTGTCTC CGCCTCGCC CGGCGCAGC 60  
 ACGGCGGGCC TGGCGCGGCG CTCTCTGAG AGCCTGCGCA CCTGTGTAGA CATCTGGAC 120  
 50 GACTGCGCAG GCGGCTGCGT GCACCTGCGA GAGATCCAGT CCTCTGGGT CGAAGCGCGG 180  
 GAGCTGCCAA GCGGGGTGCT GGAGGGGCTG AGCCAGCGGC GCGGGCCGCA GCCGGAGCA 240  
 GCTGTACGCT CCGCGCGAGG CGCGCGAGTG CCGCGCGGGG CCGGAGCGGT TCCAGAGCGC 300  
 TGGCTGGGAA CGGAGACCGG CGCGGAGCGC AGGTGCGAGG GCCTGCGAGG CCTTGGAGGC 360  
 55 GGATTCAGGG GATGCCCGGC GGACCCCTGT GCCCGAGGGG AACACCGGAG GCACACCATC 420  
 ACCAGCGCGG TGGACTGCGG CCGTCTGAAG CAGATGAAGG AGCTGGAGCA GGAGAAGGAG 480  
 GTGCTGCTAC AGGGTTTGA GATGATGGCG CAGGGCCGCG ATTGGTACCA GCAGCAGCTG 540  
 CAACAAGTGC AGGAGCGCCA GTGCGCGCTG GGCCAGAGCA GAGCCAGCGC CGACTTTGGG 600  
 GCGTGGGGA GCGCTCGCCC ACTGGGACGG CTACTGCCCA AGGTACAGGA GGTGGCCCGG 660  
 60 TGGCTGGGGG AGCTGTGCGC TGAGGCTGTG GCCGTGCGGG CCCTGCCCAC ATCTCTCTCC 720  
 GGGCCCCCTT GCTCTGCCCT GACGTCCACC TGTGCCCGG GCTGGCAGCA GCAGATCATC 780  
 CTCTGTCTGA AGGAGCAGAA CCGACTCCTC ACCCAGGAGG TGACCGAGAA GAGTGAGCGC 840  
 ATCAOGCAGC TGGAGCAGAA GTGCGCGCTC ATTAAGCAGC TATTTGAGGC CCGCGCCCTG 900  
 AGCCAGCAGG ATGGGGGCTT GTCCCGGCTT GGCCCCACA TTAGGCCCTT GACTGGGTTT 960  
 65 CGGCTTCGCG TGCTGACATG GGTGGGGCTT CTCTTGAGTC CGCATAGTCC GCAGTACTA 1020  
 CTGCGCTGTG CAGCGGACAG TGGGGGACCC CTCACGAGT TACCAGATAC CTGGTTTCCA 1080  
 GCGGTGCTGC TTTGGGTCCC ATCTCCAGGG AAAAGAACTG CTCACGCCAG GCTGCACITC 1140  
 CACCAAGGCG CAGCAGAGGG CGCGTGGCAG CTGCGATGCG GCGCTGAGGC TGGCGCCGAG 1200  
 70 ACCTGAGGGA CGCTGCCCA CTTTGAGTCC CACAAAACAA CCTGTGAGCC TGACTCCCTC 1260  
 GGAGGGCCCT GTCCCGAGGA GGGGGATCGC AGCTGGAGCC ACCTGGGCGC AGCGTTTGAT 1320  
 GTGCAACCGC CAGTGCAGAA AGTGACACCC AACGTGAGG ACGCTGAGG GAGTGGGCAC 1380  
 GGAGACATCT GTCCCTCTG TCCCAAGGGA CTGTTGACAT TCAGAGACAT AGCTATAGAA 1440  
 TTCTCTCTGG CGAGTGGGCA ATGCTTGGAT CATGCTCAGC AGAATTTATA TAGAGATGTG 1500  
 75 ATGTTAGAGA ACTAGCAGAA CCTGTTCTCC CTGGGTATGA CTGTCTCTAA GCCAGACTTG 1560  
 ATCGCTGTGC TGGAGCAAAA TAAAGAGCCC CAGAATATAA AGAGAAATGA GATGGCAGCC 1620  
 AAACACCGAG TTACATGTTT TCATTTCAAC CAAGACCTTC AGCCAGAGCA GAGCATAAAA 1680  
 GATTCACTCC AAAAAGTAAT ACCAAGAACA TATGGAAAT GTGGACATGA GAATTTACAA 1740  
 TTAAAAAAT GTTGTAAAAG AGTAGATGAG TGTGAGGTGC ACAGAGGAGG TTATAATGAC 1800  
 80 CTTAAACCAAT GTTGTCAAA TACCAAAAC AAAATATTTC AGACTATAA ATGTGTCAAA 1860  
 GTCTTCAGTA AATTTTCAAA TTCCAATAGA CACAATGCAA GATATACTGG AAAGAAACAT 1920  
 TGAATATGTA AAAATATGG CAAATCATTT TGCAATGTTT CACACCTAAA TCAACATCAG 1980  
 ATAATTCATA CTAAGGAGAA GTCCATACAA TGTGAAGAAT GTGGCAATTC CTTTAAACCAC 2040  
 TCCTCAAGCG GTACTACACA TAAAGAAAT CTTACTGGAG AGAAACCTTA CAGATGTGAG 2100  
 GAATGTGGCA AAGCCTTTAG GTGGCCCTCA AACCTTACTA GACATAAGAG AATTCACACT 2160

5	GGAGAGAAAC	CCTACGCATG	TGAAGAATGT	GGCCAAGCCT	TTAGGCGCTC	CTCAACACTT	2220
	ACTAACCAACA	AGAGAATTCA	TACTGGAGAG	AGACCCCTACA	AATGTGAAGA	ATGTGGCAAA	2280
	GCCTTTAGCG	TATCTCTAGC	CCTCATTTAC	CACAAGAGAA	TTCACTAGG	AGAGAAACCC	2340
	TACACATGTG	AAGAATGTGG	CAAAGCCTTT	AACCTGCTCT	CGACTCTTAA	GACACATAAG	2400
	ATAATTTCATA	CTGGAGAGAA	ACCCTACACA	TGTGAAGAAT	GTGGCAGAAC	CTTTAACTGC	2460
	TCCTCAACTG	TAAAGGCACA	TAAGAGAATT	CATACTGGAG	AGAAACCAT	CAAAATGTAA	2520
	GAATGTGACA	AAGCTTTTAA	GTGGCATTCA	AGTCTTGCTA	AACATAAGAT	AATTCACACT	2580
	GGAGAGAAAC	CCTACAAATG	CAGTGACAGC	AAAGCCTTAG	CCAAATCATC	AGAAATGCAA	2640
10	AAGGTCTACT	CTGGAGATGG	GGAAATGGA	ATCCGTGTAC	ATAAGAAAAA	GGAGACACAG	2700
	GGCTGGCTTG	TGAGAAACAA	GAACGAAAT	AGAACAGGGC	TGTTCCAGAT	CCGGGCTGCC	2760
	GTGAGACCTA	ACAGGGACCC	TTCTATGGGA	CAGCAAGAG	GTTCACTGAC	TGACCCCAAT	2820
	CAGAGGAAGG	AGGAACCTGA	CCTTCAAAT	CACATGACC	ATCAGAAATG	CTTAGAAGAT	2880
	CAAAGAAATA	CTGGAGTGGG	TGGACTGTG	ACATTGAGAG	ATGTAGTCAT	AGAATTCTCT	2940
15	CTGGAGGAGT	GGCAATGCCT	GGATCACGCT	CAGCAGAAAT	TATATAGAGA	TGTGATGTTA	3000
	GAGAACTACA	AAAACCTGGT	CTCCCTGGGT	ATTGCTGTCT	CTAAGCCAGA	CTTGATCACC	3060
	TGTCTGGAGC	AAAATAAAGA	GCCTTGGAA	ATAAGAGAA	ATGAGATGGT	AACCAACAC	3120
	CCAGACCTTC	CGCCAGAGCT	AGGCATAAAA	GATTCACTCC	AAAAAGTAAT	ACCAAGAAGA	3180
	TATGGAAAAA	GTGGACATGA	CAATTTACAA	GTAAGAAAT	GTAAGAAAT	GGGTGAGTGT	3240
20	GAGGTGCAAA	AAGGAGGTTG	TAATGAAGTT	AACCAATGTT	TGTCAACTAC	CCAAACAAA	3300
	ATATTTTCAG	CTCATAAATG	TGTCAAAGTC	TTGGGCAAT	TTTCAAATTC	CAATAGACAT	3360
	AAGACAAGAG	ATACTGGAAA	GAAACATTTC	AAATGTAAAA	AATATGGCAA	ATCATTTTGC	3420
	ATGGTTTCAC	AACTACATCA	ACATCAGATA	ATTCTACTTA	GGGAGAAATC	CTACCAATGT	3480
	GAAGAAATCG	GCAAAACCTT	CAACTGCTCT	TCAACCTTTT	CTAAACATAA	AGAATTTCAT	3540
25	ACTGGAGAGA	AACCTACAG	ATGTGAGGAA	TGTGGCAAAG	CTTTTACCTG	GTCTTCAACC	3600
	CTTACTAAAC	ATAGAGAGAT	TCATCTGGA	GAAAAACCTT	ACACATGTGA	AGAATGTGGC	3660
	CAAGCCTTTA	GCCGCTCCTC	AACACTTGCT	AACCAACAGA	GAATTCTATC	TGGAGAGAAA	3720
	CCATACACAT	GTGAAGAATG	TGGCAAAGCC	TTTAGCTTAT	CCTCATCCCT	CACCTTACCAC	3780
	AAGAGAATTC	ATACTGGAGA	GAAACCTTAC	ACATGTGAAG	AATGTGGCAA	AGCCTTTAAC	3840
30	TGCTCCTCAA	CCCTTAAGAA	ACATAAGATA	ATTCTACTG	GAGAGAAACC	CTACAAATGT	3900
	AAAGAATGTG	GGAAAGCCTT	TGCCTTCTCC	TCAACTCTTA	ATACTCATAA	GAGGATTCAT	3960
	ACTGGAGAGG	AACCTTACAA	ATGTGAAGAA	TGTGACAAAG	CTTTTAAGTG	GTCTTCAAGT	4020
	CTTGCTAATC	ATAAGAGTAT	GCATCTGGA	GAGAAACCTT	ACAAATGTGA	ATAA	4074

Seq ID NO: C37 DNA Sequence  
Nucleic Acid Accession #: NM\_032044  
Coding sequence: 182..658

40	1	11	21	31	41	51	
	AAAGATATAAA	AGCTCCAGAA	ACGTTGACTG	GGACCACTGG	AGACACTGAA	GAAGGCAGGG	60
	GCCCTTAGAG	TCTTGGTTGC	CAAAACAGATT	TGCAGATCAA	GGAGAACCCA	GGAGTTTCAA	120
	AGAAGCGCTA	GTAAGGCTCT	TGAGATCCTT	GCATAGCTA	CATCCTCAGG	GTAGGAGGAA	180
	GATGGCTTCC	AGAAGCATGC	GGCTGCTCCT	ATTGCTGAGC	TGCTTGCCCA	AAACAGGAGT	240
45	CCTGGGTGAT	ATCATCATGA	GACCCAGCTG	TGCTCCTGGA	TGGTTTTACC	ACAAAGTCCA	300
	TGCTATGTGT	TACTTCAGGA	AGCTGAGGAA	CTGGTCTGAT	GCGAGCTCG	AGTGTCAATC	360
	TTACGGAAAC	GGAGCCCAAC	TGGCATCTAT	CCTGAGTTTA	AAGGAAGCCA	GCACCATAGC	420
	AGAGTACATA	AGTGCTATC	AGAGAAGCCA	GCAGATATGG	ATTGGCCTGC	ACGACCCACA	480
	GAAGAGGCAG	CAGTGGCAGT	GGATTGATGG	GGCCATGTAT	CTGTACAGAT	CCTGGTCTGG	540
50	CAAGTCCATG	GGTGGGAACA	AGCACTGTGC	TGAGATGAGC	TCCAATAACA	ACTTTTTAAC	600
	TTGGAGCAGC	AACGAATGCA	ACAAGCGCCA	ACACTTCTCT	TGCAAGTACC	GACCATAGAG	660
	CAAGAATCAA	GATTCTGCTA	ACTCTGTCAC	AGCCCGCTCC	TCTTCTTTTC	TGCTAGCCTG	720
	GCTAAATCTG	CTCATTTAT	CAGAGGGGAA	ACCTAGCAAA	CTAAGAGTGA	TAAGGGCCCT	780
	ACTACACCTG	CTTTTTTAGG	CTTAGAGACA	GAAACTTTAG	CATTGGCCCA	GTAGTGGCTT	840
55	CTAGCTCTAA	ATGTTTGCCC	CGCCATCCCT	TTCCACAGTA	TCTTCTTCTC	CTCCTCCCTC	900
	GTCTCTGGCT	GTCTGAGCA	GTCTAGAAGA	GTGCATCTCC	AGCCTATGAA	ACAGCTGGGT	960
	CTTTGGCCAT	AAGAAGTAAA	GATTTGAAGA	CAGAAGGAAG	AAACTCAGGA	GTAAGCTTCT	1020
	AGACCCCTTC	AGCTTCTACA	CCCTTCTGCC	CTCTCTCCAT	TGCTGACACC	CCACCCGAGC	1080
	CACTCAACTC	CTGCTTGTTT	TTCTTTGGC	CATAGGAAGG	TTTACAGTA	GAATCCTTGC	1140
60	TAGGTTGATG	TGGGCCATAC	ATTCTTTTAA	TAAACCAITG	TGTACATAAG	AAAAAATAAA	1200

Seq ID NO: C38 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 52..3042

65	1	11	21	31	41	51	
	GCTCACCCAG	GAAAAATATG	CAATCGTCCC	ATTGATATAC	AGGCCACTAC	AATGGATGGA	60
	GTTAACTCTA	GCACCGAGGT	TGTCTACAAA	AAAGGCCAGG	ATTATAGGTT	TGCTTGCTAC	120
	GACCGGGGCA	GAGCCTGCGG	GAGCTACCGT	GTACGGTTCC	TCTGTGGGAA	GCCTGTGAGG	180
70	CCCAAACTCA	CAGTCACCAT	TGACACCAAT	GTGAACAGCA	CCATTCTGAA	CTTGGAGGAT	240
	AATGTACAGT	CATGGAAGAC	TGGAGATACC	CTGGTCATTG	CCAGTACTGA	TTACTCCATG	300
	TACCAGGCAG	AAGAGTTCCA	GGTGCTTCCC	TGCAGATCCT	GCGCCCCCAA	CCAGGTCAAA	360
	GTGGCAGGGA	AACCAATGTA	CCTGCACATC	GGGAGGAGGA	TAGACGGCGT	GGACATGCGG	420
75	GCGGAGGTTG	GGCTTCTGAG	CGGAACATC	ATAGTGTAGG	GGGAGATGGA	GGACAAATGC	480
	TACCCCTACA	GAAACCCATC	CTGCAATTTT	TTTGACTTCG	ATACCTTTGG	GGGCCACATC	540
	AAGTTTGCTC	TGGGATTTAA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTCAAGT	CCCGATTAC	TTCCACCTGG	CGGGTGTATG	AGAAGAAAGG	660
	GGAGGTTATG	ACCCACCCAC	ATACATCAGG	GACCTCTCCA	TCCATCATAC	ATTCTCTGCG	720
80	TGCGTCAAG	TCCATGGCTC	CAATGGCTTG	TGTATCAAGG	ACGTTGTGGG	CTATAACTCT	780
	TTGGGCCACT	GCTTCTTAC	GGAAGATGGG	CCGGAGGAAC	GCAACACTTT	TGACCACTGT	840
	CTTGGCCTCC	TGTTCAAGTG	TGGAACCTTC	CTCCCTCGG	ACCGTGACAG	CAAGATGTGC	900
	AAGATGATCA	CAGGAGACTC	CTACCCAGGG	TACATCCCCA	AGCCAGGCA	AGACTGCAAT	960
	GCTGTGTCCA	CCTTCTGGAT	GGCCCAATCC	AACAACAACC	TCACTCACTG	TGCCGCTGCA	1020
	GGATCTGAGG	AAACTGGATT	TTGGTTTATT	TTTACCACCG	TACCAACGGG	CCCCCTCGTG	1080

	GGAATGTACT	CCCCAGGTTA	TTGAGAGCAC	ATTCCACTGG	AAAAATTCTA	TAACAACCGA	1140
	GCACATTCCA	ACTACCGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCTGCCAAGG	ACAAGCGGGC	GTTCCTCTCA	ATCATCTCTG	CCAGATACAG	CCCTCACCAG	1260
5	GACGCCGACC	CGCTGAAGCC	COGGGAGCCG	GCCATCATCA	GACACTTCAT	TGCTTACAAG	1320
	AACCAGGACC	ACGGGGGCTG	GCTGCGCGGC	GGGGATGTGT	GGCTGGACAG	CTGCCGGTTT	1380
	GCTGACAATG	GCATTGGCCT	GACCCCTGGC	AGTGGTGGAA	CCTCCCGTA	TGACGACGGC	1440
	TCCAAGCAAG	AGATAAAGAA	CAGCTTGTTT	GTGGCGGAGA	GTGGCAACGT	GGGGACGGAA	1500
	ATGATGGACA	ATAGGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCCCTCCCT	1560
10	ATAGGCCAGA	ATTTTCCAAT	TAGAGGAATT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACTT	TCCGAAAGTT	TGTGGCCCTG	GAGGGCCGGC	ACACCAGCGC	CCTGGCCTTC	1680
	GGCTTGAATA	ATGCCCTGGC	GAGCTGCCCC	CATAACAACG	TGACCGGCAT	TGCCCTTGAG	1740
	GACGTTCCGA	TTACTTCCAG	AGTGTCTTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTT	CATGACGTCG	ACGGCTCCGT	GTCCGAGTAC	1860
	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGGTCC	GGCACCCAGA	CTGCATCAAT	1920
15	GTTCGCCACT	GGAGAGGGGC	CATTTCAGT	GGGTGCTATG	CACAGATGTA	CATTCAAGCC	1980
	TACAAGAAAT	GAGCTCTGCG	AATGAAGATC	ATCAAGAATG	ACTTCCCGAG	CCACCTCTT	2040
	TACCTGGAGG	GGGCGCTCAC	CAGGAGCACC	CATTACCAGC	AATACCAACC	GGTTGTCAAC	2100
	CTGCAGAGG	GCTACACCAT	CCACTGGGAC	CAGACGGGCC	CCGCCGAAC	CGCCATCTGG	2160
20	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGCTACCC	GCGAGGACCC	2220
	ACATCTCTCA	TCTCTCGGGA	TGTTCACAAT	CGCCTGCTGA	AGCAAAAGTC	CAAGACGGGC	2280
	GTCTTCGTGA	GAGCCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTGGG	CAGGAGCCAC	2340
	TACTACTGGG	ACGAGGACTC	AGGGCTGTTG	TTCTGAAGC	TGAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTCTGCTCT	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
25	CCAAAGAACG	CAGGCGTCAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
	GCTGTGCTAG	ACGTGCCCAT	GGCCAAAGAG	CTCTTTGGTT	CTCAGCTGAA	AACAAAGGAC	2580
	CATTCTTTGG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAACGAC	2640
	TTGCTTACA	TTGAAGTGA	TGGGAAGAA	TACCCAGTT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACCTCAAT	2760
30	CTGCAAGGCA	TACCATGGCA	GCTTTTCAAC	TATGTGGGGA	CCATCCCTGA	CAATTCCATA	2820
	GTGCTTATGG	CATCAAAAGG	AAGATACGTC	TCCAGAGGCC	CATGGACAGG	AGTGTGGGAA	2880
	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAGAGCAAAA	TGGCATTCTG	TGGCTTCAAA	2940
	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCAAAAAGC	CAAAATCTTC	3000
	CAAGTTGTGC	CCATCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
35	GCCACCTCGT	GGTAGACTAT	GACGGTGACT	CTTGGCAGCA	GACCACTGGG	GGATGGCTGG	3120
	GTCCCCACGC	CCCTGCCAGC	AGCTGCTGCG	GAAGGCCGTG	TTTCAGCCCT	GATGGGCCAA	3180
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40	GTGCTGACAG	CAAAAGATCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAGTCTGGA	3420
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45	AGGCCCCCTT	AGTTCTTGAGA	TTCCAGAAAT	CTGCTGCATT	TCACATGGTA	CCTGGAAACC	3720
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	ATGATAGAGC	ATGTGTGGTA	GAGGGGAGCA	ATGGGCTTTG	CTGCTTATGA	GCACAGAGGA	4140
	ATTGAGTCCC	CAGGACAGCC	TGCCCTCTGAC	TCCAGAGGGG	TGAAGTCCAC	AGAAGTGAGC	4200
	TTCTGCTCTA	GGGCTCTATT	TGCTCTTCAT	CCAGGGAACT	GAGCACAGGG	GGCCTCCAGG	4260
55	AGACCTTAGA	TGTTGCTGTA	CTCCCTGGGC	CTGGGATTTC	AGAGCTGGAA	ATATAGAAAA	4320
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60	CCCTCTGCT	CCCAGCGCAC	ACAAACCCGC	CCTCCCTTGG	GTGTTGGCGG	TCCCTGTGGC	4620
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	TGGTGCTACC	TGGCTCTCCT	GTCTCTGCAG	CTCTACAGGT	GAGGCCACGC	AGAGGGAGTA	4740
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	CAACCCACAA	CTCTTTCCCT	CAAGAGGGGC	CTGCCCTGGC	CCCTCCACCC	AACTGCACCC	5040
	ATGAGACTCG	GTCCAAGAGT	CCATTCCCCA	GGTGGGAGCC	AACTGTGAGG	GAGGTCTTTC	5100
	CCACCAACAA	TCTTTAGCT	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
70	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTGATGGAG	5220
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75	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
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	AGCTCTCTCT	GAAATGCTTG	TCCTTTTCT	GTGCGGAAA	TAGCTGGTCC	TTTTTCGGGA	5640
	GTTAGATGTA	TAGAGTGTGT	GTATGTAAAC	ATTTCTTGTA	GGCATCACCA	TGAACAAAGA	5700
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80	AATGTCTCTA	AATGTCAAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	5808

Seq ID NO: C39 DNA Sequence  
Nucleic Acid Accession #: NM\_014373  
Coding sequence: 322.1338

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   AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
   GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGGTCT 300
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   ATCTGCCTAT TTAATCAAAAT TATTTCTTTT ACTTATGGCT TTTTGCAATTA TCCAGTTTTC 660
   CTGACAGGCT GTATAGATTA TTGCCTGAAT TTCTCTAAAA CAACCAAGCT TTCATTAAAG 720
15  TGTCAAATAT TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTTCAGT CCTTGCTTAT 780
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   TGTCTTTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCTT TTTTCATGGT GATGATTTTA 900
   TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
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20  GTGAGATCTA AAAAATATTT CTTATCCAAG CTCATGTCCT GTTTTCTCAG TACCTGGTTA 1080
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25  TCAATAATGA TTTGTTAATA TTATTAAATA AAAGTTACAG CTGTCAATAG ATCATAATTT 1380
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   CCTGACTGA TAGCATTTC GAATGTGCT TTTGAAGGCG TATACCAGTT ATTAATAGT 1500
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   TTACAAATAT TACTTTGTTA TTAACAAAA AAGTGATAAG AGTTAAACATT TGGCTATACT 1620
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Seq ID NO: C40 DNA Sequence  
Nucleic Acid Accession #: BC012089  
Coding sequence: 1..2571

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   ATCTTTCTCT ATGTGGTACA GCCGCGTGAT TTCCCAGAAG ATACTTTGAG AAAATTTCTTA 240
   CAGAAGGCAT ATGAACTCAA AATTGATTAT GACAAGATTG TCTACTATGA AGCAGGGATT 300
45  ATTCTATGCT GTGCTCTGGG GCTGCTGTTT ATTATTCTGA TGCTCTGGT GGGGTATTTC 360
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   AGCATTGGCA TCCTCTATGG TTTTGTGGCA AATCACCAGG TAAGAACCAG GATCAAAAGG 540
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55  CATCCATCAA GTGAAACCTG CAACAGCATC AGATTGTCTC TAAGCCAGCT GAATAGCAAC 960
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   TTGGGTGCAG CAGGAAGAAA AAACCTTCAG GATTTTGCTG CTTTGGGAAT AGACAGAATG 1860
   AATTATGACA GCTACTTGGC TCAGACTGGT AAATCCCCCG CAGGAGTGAA TCTTTTATCA 1920
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   CTGAAAGAGG ATGCACAAAC TATTAAACAA ATTCACCAGC AACGAGTCTT TCCTATAGAA 2040
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Seq ID NO: C41 DNA Sequence

Nucleic Acid Accession #: NM\_033049  
Coding sequence: 28..1566

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GAAACTGCTA GCACCAAGC AAATACACCT TCTTTCCCAA CAGTACTTTC ACCTGCTCCC 240
10 CCCATAATTA GTACACATAG TTCCTCCACA ATTCCTACAC CTGCTCCCCC CATAATTAGT 300
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Seq ID NO: C42 DNA Sequence  
Nucleic Acid Accession #: NM\_001432.1  
Coding sequence: 167..676

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65 GAGGATGAGG ATGCTCTGTG CCGGCAGGGT CCTGCGCTG CTGCTCTGCC TGGGTTTCCA 240
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35	AAAAACAAGT	CATTTTGTGA	TTTTTCATCT	TTAAGAAATG	TTAAAAAAGC	TAATCCCTAA	3420
	AATAGTTAGA	TCTTTGTAAA	TGCATATTAA	ATAATAAAGT	ATGACCCACA	TTACTTTTAA	3480
	TGGGTGAAAA	TAAACACAAA	ATAATAGTTT	TAGTGAGGAT	GGTGCTGAGT	AAACATAAAA	3540
	ACTGATTGTC	TCTCAGCTGA	TGTGTCTGT	ACACAGTGGG	AAGATTTTAG	TTACACTTAA	3600
	GTCTAATCTC	CCCATTTTAC	AGATTCTTCA	CTATATATAT	TTCTAGAAGG	GGCTATGCAT	3660
40	ATTCAAATGA	TTGAGAACCA	AAGCAACCCAC	AAATGCATAA	ATGCATAATT	TATGGTCTTC	3720
	AACCAAGGCC	ACATAATAAC	CCAGTTAACT	TACTCTTTAA	CCAGGAATAT	TAAGTTCTAT	3780
	AACTATTAAC	CAAGTTTAA	CCTTAAAT	AAGATTTCCT	TAACCTTAAC	CTTAAATTTG	3840
	ATATTATATT	AAACATACAT	AATACAAATG	AACTCCACTG	TTCTCCTGAA	TATTTTTTGC	3900
	TCTAATCTCT	CTGCGGAAGG	TCARAAGTAT	GGGAGAATTG	GTATACTGGT	ATGACTACGT	3960
45	CTTAAGTCAG	CATTTTATTT	ATGAGTCTTT	GAGACTAAAT	TCAATCACC	CCAGGTATCA	4020
	AATCAACTTT	TATGCAGCAA	ATATATGATT	CTAGTGTCTG	ACTTTTGTGA	AAATCAGTAA	4080
	TGCAGTTTTT	AAAAACCTGT	ATCTGACCCA	CTTTGTAAAT	TTTGTCTCAA	TATCCATTCT	4140
	GTAGACTTTT	GAATAAAAG	TTTTTAATTT	GATGCCAAT	ATATTCTGAC	CGTTAAAAAA	4200
	TTCTTGTCTA	TATGGGAGAA	GGGGGAGTAA	TGACTGTATC	AAACAGTATT	TCTGGTGTAT	4260
50	ATTTTAATGT	TTTTAAAAAG	AGTAATTTCA	TTTAAATATC	TGTTATTCAA	ATTGTATGAT	4320
	GTAAATGTA	ATATAAGTGA	TTTTCTTTT	ATTTTGCACT	CTGTAATTGC	ACTTTTAAAG	4380
	TTTGAAGAGC	CATTTTGGTA	AACGGTTTTT	ATTAAAGATG	CTATGGAACA	TAAAGTTGTA	4440
	TGTCATGCAA	TTTAAAGTAA	CTTATTGGAC	TATGAATATT	ATCGGATTAC	TGAATTGTAT	4500
	CAATTGTGTT	GTGTTCAATA	TCAGCTTTGA	TAATTGTGTA	CCTTAAGATA	TTGAAGGAGA	4560
55	AAATAGATAA	TTTACAGAGT	ATTATTAATT	TTTATTATT	TTTCTTGGGA	ATTGAAAAAA	4620
	ATTGAATAAA	ATAAAAATGC	ATTGAACATC	TTGCATTCAA	AATCTTCACT	GAC	4673

Seq ID NO: C43 DNA Sequence

Nucleic Acid Accession #: AF011468.1

Coding sequence: 257..1468

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	CAAGTCCCTT	GTGCGTTCTT	CGTCCCTTGA	GTGTCTTGG	GGTCCCTTGG	TGCCCGCCCA	180
	GGGCTTTTGC	ATCCGCTCCT	GGGCAACGAG	GGGCTCTGTA	GGATAGTCTG	TGTACTTTAT	240
	TACAGCTAGA	GGCATCATGG	ACCGATCTAA	AGAAAACTGC	ATTTTCAGGAC	CTGTTAAGGC	300
70	TACAGCTCCA	GTGAGAGTTC	CAAAACGTTG	TCTCGTGACT	CAGCAAAATC	CTTGTGAGAA	360
	TCCATTACCT	GTAAATAGTG	GCCAGGCTCA	GCGGGTCTTG	TGTCTTCTAA	ATTCTTCCCA	420
	GGCGTTCTCT	TTGCAAGCAC	AAAAGCTTGT	CTCCAGTCAC	AAGCCGGTTC	AGAATCAGAA	480
	GCAGAAGCAA	TTGCAGGCAA	CCAGTGTACC	TCATCTCTGT	TCCAGGCCAC	TGAATAACAC	540
	CCAAAGAGAG	AAGCAGCCCC	TGCCATCGGC	ACCTGAAAT	AATCCTGAGG	AGGAACCTGG	600
75	ATCAAAACAG	AAAAATGAAG	AATCAAAAAA	GAGGCAGTGG	GCTTTGGAAG	ACTTTGAAAT	660
	TGGTCCGCTT	CTGGGTAAAG	GAAAGTTTGG	TAATGTTTAT	TTGGCAAGAG	AAAAGCAAAG	720
	CAAGTTTATT	CTGGCTCTTA	AGTGTATTAT	TAAAGCTCAG	CTGGAGAAAG	CCGGAGTGGG	780
	GCATCAGCTC	AGAAGAGAAG	TAGAAATACA	GTCCCACTTT	CGGCATCCTA	ATATTCTTAG	840
	ACTGTATGGT	TATTTCCATG	ATGCTACACG	AGTCTACCTA	ATTCTGGAAT	ATGCACCATT	900
80	TGGAACATGT	TATAGAGAAC	TTCAAGAACT	TTCAAGTTT	GATGAGCAGA	GAACCTGCTAC	960
	TTATATAACA	GAATTGGCAA	ATGCCCTGTC	TTACTGTGAT	TGGAAGAGAG	TTATTCTATG	1020
	AGACATTAA	CCAGAGAACT	TACTTCTTGG	ATCAGCTGGA	GAGCTTAAAA	TTGCAGATT	1080
	TGGGTGGTCA	GTACATGCTC	CATCTTCCAG	GAGGACCACT	CTCTGTGGCA	CCCTGGACTA	1140
	CCTGCCCTCT	GAAATGATTG	AAGGTCCGAT	GCATGATGAG	AAGGTGGATC	TCTGGAGCCT	1200
	TGGAGTTCTT	TGCTATGAAT	TTTTAGTTGG	GAAGCCTCCT	TTTGAGGCAA	ACACATACCA	1260

5	AGAGACCTAC	AAAAAATAT	CACGGGTGA	ATTACATTC	CCTGACTTTG	TAACAGAGGG	1320
	AGCCAGGGAC	CTCATTTC	GAATCTTGA	GCATAATCCC	AGCCAGAGGC	CAATGCTCAG	1380
	AGAAGTACTT	GAACCCCTC	GGATCAGAC	AAATTCATCA	AAACCATCAA	ATTGCCAAAA	1440
	CAAAGAATCA	GCTAGCAAC	AGTCTTAGGA	ATCGTGCAGG	GGGAGAAATC	CTTGAGCCAG	1500
	GGCTGCCATA	TAACCTGACA	GGAACTGCT	ACTGAAGTTT	ATTTTACCAT	TGACTGCTGC	1560
10	CCCTAATCTA	GAACGCTACA	CAAGAAATAT	TTGTTTTACT	CAGCAGGTGT	GCCTTAACCT	1620
	CCCTATTTCAG	AAAGCTCCAC	ATCAATAAAC	ATGACACTCT	GAAGTGAAAG	TAGCCACGAG	1680
	AATTGTGCTA	CTTACTACTG	TTTATAATCT	GGAGGCAAGG	TTGACTGCA	GCCTCCCTGT	1740
	CAGCCTGTGC	TAGGCATGGT	GTCTTACAG	GAGGCAATC	CAGAGCCTGG	CTGTGGGGAA	1800
	AGTGACCACT	CTGCCCTGAC	CCCGATCAGT	TAAGGAGCTG	TGCAATAACC	TTCTAGTAC	1860
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	GTGATTCCTT	TTAAGTATGA	AAATAAAGAT	ATATGTACAG	ACTTGTAATT	TTTCTCTGGT	1980
	GGCATTCTCT	TAGGAATGCT	GTGTCTCTGT	CCGGCAGCCC	GGTAGGCTTG	ATTGGGTTTC	2040
	TAGTCTCTCT	TAACCACTTA	TCTCCCATAT	GAGAGTGTA	AAAATAGGAA	CACGTGCTCT	2100
	ACCTCCATTT	AGGGATTGTC	TTGGGATACA	GAAGAGGCCA	TGTGTCTCAG	AGCTGTTAAG	2160
20	AGCTTATTTT	TTTAAACAT	TGGAGTCATA	GCATGTGTGT	AAACTTTAAA	TATGCAATAA	2220
	AAATAAGTATC	TATGTCTAAA	AAAAAATAA	AAA			2253
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	Nucleic Acid Accession #: NM_013372						
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	CGGCTGCTGA	AGGGAATAAG	AAAGGGTCCC	AAGGTGCCAT	CCCCCGCCCA	GACAAGGCCC	180
	AGCACAATGA	CTCAGAGCAG	ACTCAGTGGC	CCGAGCAGCC	TGGCTCCAGG	AACCGGGGGC	240
30	GGGGCCAAGG	GCGGCGCACT	GCCATGCCCC	GCGAGGAGGT	GCTGGAGTCC	AGCCCAAGAG	300
	CCCTGCACTG	GACGGAGCGC	AAATACCTGA	AGCGAGACTG	GTGCAAAACC	CAGCCGCTTA	360
	AGCAGACCAT	CCACGAGGAA	GGCTGCAACA	GTCCGACCAT	CATCAACCGC	TTCTGTTACG	420
	GCCAGTGCAG	CTCTTTCTAC	ATCCCCAGGC	ACATCCGGAA	GGAGGAAGGT	TCCTTTCACT	480
	CCCTGCTCCT	CTGCAAGCCC	AAGAAATTC	CTACCATGAT	GGTCACACTC	AACTGCCCTG	540
35	AACTACAGCC	ACCTCAAGAG	AAGAAGAGAG	TCACACGTGT	GAAGCAGTGT	CGTTGCATAT	600
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	AGGAAGTCCC	AGACCTAAAA	CAACCAGATT	CTTACTTGGC	TTAAACCTAG	AGGCCAGAAG	720
	AACCCCCAGC	TGCCTCTGGS	CAGGAGCCTG	CTTGTGCGTA	GTTCGTGTGC	ATGAGTGTGG	780
	ATGGGTGCTT	GTGGGTGTTT	TTAGACACCA	GAGAAAAAC	AGTCTCTGCT	AGAGAGCACT	840
40	CCCTATTGTT	TAAAGTATAT	TGCTTTAATG	GGGATGTACC	AGAAACCCAC	CTCACCCCGG	900
	CTCACATCTA	AAGGGGCGGG	GCGTGGTCT	GGTCTGACT	TTGTGTTTTT	GTGCCCTCCT	960
	GGGGACCAGA	ATCTCCTTTC	GGAATGAATG	TTATGGAAG	AGGCTCCTCT	GAGGSCAAGA	1020
	GACCTGTTTT	AGTGCTGCAT	TGCAATGGA	AAAGTCTTTT	TAACCTGTGC	TTGCATCTCT	1080
	CTTCTCTCCT	CCTCCTCACA	ATCCATCTCT	TCTTAAGTTG	ATAGTGACTA	TGTCAGTCTA	1140
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	TTTTGTGAAG	ACCTCCAGAG	CTCTGGGAGA	GGCTGGTGTG	GGCAAGGACA	AGCAGGATAG	1260
	TGGAGTGAGA	AAGGGAGGGT	GGAGGGTGAG	GCCAAATCAG	GTCCAGCAAA	AGTCAGTAGG	1320
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	TTTTCTAGT	ATTTAAACAG	ACCCAAAGTG	ACAGAGGAGA	AATGAGATTG	CCAGAAAGTG	1440
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55	GCCTCTGCTG	AGTGTACCTG	ACAGTAAGTC	TAAAGATGAR	AGAGTTTAGG	GACTACTCTG	1800
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	RAGAGAAGAC	GACGAGAGTA	AGGAAATAAA	GGGRATTGCC	TCTGGCTAGA	GAGTAAGTTA	1920
	GGTGTTAATA	CCTGTAGAG	ATGTAAGGGA	TATGACCTCC	CTTTCTTTAT	GTGCTCACTG	1980
	AGGATCTGAG	GGGACCTGCT	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCACTGC	2040
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	TCTGATTAAT	CTTGGCCTAC	TGGCAATGGC	TACTTAGGAT	TGATCTAAGG	GCCAAAGTGC	2160
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	TCAGTGTCTC	TCCATCTTAA	CAACTAAACA	GGAGCCATTT	CAAGGCGGGA	GATATTTTAA	2460
	ACACCCAAAA	TGTTGGGTCT	GATTTTCAAA	CTTTTAAACT	CACTACTGAT	GATTTCTCAG	2520
	CTAGGCGAAT	TTGTCCAAAC	ACATAGTGTG	TGTGTTTTGT	ATACACTGTA	TGACCCCAAC	2580
	CCAAATCTTT	GTATTGTCCA	CATTCTCCAA	CAATAAGGCA	CAGAGTGGAT	TTAATTAAAG	2640
70	ACACAAATGC	TAAGGCAGAA	TTTTGAGGGT	GGGAGAGAAG	AAAAGGGAAA	GAAGCTGAAA	2700
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	AGCAGTAATC	TTCTTTTAGG	AGCTTGTACC	ACAGCTCTTG	ACATAAGTGC	AGATTTTGGCT	2880
	CAAGTAAAGA	GAATTTCTCT	AACACTAATC	TCACTGGGAT	AATCAGCAGC	GTAACCTACC	2940
75	TAAAGCATA	TCACTAGCCA	AAGAGGGAAA	TATCTGTCTC	TCTTACTGTG	CCTATATTAA	3000
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80	GTCTGTAAGT	TGTTTTTTGT	TACTGTAGGT	CTTCAAGATT	AAGAGTGTAA	GTGAAAAATC	3300
	TGGAGGAGAG	GATAATTTCC	ACTGTGTGGA	ATGTAATAG	TAAATGAAA	AGTTATGGTT	3360
	ATTAAATGTA	ATTATTACTT	CAATCCTTTT	GGTCACTGTG	ATTTCAGACA	TGTTTTCTTT	3420
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	TTAGAGTCTT	TATCTGGTTC	AGGGGAAACA	AAATCTTGAC	CCAGCTGAAC	ATGTTCTCCT	3540
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5 AAGCAATATT AAGAAAGACT TTAATGTGA TTTTGAAGA CTTACGATGC ATGTATACAA 3660  
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 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 200..2932

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 20 CACTGACGGC CACGGTGGCT TCCTGGGGAA AAATGATGGC ATCAAACAA AAAAAGAACT 300  
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70 Seq ID NO: C46 DNA Sequence  
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 Coding sequence: 75..374

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 80 AGAGTGGACC ACCTCTGGCC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300  
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Seq ID NO: C47 DNA Sequence  
Nucleic Acid Accession #: NM\_005603.1  
Coding sequence: 1..3756

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50 Seq ID NO: C53 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..609

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70 Seq ID NO: C54 DNA Sequence  
Nucleic Acid Accession #: NM\_002438.1  
Coding sequence: 104..4474

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 Coding sequence: 424..2130

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	GGACACTTCA	GCGGATTGAA	TTTTCTCTTT	TTATCTGCCT	CGTCCCCGCG	CCTCCAGGCT	300
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	GCACACCACA	CCACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAC	AGATCTTTTT	420
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	CCAGAAATTA	CCCACCCGGG	ATGAGGAAC	TTTTCAGATG	CAGATCCGGG	ACAAGGCATT	540
	TTTTCATGAT	TCGTCAGTAA	TTCCAGATGG	AGCTGAAATT	AGCAGTTATC	TCTTTAGAGA	600
10	TACACCTAAA	AGGTATTTC	TTGTGGTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
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	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTAA	780
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	TCGACTGAAA	GGAAACAAGA	AAGGAGCATC	TATGTTGAAA	ATTCTAGCTA	CCCAAGGCC	1740
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Seq ID NO: C56 DNA Sequence

Nucleic Acid Accession #: BC034229.1

Coding sequence: 373..1422

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Seq ID NO: C57 DNA Sequence  
Nucleic Acid Accession #: NM\_024687.1  
Coding sequence: 138..1706

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CTTCAACAGC AAATTTTCCA CTTTCCAAC CTGTTAAAGA AAGCTCCAGT TGCCTTTTCT 1260
CCTCTCATCC TCGATCAAGA AGTGACAGCT CTCATCATC ATCTAGAGCT GCTTCTGAAA 1320
TTTCAGAAAT TGAATATATT GATATTACTG ACCAGAATGA GCTTTCCTTA GATGACACTA 1380
CTGATCAACA TACTTTAGAC AATTTGAGAA AAGAATTACA AGTGCTGAGA TCTCTTGCA 1440
ATACTTCAGA AAAGCTTAC AGCTTAACCT CAGAAGAGTT CCCAGATTTC AGCAGCCAT 1500
CACTGAATAT AAGTCAGATT TCCACAGATT TCCTTAAGAC CTCACATGTG AGGGGTCCT 1560
GTGAGATTGA GGAATTGAGC TGTCTGGA GAGATACCAA AATTCAGTCT TTGCTGTAC 1620
TTTCTGAGAG CAGTACAGAT GAGGAGGAG AAGATTTTCT CAACAAGCAA CATGTCATCA 1680
CACTACCGTG GTCAAGAGT ACTTAAAGAT TATTGTGTC TACTGTGTT CATTTGTAC 1740
CCAGAGTAAA GCAAAACACT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGCTGGAG 1800
ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAG TAAATATATA 1860
AGTTCAAAA AAAAAAAA AAAA 1884

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Seq ID NO: C58 DNA Sequence  
Nucleic Acid Accession #: NM\_005408.1  
Coding sequence: 76..372

65  
70  
75  
80

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1 11 21 31 41 51
| | | | |
AAAAGGCGG CGGAACAGCC AGAGGAGCAG AGAGGCAAG AAACATTGTG AAATCTCCAA 60
CTCTTAACCT TCAACATGAA AGTCTCTGCA GTGCTTCTGT GCCTGCTGCT CATGACAGCA 120
GCTTTCAACC CCCAGGACT TGCTCAGCCA GATGCATCA ACGTCCATC TACTTGCTGC 180
TTCACATTTA GCAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC 240
AGCAGGTGTC CCCAGAAGGC TGTCTCTTC AGAACCACAC TGGGCAAGGA GATCTGTGCT 300
GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCGGAA AGCTCACACC 360
CTGAAGACTT GAATCTGCT ACCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420
TCCATTCTCC TCTGGCTCC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480
AGGATGCAAT CGGTTTGTG ATTCAAAATG TACTATGTGT TAAGTAATAT TGGCTATTAT 540
TTGACTTGT TCTGGTTTG AGTTTATTG AGTATTGCTG ATCTTTCTA AAGCAAGGCC 600
TTGAGCAAGT AGGTTGCTGT CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660
GGGTTGTAT TCGGTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG 720
GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTGCTA AATATGTTAT 780
TGTGAAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATT 840
AAAATCTCCA AAAAAAAA 860

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Seq ID NO: C59 DNA Sequence  
Nucleic Acid Accession #: AK097746.1  
Coding sequence: 185..2224

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1      11      21      31      41      51
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5  CTTTCATGAC AGTAACAAAT CCAAGATTTT GGAAAAGCGC CTACGATATT TAAATGACCA 60
   CTTTCACATAC AACTTATATT GTAATATATG CCGATCACTA TTTGAGAAGG ACAAGCTGTT 120
   ATTTTCCTTT TTAATTATGTG CCAATCTTCT TCTGGCAAGG AAAGAGATTG AATACCAAGG 180
   ACTGATGTTT CTTTAACTG GAGGAGTAAG TCTTAAAGT GCTGAGAAAA ATCCTGATCC 240
   AACTTGGCTA CAGGACAAAA GCTGGGAGGA AATCTGTGCG GCAAGTGAAT TTCCTGCCTT 300
10  CAGAGGACTC AGSCAACATT TTTGTGAACA TATATATGAA TGGCGAGAAA TCTATGACAG 360
   TAAAGAGCCA CATATGCTA AATTTCCAGC ACCAATGGAT AAGAACCTAA ATGAACCTACA 420
   GAAAAATAATA ATTCTTCGGT GTTAAAGACC TGATAAGATA ACCCCAGCTA TAACAAACTA 480
   TGTAACTGAC AAACAGGGA AAAAGTTTGT AGAGCCTCCA CCATTTGATT TGACAAAGAG 540
   TTACTTGGAT TCAAAATGCA CCATTCCCTT AATTTTGTG CTATCTCCAG GAGCAGATCC 600
   TATGGCCAGC CTGCTGAAAT TTGCAAAATG TAAATCTATG TCTGGAAATA AGTTTCAAGC 660
15  TATTTCACTG GGCAGGAGAC AAGGACCGAT TGCAGCAAAA ATGATTAAG CAGCAATTTGA 720
   AGAAGGAATC TGGGTGTGCC TACAGAAATT CCATCTTGCA GTGTCTGGA GCCCATGTT 780
   GGAAAAAATA TGTGAAGATT TTACTCTGA AACCTGTAAC TCATCCTTTA GGCTTTGGCT 840
   GACAAGCTAT CCATCTTCAA AATTCACAGT AACAAATCTA CAGAATGGAG TAAAAATGAC 900
   TAATGAACCT CCCACGGGTC TTGGGCTGAA TCTCCTTCAA TCATATCTCA CTGATCCAGT 960
20  TTTCTGATCT GAGTTTTTCA AGGGATGCGG TGGAAAAGGAA CTGTTATTTA TCAATGAATA 1020
   TGATACAACT CCATTTGAAG CTATATCTTA CTTGACTGGG GAGTGTAAAT ATGGAGGAAG 1080
   AGTGACAGAC GATTGGGACA GAGCTCTTCT ATTAACCATG CTGGCTGACT TTTATAATCT 1140
   GTACATAGTT GAAAACCTTC ATTATAAGTT TTTCTCCAGT GGAAACTATT TTGCACCTCC 1200
25  TAAAGGCACCT TATGAGGACT ACATTGAATT CATTAAGAAA CTTCATTTA CTCACACCCC 1260
   TGAGATATTT GGATTACATG AAAACGTTGA CATCTCCAAG GATCTTCAAC AAACAAAAAC 1320
   CCTCTTTGAG TCGTGTGCTC TCACCCAGGG AGGCTTCAAA CAGACAGGAG CCTCAGGAAG 1380
   TACTGATCAG ATTCTGTTAG AAATTACCAA AGATATCCTC AACAGCTCC CTAGTGATT 1440
   CGACATTGAA ATGGCACTAC GGAAGTATCC TGTGAGATAT GAAGAAAGCA TGAATACTGT 1500
30  GTTAGTACAA GAAATGGAAA GATTAAACAA TTTAATTATA ACTATACGTA ACATCTACG 1560
   GGACCTTGAA AAAGCTATTA AGGGTGTGGT TGTGATGGAT TCTGCAATGG AGGCACTCTC 1620
   CAGTAGCTTA CTGTGTGGA AGGTTCCAGA AATATGGGCC AAACGTTTAT ACCCAAGCCT 1680
   TAAGCCCTTG GGAAGTTACA TCACAGATTT CTTAGCCCGG TTGAACCTTT TACAGGACTG 1740
   GTATAATTCA GGAACCCCTT GTGTGTTTTG GCTGTCAAGT TTTCTTTTCA CTCAGGCCTT 1800
35  TTTAACTGGA GCTATGCAGA ATTATGCCAG AAAATATACC ACCCTATTG ATTTGCTAGG 1860
   ATATGAATTT GAGGTATATC CATCTGATAC ATCTGACACA TCACCAGAAG ATGGTGTTTA 1920
   TATCCACGGA CTGTATCTCG ATGGCGCACG CTGGGACCGA GAAAGTGGAT TGCTTGCTGA 1980
   ACAATATCCC AAATCTCTGT TTGACCTGAT GCCCATCATA TGGATAAAAC CAACTCAAAA 2040
   ATCTCGGATT ATAAAGTCGG ATGCCATATG CTGTCCCCTC TACAAGACAA GTGAACGTAA 2100
40  AGGAACCTCT TCCACTACGG GACATCTTAC TAACTTTGTC ATTGCAATGT TGTAAAAAAC 2160
   AGACCAACCT ACTCGGCACT GGATCAAGCG CGGGGTGCTT TTGCTTTGTC AGTTGGATGA 2220
   CTAATTTGGA CAAATTTATA AAACATCCAA AAGTTT 2256

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Seq ID NO: C60 DNA Sequence  
Nucleic Acid Accession #: J02761.1  
Coding sequence: 14..1159

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1      11      21      31      41      51
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50  GAATTCGGGT GCCATGGCTG AGTCACACCT GCTGCAGTGG CTGTGCTGTC TGCTGCCCCAC 60
   GCTCTGTGGC CCAGGCACTG CTGCTGAGAC CACCTCATCC TTGGCCTGTG CCCAGGGCCCC 120
   TGAGTTCTGG TGCCAAAGCC TGGAGCAAGC ATTGCAGTGC AGAGCCCTAG GGCATTGCCT 180
   ACAGGAAGTC TGGGACATG TGGGAGCCGA TGACCTATGC CAAGAGTGTG AGGACATCGT 240
   CCACATCCTT AACAAGATGG CCAAGGAGGC CATTTTCCAG GACACGATGA GGAAGTTCTT 300
55  GGAGCAGGAG TGCAACGTCC TCCCTTGAA GCTGCTCATG CCCAGTGCA ACCAAGTGCT 360
   TGACGACTAC TTCCCCCTGG TCATCGACTA CTTCACAGAC CAGACTGACT CAACCGGCAT 420
   CTGTATGCAC CTGGGCTGTG GCAAAATCCG GCAGCCAGAG CCAGAGCAGG AGCCAGGGAT 480
   GTGAGACCCC CTGCCCAAAC CTCTGCGGGA CCTCTGCGCA GACCCTCTGC TGGACAGCT 540
   CTTCTCTCCT GTCTGCGCGG GGGCCCTCCA GGGGAGGCTT GGGCCTCACA CACAGGATCT 600
60  CTCCGAGCAG CAATTCCTCA TTCTCTCCC CTATTGCTGG CTCTGCAGGG CTCTGATCAA 660
   GCGGATCCAA GCCATGATTC CCAAGGGTGC GCTAGCTGTG CAGTGGGCC AGGTGTGCCG 720
   CGTGTACTCT CTGGTGGGCG GCGGCATCTG CCAGTGCCCTG GCTGAGCGCT ACTCCGTCAT 780
   CTGCTCGAC AGCTGTCTGG GCGCATGCT GCCCAGCTG GTCTGCCGCT TCGTCTCCCG 840
   GTGCTCCATG GATGACAGCG CTGGCCCAAG GTGCGGACA GGAGAATGGC TGCGCGGAGA 900
65  CTCTGAGTGC CACCTCTGCA TGTCCGTGAC CACCCAGGCC GGGAACAGCA GCGAGCAGGC 960
   CATACCACAG GCAATGTGCC AGGCTGTGTG TGGCTCTGG CTGGACAGGG AAAAGTGCAA 1020
   GCAATTTGGT GAGCAGACA CGCCCCAGCT GCTGACCCTG GTGCCAGGG GCTGGGATGC 1080
   CCACACCACT TGCCAGGCCCT TGGGGTGTG TGGGACCATG TCCAGCCCTC TCCAGTGAT 1140
   CCACAGCCCC GACCTTTGAT GAGAATCTAG CTGTCCAGCT GCAAGGAAAG AGCCAAGTGA 1200
70  GACGGGCTCT GGGACCATGG TGACCAAGCT CTTCCCTGTC TCCCTGGCCC TCGCCAGCTG 1260
   CCAGGCTGAA AAGAAGCCCT AGCTCCACA CCGCCCTCTT CACCTCCCTT CCTCGGCAGT 1320
   CACTTCCACT GGTGGACAC GGGCCCCAG CCGTGTGTC GCTTGTCTG TCTCAGCTCA 1380
   ACCACAGTCT GACACAGAG CCCACTTCCA TCCTCTCTGG TGTGAGGCAC AGCGAGGGCA 1440
   GCATCTGGAG GAGCTCTGCA GCTTCCACAC CTACCAAGAC CTCACAGGGC TGGGCTCAGG 1500
75  AAAAAACAGC CACTGCTTTA CAGGACAGGG GGTGGAAGCT GAGCCCCGCC TCACACCCAC 1560
   CCCCATGCAC TCAAGATTG GATTTTACAG CTACTTGCAA TTCAAAATTC AGAAGAATAA 1620
   AAAAAAGGAA CATAAGAAAC TCTAAAAGAT AGACATCAGA AATTGTTAAG TTAAGCTTTT 1680
   TCAAAAAATC AGCAATTTCC CAGCGTAGTC AAGGGTGGAC ACTGCACGCT CTGGCATGAT 1740
   GGGATGGCGA CGGGGCAAGC TTTCTTCTC GAGATGCTCT GCTGCTTGTG AGCTATTGCT 1800
80  TTGTTAAGAT ATAAAAAGGG GTTCTTTTTT GTCTTTCTGT AAGGTGGACT TCCAGATTTT 1860
   GATTGAAGAT CCTAGGGTGA TTCTATTCTT GCTGTGATTT ATCTGCTGAA AGCTCAGCTG 1920
   GGGTGTGCA AGCTAGGGAC CCATTCTCTG GTAATACAA GTCTGCACCA ATGCTAATAA 1980
   AGTCTTATTC TCTTTTAAAA AAAAAAAACG GAAATTC 2026

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Seq ID NO: C61 DNA Sequence



Nucleic Acid Accession #: NM\_139172.1  
Coding sequence: 19..552

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5      1      11      21      31      41      51
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      GGGGCTCTGGG GAGGTGACAT GTTGGGCTGT GGGATCCCAG CGCTGGGCGCT GCTCCTGTCTG 60
      CTGCAGGGCT CGGCAGACGG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG 120
      GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180
10     TGCCCTGCGTC TCOGTGCTG CTACCGCAAT GGGGTCTGCT ACCACCACGG TCCAGACGAA 240
      AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGACGT GCAGCGGCTT CCTCCTCCTG 300
      AGCTGCAGCA TCTGCTTGT CTGGTGGGCC AAGCGCCGGG ACGTGTCTCA TATGCCCGGT 360
      TTCTTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCA GCACCGAGGG 420
      ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCACTCGCCC TGTCCTAAGA GTCCAGGGAT 480
      GTGGAGGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA 540
15     GAGGAGGATT AGGGAGTTC CCGGGGACT GCTCAATACA GATACGGTGG ACG 593

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Seq ID NO: C62 DNA Sequence  
Nucleic Acid Accession #: NM\_054023.2  
Coding sequence: 98..379

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20     1      11      21      31      41      51
      |      |      |      |      |      |
      GGGGACACTT TGTATGGCAA GTGAACCAC TGGCTTGGTG GATTTTGCTA GATTTTCTG 60
      ATTTTAAAC TCCTGAAAAA TATCCAGAT AACTGTCAAT AAGCTGGTAA CTATCTTCCT 120
      GCTGGTGACC ATCAGCCTTT GTAGTTACTT TGCTACTGCC TTCTCATCA ACAAAGTGCC 180
      CCTTCTGTT GACAAGTTGG CACCTTTACC TCTGGACAAC ATTCTTCCTT TATGGATCC 240
      ATTAAGCTT CTCTGAAAA CTCTGGGCAT TTCTGTGAG CACCTTGGG AGGGGCTAAG 300
      GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAAC TGCTGGAGGC 360
      GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGAAGATGA 420
      TGCTCTCATC CTCCCTGCTT GAAACCTGTT CTACCAATTA TAGATCAAT GCCCTAAAT 480
      GTAGTGACCC GTGAAGAGA CAAATAAAGC AATGAATACT AAAAAAAAAA AAAAAAAAAA 540
      AAAAAAAAAA 550

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Seq ID NO: C63 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2874

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35     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCCTGT CCTATGCCTA TAAAAACGCT GAGACCCCTAG CAGGCAGACA CACAAGCAGC 60
      TGGATGTGCA GAGGAGCATA TCAGCGGAGG AACACACGGG CAGCTGGACG TCCAGAGGAA 120
      TGCACTGACA GAAACTGGCA TGCTGGCAGA ACACGTGGAA TTGGCTGGG GCAGTTGGAG 180
      GAGAGATGTT CAGATGTGTT CGGAGTTTCT TTCTTCTGTT GGGTTCTGG TCTCGTGGC 240
      TCAGGAGCGA AGCTGCAGAC CTTACGCCA GCCCAGGAAG GGGCTCCAC AGTGACGCG 300
      CAGGCTGAAG CGCTCTCAA GTGCCGCCAG AGTGGCGCTC CAGGCAGAGG AGGCGCCGAG 360
      AGCAGAGGAG CGAGGATGCG CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC 420
      CCAACGTCTT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACCGAAAT TGCTCACAAG 480
      AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCCCTCCTT 540
      GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTAC CATTCTTGT GACTCATTG 600
      TACTTCTCGG GGGTGTGAC CACTGGGATG GAACAACAG ATTTTGAAAC AGGACCAAC 660
      ATATTGATT TGCAAGTTTA TGTGAAGGAT GAGGTGGTG TCACAGACCT GCAAGTCTG 720
      ACTGTCCAGG TAAACAGATG GAAAGAGCCA CCTCAGTTTC AAGGCAACTT GGCAGAAGAT 780
      CATCTCGGTG CAGACCGACC ACATTTCAAT GCTCATAGTC ACACGTACGT GAGGGTAGTG 840
      GCTACTGCAT TGGCCAGGCA CAGGCTTAGA TCTAGCATTG GTTCCCTCTT CTTGGGCACC 900
      TTCTGTGTTG TGGTGGGATC CAGATATTTT CTGATTTCTC CCCCAGAGAG CTTTCAAGAT 960
      TCTGCTAATG GCACCTCTT TCCACAACA GAATGGAGT TTGAAGCAGG ACACAGAACT 1020
      TTCCATCTCA TGTGGGAGGT GAGGACAGT GGAGGCTCCA AAGCTCCAC AGAGCTCCAG 1080
      GTGAACATCG TGAACCTCAA CGACGAAGTC CCTGCTTTA CCAGCCGAC ACGAGTGTAC 1140
      ACAGTCTCTG AGGAACGTAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1200
      GATGATGAAG GTTTTCCAG CCACCTCTCT TACAGCATTA CCACTGTTAG CAAATATTT 1260
      ATGATAATC AGTTGACTGG TACAATCCAA GTGGCCCAAA GGATAGACCG AGATGCAGGT 1320
      GAATTGAGAC AAAATCCCA CATTTCCTG GAAGTTCTAG TGAAGGACAG ACCATATGGG 1380
      GGTACAGGAGA ATCGCATCCA GATAACCTTC ATGTGGAAG ACGTCAACGA CAATCCTGCC 1440
      ACATGCCAAA AGTTCACTT CAGATCCAGT CTCACCCCTG CTCTGTGCTC CAAGACGCTG 1500
      ACCTGGATGG ATACCGTATT AGACTGTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1560
      GGGCGATTTA CAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1620
      CTCACATCA TGGCAGAAGG CAAGGAGGAG CAAGTCACAT CTTACATGGA TGGCAGCAGG 1680
      CAAAGAGATA GAGCTTGTGT AGGGAACCTC CTCCTTATA AGCCATCAGA TCTCATGAGA 1740
      CTTAGTCACT ATCAGGAGAA CAATCAGGA AAGACTTGCC CCCATGATC CATTTCCTCC 1800
      TACCAAGTCC CTCCACACAC ATGTAGGAAT TCAAGAATCC AGGCCACCAA CAAGGAAGAC 1860
      ACAAGCTCTG TCACTGTAC TGTGAACATC CTTGAAGAAA ATGATGAAAA GCCAATTTGT 1920
      ACTCCAACT CTTATTTCTT GGCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATTCTAG 1980
      AATTTCAAGC TGACATGTAC CGACCTTGAT TCCAGCCCA GATCTTTCCG TTATTCCATT 2040
      GGCCAGGTA AGCTCAACAA TCATTTTACC TTCTCTCCA ATGCTGGTTC CAATGTACA 2100
      CGCTGCTGC TTACATCTCG CTTTGTACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC 2160
      AAGCTACTTG TTAAGTAAAC TGATGACAA TGTAGTCTG ACAGGAAGAA AGCGAGGCT 2220
      CTTGTTGAGA CAGGAACAGT GACACTGAGT ATTAAGTCA TTCCCCACC AACCACTATC 2280
      ATCACCACGA CCCCCAGGCC CAGGTCACC TATCAGTCC TGAGGAAGAA CGTTTACTCT 2340
      CCATCTGCAT GGTACGTGCC GTTTGTATC ACTTTGGGCT CCATATTGCT TCTGGGTCTC 2400
      CTCGTGTACC TGGTCTGCTT ATTGGCCAAA GCCATCCACA GACACTGCC CTGCAAGACT 2460
      GGGAGAAGCA AGGAACCTCT GACAAAGAAA GGAGAAACGA AGACTGCAGA GAGAGACGTC 2520
      GTGGTGGAAA CTATCCAGAT GAACACTATC TTGATGGAG AAGCCATAGA TCCAGAGCCT 2580
      GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCAGCT GCTGCGACCC TAGTCCAGTA 2640
      ACCCTAAGAA AGGTCCAGGT GTGTGGGGAG AGTGAAGAGA COGTCAGTG TTCCGGCCAC 2700

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ATCACACTTC CCGGCAAGAT TCCAGTCGAT GACCCAAGGA AACAGGAAAC AGGCCTGCAG 2760  
 GGTGATTTCG AGGTCTGGAC TCTATGCCCC GCTGTGAAGG TGGTTGTAGG CAGCCCTCAA 2820  
 GCTGAACGGT GCATTTCGATT GGCCTCAGT CTGAAAAAGT ACAGTTCTGA TTAA 2874

5

Seq ID NO: C64 DNA Sequence  
 Nucleic Acid Accession #: XM\_168571.1  
 Coding sequence: 155..988

10	1	11	21	31	41	51	
	TACACAGTCC	TGGAGGAACT	GAGTCCAGGA	ACCATCGTGG	CCAATATCAC	AGCGGAGGAT	60
	CCTGATGATG	AAGGTTTTTC	CAGCCACCTC	CTCTACAGCA	TTACCACTGT	TAGCAAAATAT	120
	TTTCATGATAA	ATCAGTTGAC	TGGTACAATC	CAAGTGGCCC	AAAGGATAGA	CCGAGATGCA	180
	GGTGAATTGA	GACAAAATCC	CACCAATTCC	CTGGAAGTTC	TAGTGAAGGA	CAGACCATAT	240
15	GGGGGTCAGG	AGAATCGCAT	CCAGATAACC	TTCAATTGTG	AAGACGTCAA	CGACAATCCT	300
	GCCACATGTC	AAAAGTTTCA	CTTCAGCATT	ATGGTGCCGG	AAAGAACAGC	CAAGGGGAAG	360
	TTGCTTCTTG	ACCTAAACAA	GTCTGCTTTT	GATGATGACA	GTGAGGCACC	AAACAACAGA	420
	TTCAACTTCA	CCATGCCATC	TGGAGTGGGG	AGCGGCAGCA	GATTTTTCAC	GGATCCAGCT	480
20	GGCTCTGGGA	AGATTGTGCT	GATTGGTGAT	CTAGACTACG	AAAATCCAAG	TAACCTAGCA	540
	GCGGGCAATA	AATATACGGT	GATAATCCAG	GTGCAGGATG	TGGCCCCCCC	TTACTATAAA	600
	AATAAGCTCT	ACGTTTATAT	CCTAACCAAG	CCAGAAAATG	AGTTTCTCTT	CATTTTGTAT	660
	AGGCCATCCT	ATGTTATTTG	TGTGTGAGAA	AGAAGGCCCG	CCCAGGGTCA	CCTATCAGGT	720
	CCTGAGGAAA	AACTGTTTAT	CTCCATCTGC	ATGGTACGTG	CCGTTTGTCA	TCACTTTGGG	780
25	CTCCATATTG	CTTCTGGGTC	TCCTCGTGTA	CCTGGTCTGC	CTATTGGCCA	AAGCCATCCA	840
	CAGACACTGC	CCCTGCAAGA	CTGGGAAGAA	CAAGGAACCT	CTGACAAAGA	AAGGAGAAAC	900
	GAAGACTGCA	GAGAGAGAGC	TGCTGGTGGG	AACTATCCAG	ATGAACACTA	TCTTTGATGG	960
	AGAAGCCATA	GATCCAGTGA	CCGGGGAAGC	ATATGAATTC	AACTCAAAAA	CTGGAGCCAG	1020
	AAAGTGGAAA	GATCCACTAA	CCCAATGCC	AAAATGGAAA	GAGTCCAGCC	ACCAGGGAGC	1080
30	TGCCCCACGC	AGAGTCACTG	CTGGGAAGAG	GATGGGGTCA	CTGAGAAGTG	CCAACCTGGG	1140
	AGAAGATGAG	CTGAGTGGCA	AAGGTGGGTC	TGAGGATGCT	GGTCTGGGTT	CCAGAAATGA	1200
	GGGTGGCAAG	CTGGGCAACC	CAAGAAGACG	AAATCCAGCC	TTCTGTAACA	GGGCTTACCC	1260
	CAAAACACAC	CCAGGAAAGT	AAACGGGGTC	TAAGGAGGGG	CCTGTCAATC	ACTGAGATGC	1320
	TGCTCACTCC	TAAATCTCAT	GGGGATGGTG	TGGCATGGTG	GTAGGGGGGA	AAATGTGGGC	1380
35	TGAGGGGATT	CAGACATCCA	GGGTCAAACA	TGGGATGTTT	GACAAATTTT	TAAACAATA	1440
	GAAAGGGGTT	TGATCACATA	GTTCGCTGTT	CTGAAATGAT	ACAGGAACAT	TTTCTATCAG	1500
	ATTTCAAGAC	TACCTGTGCT	TCTGATAAGC	AAGACTGTTA	ACTTTGGGGT	GTGGAATTGT	1560
	TGTTTCTCTT	CTTTGCAATT	ACTGCTAGGA	AGCTCTATTC	TGTTCAACAT	AGAAAGTTTG	1620
	TAGGAATTCC	TGACATAAAT	AGTGAAGACT	ATCCTTACAT	CTGGTTTCCA	CCTTATTTTC	1680
40	CTGCCCTCGT	TTTAACTACA	CCCAGATTTC	TTCAAGTTATA	AATATGCCAT	ACACCTTTGT	1740
	AAGTCACCTC	AAATCTTCTT	CAAAAGAAGC	AGAACAGTGA	AAAAAACAGA	TGAGTAAGTT	1800
	AAGAGTTGGT	CATCTGGAAA	GAAGAAACT	CAGTAGGCAC	CTTCTTTTGT	TTTTTCTGTT	1860
	GGGTGTCGGA	TCAGCATCCT	GCATGTGAGA	TTATCCACG	TTGCTCTGTC	TAGCAGTAGT	1920
	TCAGTTCTCT	TCATGGTTAT	GTCTGGTTTC	ATTCTATGAT	TATATCACA	TTTATCTATT	1980
45	CTACACTTGG	GTGGCAGCTG	CTTCAGATTT	TTTACTTTTA	AAAAATATAC	TTAAAAGTGA	2040
	ACTACAGGCA	GGGCATGATG	GCTCATGCCT	GTAATGCCAG	CACCTTGCCA	AGGTGGGCAG	2100
	ATCACCTAAG	CTCAGGAGTT	CAAGATCAGC	CTGGCCTAGA	TGGCAAAACC	CTGCTCTTAC	2160
	TAAAAAATAC	AAAAATTAGC	TTGGTGTGGT	GGTGGGCACA	TGTAATCCCA	GCTACTTGGG	2220
	AGGCTAGGT	AGGGAGAACT	GCTTAAACCT	GAGAGGTGGA	GGTTACAGTG	AGTTGAGATT	2280
50	GTGCCACTGC	ACTCTAGCCT	GGGTGACAAA	GCAAGACTCC	ATCTCAGAAA	AAAAAATAA	2340
	AAGTGAATTA	CAACACT					2357

Seq ID NO: C65 DNA Sequence  
 Nucleic Acid Accession #: NM\_005266.3  
 Coding sequence: 122..1198

55

1	11	21	31	41	51		
	GGCAGGAGGC	CATTTTCAA	CAGTCCCTCC	TGGGAGAACA	CAGACAGGCA	GAGGATTACA	60
	ACACAAGGCA	GCAAGCACTG	GGAGACGAAA	GTTTTGGCAT	CTGTTCCCTG	GCTGTGCCAA	120
60	GATGGGCGAT	TGGAGCTTCC	TGGGAAATTT	CCTGGAGGAA	GTACACAAGC	ACTCGACCGT	180
	GGTAGGCAAG	GTCTGGCTCA	CTGTCTCTTT	CATATTCGGT	ATGCTGTGTC	TGGGCACAGC	240
	TGCTGAGTCT	TCTTGGGGGG	ATGAGCAGGC	TGATTTCCGG	TGTGATACGA	TTCAGCCTGG	300
	CTGCCAGAA	GTCTGTACAG	ACCAGGCTTT	CCCATCTCC	CACATTCCGT	ACTGGGTGCT	360
65	GCAGATCATC	TTGCTCTCCA	CGCCCTCTCT	GGGTATACATG	GGCCACGCCA	TGCACACTGT	420
	GCGCATGCAG	GAGAAGCGCA	AGCTACGGGA	GGCCGAGAGG	GCCAAAGAGG	TCCGGGGCTC	480
	TGGCTCTTAC	GAGTACCCGG	TGGCAGAGAA	GGCAGAACTG	TCCGTCTGGG	AGGAAGGGAA	540
	TGGAAGGATT	GCCTCCAGG	GCACTCTGCT	CAACACCTAT	GTGTGCAGCA	TCCTGATCCG	600
	CACCAACATG	GAGGTGGGCT	TCATTGTGGG	CCAGTACTTC	ATCTACGGAA	TCCTCTGAC	660
70	CACCTGCTAT	GTCTGGCGCA	GGAGTCCCTG	TCCCAACCCG	GTCAACTGTT	ACGTATCCCG	720
	GCCCCAGAG	AAGAATGTCT	TCATTGTCTT	TATGCTGGCT	GTGGCTGCAC	TGTCCTCTCT	780
	CTTAGGCTG	GCTGAACCTT	ACCACCTGGG	CTGGAAGAA	ATCAGACAGC	GATTTGTCAA	840
	ACCGCGGAGT	CACATGGCTA	AGTGCCAGCT	TTCTGGCCCC	TCTGTGGGCA	TAGTCCAGAG	900
	CTGCACACCA	CCCCCGACT	TTAATCAGTG	CCTGGAGAA	GGCCCTGGGG	GAAAATCTTT	960
75	CAATCCCTTC	AGCAATAATA	TGGCCTCCCA	ACAAAACACA	GACAACCTGG	TCACCGAGCA	1020
	AGTACAGGTT	CAGGAGCAGA	CTCCTGGGGA	AGGTTTCAATC	CAGGTTCTGT	ATGCCAGAGA	1080
	CCCTGAGCTG	CCCAATGGAG	TCTCACAGG	TCACCGCCTT	CCCCATGGCT	ATCATAGTGA	1140
	CAAGCGAGCT	CTTAGTAAGG	CCAGCAGCAA	GGCAAGGTCA	GATGACCTAT	CAGTGTGACC	1200
	CTCCTTTATG	GGAGGATCAG	GACCAGGTGG	GAACAAGGA	GGCTCAGAGA	GGAAAGACGT	1260
80	GTCCCTTCTG	AACATGATCT	TTCTCACTGT	CATCACTGCT	TGGCTCTCTT	GAGCCCGGGG	1320
	TCTCAATGAC	GTGTCTCAT	AATTTAGAAA	ACTATAACCA	GGGCTCTGGG	ATAGTAAGAG	1380
	AGGTGACAA	ACCCAGAGAC	TGCAGTTCCC	TCCCACCTT	CTACCCAGTA	TACGAAGCCT	1440
	TTCAGATTAC	TCAATGAAAC	GGGTAGAGGG	AAAGAAGGGA	AGCATGGCAA	AAGCTGGCCT	1500
	GGAGGGGATA	GCCAGAGGGA	TAGAATGACT	CTCTCTCTAC	ATACCCAGCAG	CATACCAAT	1560
	GCGTTCTCTA	AGTTCTTACC	TCCTTGACCT	GATCACCTTC	CCTCCTCCAA	GGAAGAGCTC	1620

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AAAGTTCCCA GCCAATAGAC AGCATGAATC AAGGAACCTG CATTATATGT GCTCTTGAAT 1680  
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 CTTTACAAAT GCCTTGGTAT GTACCTCTGG CAAATGCCCT GGTATGTACC TCTGGCAAAT 1860  
 GCCCCACCTT GGTGATGTTG CAACCTTTCC TTCTGTCTAGG GTGTACACCT AGCCTGTGCA 1920  
 GGTGTGAGCC CTGCTAGGGA GTCACTGTAC ACACAAATC TACTGGAATT CCTGCCAACA 1980  
 TCTGTACACC TGCAGTCTCT TTACAGTTCA ATCCAATGAT AGAAACCATC CCTTCCCTTT 2040  
 CTCCCTTGGC TGTTACCCCA GCCATTCCCT GAAGGCCCTT CCAACAGGAA TATCCAAGAA 2100  
 GCTGTTGTCC TCTCTCGAAC CCTGACCAGA TCATCAGCCA CTGAGGCCAG TGGAAATTTCC 2160  
 CCAAGGCTTG TTAACAAAAA AAAAAAATA 2190

Seq ID NO: C66 DNA Sequence  
 Nucleic Acid Accession #: NM\_014459.2  
 Coding sequence: 738..3407

1 11 21 31 41 51  
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 GCTGGGAAG CTTCAAAATA TATCTGTGAC TCTGTCTTGG TTGCTCTTCA TCCCATCAAA 180  
 TTTTCATCAG GGAGGCGAGC AGCAAGTAAG AATTTCACCT TGGGATCTGC CTAGAGACAC 240  
 ACCTCCCTGC TCCCTCCCCC ACTCGATGTG AAGAGTATTC CGGAGTCTCC GGGCGGGAGT 300  
 AGATTTCGAG CACCTTAGCG GGAGCGAGGA AAACCTACTG ATTCTTTAGC TCATTATCAT 360  
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 AAGTCCGGGC GGGAGAGAGC AAACCCCTGG CTCACCCCCA GCCGCGAGAA GCCACCGCCT 480  
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 ATCAACAGGT TCAGGGAACCT TGAGCAGAAAT AAGGAGAGAC CACCGGGTGC CGCAGCTCGG 600  
 GTGCAGAGGG AAAAAGGAC CCATAGACTT GTGGCTCGCG TCGCGCGCGC ACGCTGCGCC 660  
 AGGGCCCCAG GCTGGCGCGC ACTCCCTCTC TGGCTCTCTC AGTCCGATTG CTCCTGCCCC 720  
 CACCTTACAG GTCTGGGATG TACCTTTCCA TCTGTTGCTG CTTTCTTCTA TGGGCCCTCG 780  
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 TGGAGCTGGA CGCAGACAGC GGGCTCTCT ACACCAAGCA CGCATCGAC CGCAGTCCC 1020  
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 TCTGATGAT CAAGGTAGAG ATCCAGGACA TCAACGACAA CGGCGCCTCC TTCTCTCGG 1140  
 ACCAGATGCA AATGGACATC TCGGAGAACG CTGCTCCGGG CACCGCTTCC CCCTCAGCA 1200  
 GCGCACATGA GCGGAGCGCC GCGGAGAAAT GGCTCCGAC CTACCTGCTC ACGCGGAGC 1260  
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 GGCTCTACGT GCTTCAGGTG CACGAGAACA ACATCCCGGG AGAGTACCTG GGCTCTGTGC 2220  
 TGCGCCAGGA TCCCGACCTG GGCCAGAAAG GCACCGTATC CTACTCTATC CTGCCCTCGC 2280  
 ACATGCGGCA CGTGTCTATG TACACCTATG TGTCTGTGAA TCCACGAAAC GGGGCCATCT 2340  
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 CAGTGCCCAA GCTCATCATC CGCTCGGTGA GCGATCCCT TCCGAGGGGG GTACCAAGGG 2820  
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 TCTCCATCAT CCTCTAGCG GCCATGATCA CCATCGCCGT CAAGTGCAAG CGCGAGAAC 2940  
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TTCGATCAG ATGGCAAGGG TCTTTGCAGA TGTGCATTC AGAGCCAGCC GGGATTCCAG 4080
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TGTGGATGCA GAGGAAGTTG TGAGAGAAAT TGATAAGCTT TTGCAAGACT GCCGGGGAAA 4200
CGACCCCTGT GCTGTGAGAA AGTGAAAAAA GAAAAAAAAG AAGGCATTGG CATTTCCTTG 4260
TCTCTTCTGT TGATTTAAAA ATGATCCCTC CTGGTGATAA CCCATTTTAC AGGGATGAAG 4320
AAAGACCAAT GCTGCTTTAA GGCTTTTAGT GAACATCTGA AGTGCCCA CA AGTATGTTCT 4380
TTCCACTGCT GATTTCCTTT TCAGAGATAA CAATGGTTTC GTTTTGACCA AACTTGTATT 4440
AGGACAGAAT TAATGATGCT TAAAGAGAAA AGAAAAAAG AGAGAAGAAA AAGGAGAGAT 4500
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TGAGAACTGA AGTATTTCTG ATCACTCTCA GACTGTCCTC CGTGATTAT GCTGACTTAA 4620
CTGTTTACCT ATAAACCCCA TACAAAGCAG GGTCTAATT TGTGATCTGT GGTGGATTTC 4680
TAGCAGTCAT CACAGGCTTC TACTGAAAGT CCGTAAAAGA CCTTGCACTA GTCCAGCTA 4740
CACCAACAT TAACACATAT TTGTGGTAAA CATTTCCTGA TAAAGTTACC TGACACACAT 4800
ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAAACA AAACAAAAAA AAAACCTTTG 4860
GTCATTTGTA AGACATCTCA TGTATATAA AAGTTAAATG TAAAAAGATA CAGTCCATTT 4920
TGTCCTGCAC ACAGGTAGAC TAATTCAGT CAAAAAAA AAAA 4966
  
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Seq ID NO: C67 DNA Sequence
Nucleic Acid Accession #: NM_005601.2
Coding sequence: 101..598
  
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TCTTCTCTCT CCAGGACCCA GAAGCCCTGA GCTTATCCCC ATGGAGCTCT GCCGGTCCCT 120
GGCCCTGCTG GGGGGCTCCC TGGGCTGAT GTTCTGCCCTG ATTGCTTTGA GCACCGATT 180
CTGGTTTGA GCTGTGGGTC CCACCCACTC AGCTCACTCG GGCCCTGTCG CAACAGGGCA 240
TGGGACATC ATATCAGGCT ACATCCAGCT GACGACAGCC TTCAGCATT TGGCTGTTCT 300
GTGGGCCCTG GTGTCCGTGA GCTTCTGCTG CTGTCTCTCG TCCCCCTCAC TGTTCCTCCC 360
AGGCCACGGC CGGCTGTGCT CAACCCACGC AGCCTTTGCT GCAGCCATCT CCATGGTGGT 420
GGCCATGGCG GTGTACACCA GCGAGCGGTG GGACCCAGCT CCACACCCCA AGATCCAGAC 480
CTTCTTCTCC TGGTCTTCT ACCTGGGCTG GGTCTCAGCT ATCCTCTTGC TCTGTACAGG 540
TGCCCTGAGC CTGGGTGCTC ACTGTGGCGG TCCCGTCTCT GGCTATGAAA CCTTGTGAGC 600
AGAAGGCAAG AGCGGCAAGA TGAGTTTGA GCGTGTGATT CCAAGGCCCT CATCTGGAGC 660
CTCGGGAAG TCTGTCTCTA CATTGCCCCG CCCTTCCAGC CCTTCCCCAG CCCTCCTCT 720
TGTTTCTTCA TTCATTCAAC AAAATTGGC TGGAAAAAAA AAAAAAAA AAAAAAAA 780
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Seq ID NO: C68 DNA Sequence
Nucleic Acid Accession #: NM_006433.2
Coding sequence: 129..566
  
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GCCCCACCAT GGCTACCTGG GCCCTCCTGC TCCTTGACAG CATGCTCCTG GGCAACCCAG 180
GTCTGTCTCT CTCTGCTCTG AGCCCTGAGT ACTACGACCT GGCAAGAGCC CACCTGGCTG 240
ATGAGGAGAA ATCCTGCCCG TGCCCTGGCC AGGAGGGCCC CCAGGGTGAC CTGTTGACCA 300
AAACACAGGA GCTGGGCGGT GACTACAGGA CCTGTCTGAC GATAGTCCAA AAACCTGAAGA 360
AGATGTGTGA TAAGCCCAAC CAGAGAAGTG TTTCCAATGC TGCGACCCGG GTGTGTAGGA 420
CGGGGAGGTC ACGATGGCGC GACGCTGCA GAAATTTTAT GAGGAGGTAT CAGTCTAGAG 480
TTACCCAGGG CCTCTGGGCC GGAGAACTG CCCAGCAGAT CTGTGAGGAC CTCAGGTTGT 540
GTATACCTCT TACAGTCCC CTCTGAGCCC TCTCACCTTG TCCTGTGGAA GAAGCACAGG 600
CTCCTGTCTT CAGATCCCGG GAACCTCAGC AACCTCTGCC GGCTCCTCG TTCTCTGATC 660
CAGATCCAC TCTCCAGTCT CCCTCCCTCG ACTCCCTCTG CTGTCTCTCC CTCTCAGAG 720
AATAAAGTGT CAAGCAAG
  
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Seq ID NO: C69 DNA Sequence
Nucleic Acid Accession #: NM_002985.2
Coding sequence: 69..344
  
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1 11 21 31 41 51
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GCGTCTCTGC ATCTGCCTCC CCATATTCTT CGGACACCAC ACCCTGCTGC TTTGCTTACA 180
TTGCCCGCCC ACTGCCCGGT GCCCACAATCA AGGAGTATTT CTACACCACT GGCAAGTGTCT 240
CCAAACCCAGC AGTCTCTTT GTCAACCCGAA AGAACCCGCA AGTGTGTGCC AACCAGAGA 300
AGAAATGGGT TCGGGAGTAC ATCAACTCTT TGGAGATGAG CTAGGATGGA GAGTCTTGA 360
ACCTGAACCT ACACAAATT GCCTGTTTCT GCTTGCTCTT GTCTAGCTT GGGAGGCTTC 420
CCCTCACTAT CCTACCCCAT CGGCTCCTTG AAGGGCCAG ATTCTACCAC ACAGCAGCAG 480
TTACAAAAAC CTTCGCCAGG CTGGACGTGG TGGCTCAGC CTGTATATCC AGCATTGTTG 540
GAGGCCAAGT TGGGTGGATC ACTTGAGGTC AGGAGTTGCA GACCAGCCTG GCCAACATGA 600
TGAAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGGTAGC GGGGCGCTGT 660
AGTCCAGCT ACTCGGGAGG CTGAGGCAGG AGAATGGGCT GAACCCGGA GCGGAGCTT 720
GCAGTGAGCC GAGATCGCGC CACTGCACCT CAGCCTGGGC GACAGAGGGA GACTCCGTCT 780
CAAAAAAAA AAAAAAAA AAAATACAAA AATTAGCCGG GCGTGGTGGC CCACGCTGT 840
AATCCAGCT ACTCGGAGG CTAAGGCAGG AAAATTGTTT GAACCCAGGA GGTGGAGGCT 900
GCAGTGAGCT GAGATTGTGC CACTTCACCT CAGCCTGGGT GACAAAGTGA GACTCCGTCA 960
CAACACACAC AAAAAAAGC TTCCCAACT AAAGCTAGA AGAGCTCTG AGGCGTGTCT 1020
TTGTCAAAAG GAAGTCTCTA GGTCTGAGC TCTGGCTTTG CCTTGGCTTT GCCAGGGCTC 1080
  
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TGTGACCAGG AAGGAAGTCA GCATGCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC 1140  
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Seq ID NO: C70 DNA Sequence  
 Nucleic Acid Accession #: NM\_022154.2  
 Coding sequence: 1381..1722

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1      11      21      31      41      51
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CCGGCCGGGC GTTTGAGGGC TACTGCCACG CAGCGTTTCT GGAGCCTGCC GGCTGGTGCC 180
CTGGTGCCCT TTATCTCTGT CCCCTTTTGT CCTCTTTATC TCAGGCTCTC CAGGAGGCCG 240
GGGGGCCAC TCAGCTATC GCTCCCTCG GCTACGCTGC CACTCCAATG CCCGCGAGGT 300
CGGAGCTGCG TGTTCTTTGG AAGCGCGCGG AGAACCAGGG CGCTCCCGCG CCACCTCTGA 360
CTOGGAGCAG CGCCGAGCAC TGACGCTCCC GCCCTTGGGC AAGGACGCCA GTGCGCCCGC 420
GCGCGTCCCT CTGCGCGGCA GCCGTCGCG GGCCCTCAAG GGGGAGCCCA GGCCAGGATG 480
GCCCGGGGTC GCGCGTGGC CGGCTCCTG TTGCTGGCGG CCGCCGGCCT CGGAGGAGTG 540
CGGAGGGGCG CAGGCTAGC CTTCAGCGAG GATGTGCTGA CGGTGTTCCG CGCGAATCTG 600
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TCCTTCTATG GCTTTTCAAA TGCTACCCAA ATAACCAGCT CCAATTTCTC TGTCTCTCTG 780
CCAGCAGTCT TACAGCAATT GAACCTTTCAC CCATGTGAGG ATCGGCCCAA GCACAAACAA 840
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ATTCCAGAGG CATTGAGATT TGATCCCAAA GTGACAGATT ATGTTGAGAA GGCAGTTGCT 1080
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ACTCATCAAC CTAAGCATT ACCTGCCATC AATGGTGTGA CATGCTATGC AAATCCTGCT 1260
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TTTGGCATTT TGGTGGGCAA CAATTTGCTT CCAATATTA TATTGCACT TGCTGGAGGC 1680
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GAACATCCTA GATTCACTCT CCCAAGTCAC TTAAGGTGAT TTGATGGTGA GGAATATGAT 3060
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ATGTAGCAGC AATGCAGATT TGGTGAATAT TTAATATATA TTTTAGTATG TATTTCACIT 3180
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Seq ID NO: C71 DNA Sequence  
 Nucleic Acid Accession #: NM\_004184.2  
 Coding sequence: 188..1603

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AGCAACATG CCCACAGTG AGCCCGCATC TCTGCTGGAG CTGTTCAACA GCATCGCCAC 240
ACAAGGGGAG CTCGTAAGGT CCTCAAAGC GGGAAATGCG TCAAGGATG AAATTGATTC 300
TGCACTAAGG ATGTTGGTGT CATTAAAAAT GAGCTACAAA GCTGCCCGCG GGGAGGATTA 360
CAAGGCTGAC TGTCTCCAG GGAACCCAGC ACCTACCAGT AATCATGGCC CAGATGCCAC 420
AGAAGCTGAA GAGGATTTTG TGGACCATG GACAGTACAG ACAAGCAGTG CAAAAGGCAT 480
AGACTACATG AAGCTCATTT TCGGTTTGG AAGTAGTAAA ATTGACAAAG AGCTAATAAA 540
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	TTTCACAAAG	TGGCTCCAGG	ATGTATTTAA	CGTGCCCTTG	GTATCCAGCA	TGACGGATGA	780
	CGAGAAGTAT	CTGTGAAGG	ACCTGACCC	GGACCCAGCC	TATGGCGATG	CTGTGAGAA	840
	TGCCAAGGAC	ATCATGCGCT	GTGGCTTTGA	CATCAACAAG	ACTTTCATAT	TCTCTGACCT	900
	GGACTACATG	GGGATGAGCT	CAGGTTTCTA	CAAAAATGTG	GTGAAGATTG	AAAAGCATGT	960
	TACCTTCAAC	CAAGTGAAAG	GCATTTTCGG	CTTCACTGAC	AGCGACTGCA	TGGGAAGAT	1020
	CAGTTTTCCT	GCCATCCAGG	CTGCTCCCTC	CTTCAGCAAC	TCATTCCAC	AGATCTTCCG	1080
10	AGACAGGACG	GATATCCAGT	GCCTTATCCC	ATGTGCCATT	GACCGGATC	CTTACTTTAG	1140
	AATGACAAAG	GAGCTGCGCC	CCAGGATCGG	CTATCTCTAA	CCAGCCCTGT	TGCACTCCAC	1200
	CTTCTTCCCA	GCCTGCGAGG	GCGCCAGAC	CAAAATGAGT	GCCAGCGACC	CAAACTCCTC	1260
	CATCTTCCCT	ACCGACACGG	CCAAGCAGAT	CAAAACCAAG	GTCAATAAGC	ATGCGTTTTC	1320
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	AGGCCCTCAC	AGATGTCTAG	GCAGGCCCTCA	TTTCATCACG	CAGCATGTGC	AGGCGTGAA	2580
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Nucleic Acid Accession #: NM\_004938.1  
Coding sequence: 337..4632

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Seq ID NO: C73 DNA Sequence  
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 Coding sequence: 222..1898

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45 Seq ID NO: C74 DNA Sequence  
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80 Seq ID NO: C75 DNA Sequence  
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	AATGGTCACT	GCTTTGGGGC	CAACCCCAAC	CAGTGCTGCC	ATGATGAGTG	TGCCGGGGGC	900
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	TGTGTACCTC	GCTGTCCACA	GCCTCTTGTG	TACAACAAGC	TAACTTTTCCA	GCTGGAAACC	1020
	AATCCCAACA	CCATGGACAC	GTATGGAGGA	GTTTGTGTAG	CCAGCTGTCC	CCATAACTTT	1080
	GTGGTGGATC	AAACATCCTG	TGTCAGGGCC	TGTCCTCTGT	ACAAGATGGA	AGTAGATAAA	1140
	AATGGGCTCA	AGATGTGTGA	GCCTTGTGGG	GGACTATGTC	CCAAAGCCTG	TGAGGGAACA	1200
20	GGCTCTGGGA	CGCGCTTCCA	GACTGTGGAC	TCGAGCAACA	TTGATGGATT	TGTGAACCTG	1260
	ACCAAGATCC	TGGGCAACCT	GGACTTTCTG	ATCACCGGCC	TCAATGGAGA	CCCTTGGCAC	1320
	AAGATCCCTG	CCCTGGACCC	AGAGAAAGCT	AATGTCTTCC	GGACAGTACG	GGAGATCACA	1380
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30	TTTCTGAATG	GGGAGCCTCG	AGAATTGGCC	CATGAGGCGG	AATGCTTCTC	CTGCCACCCG	1860
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	CAATGTGCCC	ATTTTGTAGA	TGGGCCCCAC	TGTGTGAGCA	GCTGCCCCCA	TGGAGTCCCTA	1980
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70	CCCAAGGCTA	ATGCCAGAG	AACGTAACTC	CTGCTCCCTG	TGGCACTCAG	GGAGCATTTA	4260
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	AGAAAGCTAA	AATCTGTGAA	GAAAGAGGTT	AGGAGTAGAT	ATTGATTACT	ATCATAATTC	4740
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Nucleic Acid Accession #: NM\_001216.1  
Coding sequence: 43..1422

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Seq ID NO: C77 DNA Sequence

Nucleic Acid Accession #: NM\_004207.1  
Coding sequence: 63..1460

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70 CGCAGACAG GCTGGCAGGG CAGGTGCTGC GTGGGGCCCT CTCAGCCCG TCCTACCCCTG 1860
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Seq ID NO: C78 DNA Sequence

Nucleic Acid Accession #: NM\_000358.1  
Coding sequence: 48..2099

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	ACCTTTACGA	GACCCCTGGG	GTCCGTTGGAT	CCACCACCAC	TCAGCTGTAC	ACGGACCGCA	420
	CGGAGAGGCT	GAGGCCTGAG	ATGGAGGGGG	CCGGCAGCTT	CACCATCTTC	GCCCCTAGCA	480
	ACGAGGCGTG	GGCCTCCTTG	CCAGCTGAAG	TGCTGGACTC	CCTGGTCAGC	AATGTCAACA	540
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	TGAAACACGG	CATGACCCTC	ACCTCTATGT	ACCAGAATTC	CAACATCCAG	ATCCACCACT	660
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20	CCTCTAAGTA	TCTGTACCAT	GGACAGACCC	TGGAACTCT	GGGCGGCAAA	AAACTGAGAG	1440
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45 Seq ID NO: C79 DNA Sequence  
Nucleic Acid Accession #: NM\_006536.2  
Coding sequence: 109..2940

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	GAACTCCCAT	TCCTGGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
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	TTTACACACA	GCCTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCAC	ATTCTCGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCAGCAAA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAACAAGCC	GCAGAAATTT	ATTTGATGCA	GATTGTTGAA	1140
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Seq ID NO: C80 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

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Seq ID NO: C81 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

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Seq ID NO: C82 DNA Sequence  
Nucleic Acid Accession #: NM\_006952.1  
Coding sequence: 11..793

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Seq ID NO: C83 DNA Sequence  
Nucleic Acid Accession #: NM\_001793.2  
Coding sequence: 71..2560

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5 Seq ID NO: C84 DNA Sequence  
 Nucleic Acid Accession #: NM\_005629.1  
 Coding sequence: 639..2546

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80 Seq ID NO: C85 DNA Sequence  
 Nucleic Acid Accession #: NM\_006516.1  
 Coding sequence: 180..1658

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 ATGAGATCGC TTCGCGCTTC CGGCGGGGG GAGCCAGCCA AAGTGATAAG ACACCCGAGG 1620  
 AGCTGTTCCA TCCCTCGGGG GCTGATTCCT AAGTGTGAGT CGCCCGAGAT CACGAGCCCG 1680  
 GCGTGTCTCC AGCAGCTCTC AGGATCTCTC AGGAGCAGAG GCAGCTGGAT GAGACTTCCA 1740  
 30 AACCTGACAG ATGTGACCGG AGCCGGGCTT GGGCTCTCTT TCTCCAGCCA GCAATGATGT 1800  
 CCAGAAGAAT ATTCAGGACT TAACGGCTCC AGGATTTTAA CAAAAGCAAG ACTGTTGCTC 1860  
 AAATCTATTC AGACAAGCAA CAGGTTTTAT AATTTTTTFA TTACTGATT TGTATTTTTT 1920  
 ATATCAGCCT GAGTCTCTCG TGCCACATC CCAGGCTTCA CCTGTAATGG TTCCATGCCT 1980  
 GAGGTTGGAG AGTGAAGCCT GTGAGACAC TTGCTTCTT CACCCAGCTA ATCTGTAGGG 2040  
 35 CTGGACCTAT GTCCTAAGGA CACACTAATC GAACTATGAA CTACAAAGCT TCTATCCAG 2100  
 GAGGTGGCTA TGGCCACCGG TTCTGCTGGC CTGGATCTCC CCACTCTAGG GGTGAGGCTC 2160  
 CATTAGGATT TGCCCTTCC CATCTCTCC TACCCAAACA CTCAAATTAA TCTTTCTTTA 2220  
 CCTGAGACCA GTTGGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAAAGGCC AGTCTGGGCT 2280  
 CGCGGTTCT AGTCTCTTTT GCACTGAGG GCACTAAT ACCATGAGAA GAGGGCTCTG 2340  
 40 GGGAGCCTGC AAACCTACTG CTCAGAAGA CATGGAGACT CCTGCCCTGT TGTGTATAGA 2400  
 TGCAAGATAT TTATATATAT TTTTGGTTGT CAATATTAAA TACAGACACT AAGTTATAGT 2460  
 ATATCTGAGC AAGCCCACTT GTAAATACAC CACCTCACTC CTGTACTTCA CCTAAACAGA 2520  
 TATAAATGGC TGGTTTTAG AAACATGGTT TTGAAATGCT TGTGGATGA GGGTAGGAGG 2580  
 TTTGATGGAG AGTGAGACAG AAGTAAGTGG GGTGCAACC ACTGCAACGG CTAGACTTC 2640  
 45 GACTCAGGAT CCACTCCCTT ACACGTACCT CTCATCAGTG TCCTCTGTCT CAAAATCTG 2700  
 TTTGATCCCT GTTACCCAGA GAATATATAC ATTCTTTATC TTGACATTCA AGGCATTCT 2760  
 ATCACAATTT TGATAGTTGG TGTTCAAAA AACACTAGTT TTGTGCCAGC CGTGATGCTC 2820  
 AGGCTGAAA TCGCATTATT TTGAATGTGA AGGGAA 2856

Seq ID NO: C86 DNA Sequence  
 Nucleic Acid Accession #: XM\_035292.2  
 Coding sequence: 53..1576

55 1 11 21 31 41 51  
 | | | | | |  
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCGCGGCC GGTGCGCAGA GCATGGCGGG 60  
 TCGGGGCCCG AAGCGGCGCG CGCTAGCGGC GCGCGCGGCC GAGGAGAAGG AAGAGGCGCG 120  
 GGAGAAGATG CTGGCGGCCA AGAGCGCGGA CGGCTCGGCG CCGCGAGCGG AGGGCGAGGG 180  
 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240  
 60 TATCGGCTCG GGCATCTCG TGACGCCAC GGGGCTGCTC AAGGAGGCG GCTCGCGGG 300  
 GCTGGGCGTG GTGGTGTGGG CCGGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360  
 CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTACA TGCTGGAGGT 420  
 CTACGGCTCG CTGCGCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCGGCGCTTC 480  
 ATCGCAGTAC ATCGTGGGCC TGGTCTTCC CACCTACCTG CTCAGCGCG TCTTCCCCAC 540  
 65 CTGCGCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCTGTC TGCTGCTCAC 600  
 GGCCTGGAAC TGCTACAGCG TGAAGGCCGC CACCGCGGTC CAGGATGCTT TTGCGCGCGC 660  
 CAAGCTCCTG GCCCTGGCCC TGATCATCTT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720  
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAATCTGGAT TGGGGAAAT 780  
 70 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTAAT TGAATTTCTG 840  
 CACAGAGGAA ATGATCAACC CCTACAGAAA OCTGCCCTG GCCATCATCA TCTCCCTGCC 900  
 CATGCTGAGC CTGGTGTACG TGCTGACCAA CCTGGCTTAC TTCACCAACC TGTCCACCGA 960  
 GCAGATGCTG TCGTCCGAGG CGTGGCGGT GGAATTCGGG AACTATCACC TGGGCGTCAT 1020  
 GTCTGAGATC ATCCCGTCT TCGTGGGCTT GTCTGCTTC GGCTCCGTC ATGGGTCTCT 1080  
 GTTCAATATC TCCAGGCTCT TCTTCTGGG GTCCCGGGA GGCACCTGC CCTCATCTCT 1140  
 75 CTCCATGATC CACCAACAGC TCCTCACCCC CGTGGCGTCC CTGCTGTTC CTGTGTGAT 1200  
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTCTCGCTC ATCAACTTCT TCAGCTTCTT 1260  
 CAACCTGGCT TCGTGGGCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320  
 TGAGCTTGAAG CGGCCATCA AGGTGAACCT GGCCCTGCTT GTGTCTTCA TCCTGGGCTC 1380  
 CACTTCTCTG TCGCGCTCT CCTTCTGGAA GACACCGGTG GAGTGTGGCA TCGGCTTCA 1440  
 80 CATCATCTCT AGCGGCTGC CGCTCACTT CTTCGGGCTC TGGTGGAAA ACAAGCCCAA 1500  
 TGGGCTCTCT CAGGCGATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TCGAGGTGGT 1560  
 CCCCAGGAG ACATAGCCAG GAGGCGAGT GGCTGCCGGA GGAGCATGC 1609

Seq ID NO: C87 DNA Sequence  
 Nucleic Acid Accession #: NM\_005268.1

Coding sequence: 168..989

	1	11	21	31	41	51	
5							
	TAAAAAGCAA	AAGAATTGCG	GGCCGGGTGCG	ACACGGGGCTT	CCCCGAAAAC	CTTCCCCGCT	60
	TCTGGATATG	AAATTCAAGC	TGCTTGCTGA	GTCTATTGCG	GGCTGCTGCG	GAGCCAGGAG	120
	AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGGGTGG	GTCCACCATG	AACTGGAGTA	180
	TCITTTGAGG	ACTCCTGAGT	GGGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
10	TGTCCTGGT	CTTCATCTTC	CGCGTGCTGG	TGTACTGGT	GACGGCCGAG	CGTGTGTGGA	300
	GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTGCCAGGCC	CGGCTGCTCC	AACGTCTGCT	360
	TTGATGAGTT	CTTCCTCTGT	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGGTGA	420
	CATGCCCTCT	ACTGCTCGTG	GTCATGCAGC	TGGCCTACCG	GGAGGTTTCAG	GAGAAGAGGC	480
	ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGGGG	540
15	GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT	600
	TTCTCTATGT	GTTCACACTA	TTCTACCCCA	AAATATATCT	CCCTCTGTGT	GTCAAGTGCC	660
	ACGCAATCC	ATGCCCAAT	ATAGTGGACT	GCTTCATCTC	CAAGCCCTCA	GAGAAGAAC	720
	TTTTCAACCT	CTTCATGGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
	TCATCTACCT	GGTGAGCAAG	AGATGCCACG	AGTGCCCTGC	AGCAAGGAAA	GCTCAAGCCA	840
20	TGTGCACAGG	TCATCACCCC	CACGGTACCA	CCTCTTCCCT	CAAAACAAGAC	GACCTCCTTT	900
	CGGGTGACCT	CATCTTTCTG	GGCTCAGACA	GTCTCTCTCC	TCTCTTACCA	GACCGCCCCC	960
	GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGGTCTG	GCAGGTTGGG	1020
	CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGG	GGAGCTAAGC	1080
	CATGAGGTAG	GGGACGGCAA	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCTAGTCC	1140
25	TCAACTCCAG	CCACCTGCCC	CAGCTCGACG	GCACTGGGCC	AGTTCCCCCT	CTGCTCTGCA	1200
	GCTGGTTTC	CTTTTCTAGA	ATGGAATAG	TGAGGGCCAA	TGC		1243

Seq ID NO: C88 DNA Sequence

Nucleic Acid Accession #: NM\_005130

Coding sequence: 98..802

30	1	11	21	31	41	51	
	CTCTACCTGA	CACAGCTGCA	GCCTGCAATT	CACTCCCACT	GCCTGGGATT	GCACTGGATC	60
35	CGTGTGCTCA	GAACAAGGTG	AACGCCACGC	TGCAGCCATG	AAGATCTGTA	GCCTCACCTT	120
	GCCTCTCTTC	CTCTACTCTG	CTGCTCAGGT	GCTCCTGGTG	GAGGGGAAAA	AAAAAGTGAA	180
	GAATGGACTT	CACAGCAAAG	TGGTCTCAGA	ACAAAAGGAC	ACTCTGGGCA	ACACCCAGAT	240
	TAAGCAGAAA	AGCAGGCCCG	GGAAACAAAG	CAAGTTTGTC	ACCAAAGACC	AAGCCAACTG	300
	CAGATGGGCT	GCTACTGAGC	AGGAGGAGGG	CATCTCTCTC	AAGGTTGAGT	GCACTCAATT	360
40	GGACCATGAA	TTTTCTGTGT	TCTTTGCTGG	CAATCCAACC	TCATGCCTAA	AGCTCAAGGA	420
	TGAGAGAGTC	TATTGGAAAC	AAGTTGCCCG	GAATCTGCGC	TCACAGAAAG	ACATCTGTAG	480
	ATATTCCAAG	ACAGCTGTGA	AAACCAAGAT	GTGCAGAAAG	GATTCTCCAG	AATCCAGTCT	540
	TAAGCTAGTC	AGCTCCACTC	TATTTGGGAA	CACAAAGCCC	AGGAAGGAGA	AAACAGAGAT	600
	GTCCCCCAGG	GAGCACATCA	AGGGCAAAGA	GACCAACCCC	TCTAGCCCTAG	CAGTGACCCA	660
45	GACCATGGCC	ACCAAAGCTC	CCGAGTGTGT	GGAGGACCCA	GATATGGCAA	ACCAGAGGAA	720
	GACTGCCTGT	GAGTTCGTGT	GAGAGACTTG	GAGCTCTCTC	TGCACATTCT	TCCTCAGCAT	780
	AGTCAGGAC	ACGTCTGTGT	AATGAGGTCA	AAAGAGAACG	GTTTCTTTTA	AGAGATGTCA	840
	TGTCGTAAGT	CCCTCTGTAT	ACTTTAAAGC	TCTCTACAGT	CCCCCAAAAA	TATGAACTTT	900
	TGTGCTTAGT	GAGTGCAACG	AAATATTTAA	ACAAGTTTGT	TATTTTGTGT	TTTTGTGTTT	960
50	TGGAATTGCG	CTTATTTTTC	TTGGATGCGA	TGTTCAAGAG	CTGTTTCTGT	CAGCATGTAT	1020
	TTCCATGGCC	CACACAGCTA	TGTGTTTGAG	CAGCGAAGAG	TCCTTGAGCT	GAATGAGCCA	1080
	GAGTGATAAT	TTCAAGTGCA	CGAACCTTCT	GCTGAATTAA	TGGTAATAAA	ACTCTGGGTG	1140
	TTTTTCAAAA	AAAAAATAAA	AAA				1163

Seq ID NO: C89 DNA Sequence

Nucleic Acid Accession #: BC022542

Coding sequence: 274..927

60	1	11	21	31	41	51	
	ACTTGGTCCC	AGCCGATAAA	TCTGGGGCAG	CGCGCGGTAG	GAGCTGCGGG	CGGCCAGGCC	60
	CCTTCCTGCG	TCCGCACCTG	GCCCGCGCGG	CCCTCTCGGG	GGGTCCGGCT	TCCGGCGTCC	120
	TGGCGGCTCG	GGTGGCGGGG	GTTGCGGGCG	CCGCTCGGCT	GCTCTCGGG	GCGGGGAGGG	180
	GGCTCAGCGG	CGGGCCCGCC	ACGGCCTTCA	CCGCGCGCGG	CTCTGACGCC	GGCATAAGGG	240
65	CCATGTGTTT	TGAAATTATT	TTGAGGCAAG	AAGTTTGTAA	AGATGGTTTC	CACAGAGACC	300
	TTTTAATCAA	AGTGAAGTTT	GGGGAAGCA	TTGAGGACTT	GCACACGTGC	CGTCTCTTAA	360
	TTAAACAGGA	CATTCTTGCA	GGACTTTATG	TGGATCCGTA	TGAGTTGGCT	TCATTACGAG	420
	AGAGAAACAT	AACAGAGGCA	GTGATGGTTT	CAGAAAAATT	TGATATAGAG	GCCCCTAAC	480
	ATTTGTCCAA	GAGGCTGGA	GTTCTCATT	ATGCCAGACG	AGATTACAG	TGCATTGACT	540
70	GTTTTCAGCG	CTTTTTCCTT	GTGCACTGCC	GCTATCATCG	GCGCACAGT	GAAGATGGAG	600
	AAGCCTCGAT	TGTGGTCAAT	AACCCAGATT	TGTTGATGTT	TTGTGACCAA	GAGTTCGCGA	660
	TTTTGAAATG	CTGGGCTCAC	TCAGAAAGTG	CAGCCCTTGT	TGCTTTGGAT	AATGAGGATA	720
	TATGCCAATG	GAACAAGATG	AAGTATAAAT	CAGTATATAA	GAATGTGATT	CTACAAGTTC	780
	CAGTGGGACT	GACTGTACAT	ACCTCTCTAG	TATGTTCTGT	GACTCTGCTC	ATTACAATCC	840
75	TGTGCTCTAC	ATTGATCCTT	GTAGCAGTTT	TCAAATATGG	CCATTTTTC	CTATAAGTTT	900
	TATGTAGTTA	AATGCTTCTT	AGAAACCTAA	ATAAGATCTA	TTAATTTCTG	ACGAGAGGTG	960
	TTCTTCTAGA	ATTAAATTACT	TTTATCTTTT	GTCTTCATTT	GTGGCCAAAA	TTATGTTTAC	1020
	TAGAGGAAAT	TTGGGATCAT	TCTCAGCTAA	TTCCAAAAAT	TAGTGTCTTA	TTGCATGGAT	1080
	CCTTGGTAAT	CCTCAAGCAT	CAGATGCCAT	AAGGGGAAAC	TTAATTTCTG	TAAATTAATG	1140
80	TTTATTTTGT	GAGAAAGTAC	TTTATCTTCA	TTTGGGGTAG	AAAAATTATT	TCITTATGTA	1200
	GTAGAGACAA	ATTATTTCTA	TTTTGCAAGT	ACTTTCAATT	TAAGCTACAA	ATTGAGAAAA	1260
	CGGTTATAAA	TAAGAAATAA	ATAGGCCAGG	CACAGTGGCT	CACACCTGTA	ATCCAGCAC	1320
	TTTGGGAGCC	CGAGGTGGGC	GGATCACCAG	AGGTCAAGAG	TTTGAGACCA	GCTTGGTGAA	1380
	ACCCGTCTCT	TACTAAAAAT	ACAAAAGTTA	GCTGGGGCTG	GTGGTGGGCA	TCTGTAGTCC	1440
	CAGCTAATTG	GAAGGGTGAG	GCGGGAGGAT	CGCTTGAACC	TGGGAGGCGG	AGGTTCCAGA	1500



5 GAGCCAAAGT CGCACCAGT CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA 1560  
 GGAAAAACAA AAAAGAGAA TAAATAATT TGGATGAAAA TCATGTTTAT TTAATAGTA 1620  
 ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCATGA AAATCATTAA AGTAGGACAG 1680  
 CTAAGAAATT AATATTAAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCCTTA 1740  
 ACGCACTCCA TTCTCCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800  
 GGACTTGATG AAACCTGAGTA CTAAGATTG GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860  
 TTGCCATTTT AAATAAGTT GTACATGAAC AAAAAA AAAA 1906

10 Seq ID NO: C90 DNA Sequence  
 Nucleic Acid Accession #: NM\_004994  
 Coding sequence: 20..2143

15 1 11 21 31 41 51  
 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTG GTCTTGGTGC TCCTGGTGCT 60  
 GGGCTGCTGC TTTGCTGCC CCAGACAGCG CCAGTCCACC CTGTGCTCT TCCTGGAGA 120  
 CCTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180  
 CACTCGGTG CGACGATGC GTGGAGATC GAAATCTCTG GGGCTGCGC TGCTGCTTCT 240  
 CCAGAAGCAA CTGTCCCTGC CCGAGACCG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300  
 GCGAACCCCA CGGTGCGGGG TCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT 360  
 CAAGTGGCAC CACACACAAC TCACCTATTG GATCCAAAC TACTCGGAAG ACTTGGCGG 420  
 GGGCGTGTG GACGAGCCCT TTGCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCGCT 480  
 CACCTTCACT CGCGTGACA GCGGGGACG AGACATCGTC ATCCAGTTTG GTGTGCGGA 540  
 GCAAGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACAGC CCTTTCCTCC 600  
 TGGCCCGCGG ATTGAGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660  
 GGGCGTGTG GTTCCAACTC GGTTTGAAA CGCAGATGGC GGGCGCTGCC ACTTCCCTTT 720  
 CATCTTCGAG GGGCGCTCCT ACTCTGCTG CACCACGAC GGTGCTCCG ACGGCTTGCC 780  
 CTGGTGCAGT ACCACGGCCA ACTAGCACAC CGACGACCGG TTTGGCTTCT GCCCCAGGA 840  
 GAGACTCTAC ACCCGGACG GCAATGTGA TGGGAAACCC TGCCAGTTTC CATTATCTT 900  
 CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTGGC TCGACGGCT ACCGCTGGTG 960  
 CGCCACCAAC GCCAATACG ACCGGGACAA GCTCTTCGGC TTCTGCCGA CCGAGCTGA 1020  
 CTCGACGGTG ATGGGGGCGA ACTCGGCGG GGAGCTGTGC GTCTTCCCT TCACTTTCT 1080  
 GGGTAAGGAG TACTGACCT GTACCAGCA GGGCGCGGA GATGGCGCC TCTGGTGGC 1140  
 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGCTTC TGCCCGGACC AAGGATACAG 1200  
 TTTGTCTCT GTGGCGGCG ATGAGTTCGG CCACGGCTG GGTCTAGATC ATTCTCAGT 1260  
 GCGGAGGCG CTATGTACC CTATGTACC GTCTACTGAG GGGCCCCCT TGCATAAGGA 1320  
 CGAGCTGAAT GGCATCGGCG ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCTCC 1380  
 AACCAACAGT AACCAGCAGC CCAAGGCTCC CCGACGGTTC TGCCCGGACC GACCCCGAC 1440  
 TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500  
 AGGTCCCCC ACTGCTGGCC CTCTACGGC CACTACTGTG CCTTGTAGTC CGGTGGACGA 1560  
 TGCCTGCAAC GTGAACATCT TCGACGGCAT CGCGGAGATT GGGAAACGAG TGTATTGTT 1620  
 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCGGCGCG AGGGCCCTT 1680  
 CCTTATCGCC GACCAAGTGG CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740  
 GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGGCTC 1800  
 GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCGGAGTGG CCCAGGTGAC 1860  
 GGGGCGCTCG CGGAGTGGA GGGGGAAGAT GCTGCTGTT AGCGGCGCGC GCTCTGGAG 1920  
 GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGATGTT 1980  
 CCGCGGCTCG CTTTGGACA CGCACGAGCT CTTCAGTAC CGAGAGAAG CCTATTCTG 2040  
 CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACGAG TGGACCAAGT 2100  
 GGGTACGTG ACCTATGACA TCCTGCAGTG CCTGAGGAC TAGGCTCCG GTCTTCTCTT 2160  
 CGAGTGGCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCGGATA 2220  
 CAACTGTGTA TCTGTCTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGG CCCTCTCTTC 2280  
 TCACCTTTGT TTTTGTGG AGTGTCTTA ATAACTTGG ATTCTCTAAC CTTT 2334

55 Seq ID NO: C91 Sequence  
 Nucleic Acid Accession #: NM\_000213  
 Coding sequence: 188..5656

60 1 11 21 31 41 51  
 GGGCTGCGG CCTGCTCCC ACCCCCCAAC CCCCCGCGC CGCCCTGGA CAGTCCCTGC 60  
 TGGCCGCGC GCTGACGCC CATCTCTAG CCGCAGCCCA GCGCGGAGG GAGCGAGTCC 120  
 GCGCGAGGT AGGTCCAGGA CGGGCGACA GCAGCAGCG AGGCTGGCG GAGAGGGAG 180  
 GAAGAGGATG GCAGGGCCAC GCGCCAGCC ATGGGCCAGG CTGCTCTGG CAGCCTTGAT 240  
 65 CAGCGTCAGC CTCTCTGGGA CCTTGGCAA CCGCTGCAAG AAGGCCCGAG TGAAGAGCTG 300  
 CACGGAGTGT GTCCGTGTGG ATAAGGACTG CGCCTACTGC ACAGACGAGA TGTTCAGGA 360  
 CCGGCGCTGC AACACCCAGG CGGAGCTGCT GCGCGCGGG TGCCAGCGGG AGAGCATCGT 420  
 GGTGATGGAG AGCAGCTTCC AAATCACAGA GGAGACCCAG ATTGACACCA CCCTGCGCG 480  
 CAGCCAGATG TCCCCCAAG GCCTGCGGGT CCGTCTGCGG CCGGTGAGG AGCGGCATTT 540  
 70 TGAGCTGGAG GTGTTTGAGC CACTGGAGAG CCCCCTGGAC CTGTACTACC TCATGGACTT 600  
 CTCCACTCC ATGTCCGATG ATCTGGACAA CCTCAAGAAG ATGGGCGAGA ACCTGGCTCG 660  
 GGTCTGAGC CAGCTCACCA GCGACTACAC TATTGGATT GGCAGTTTG TGGACAAAGT 720  
 CAGCGTCCCG CAGACGGACA TGAGGCTGGA GAAGCTGAAG GAGCCTGGC CCAACAGTGA 780  
 75 CCCCCCTTC TCCTTCAAGA ACCTCATCAG CTTGACAGAA GATGTGGATG AGTTCGGGAA 840  
 TAAACTGCAG GGAGAGCGGA TCTCAGGCAA CTTGAGTGT CTGAGGGCG GCTTCGATGC 900  
 CATCTGCGAG ACAGCTGTGT GCACGAGGGA CATTGGCTGG CCGCCGAGCA GCACCCACT 960  
 GCTGGTCTTC TCCACGAGT CAGCCTTCCA CTATGAGGCT GATGGCGCA AGTGCTGGC 1020  
 TGGCATCATG AGCGCAACG ATGAACGGTG CCACTGGGAC ACCACGGGCA CCTACACCA 1080  
 80 GTACAGACA CAGACTACC GGTGCGTCC CACCTGGTG CCGCTGCTCG CCAAGCACAA 1140  
 CATCATCCCC ATCTTTGCTG TCACCAACTA CTCCTATAGC TACTACGAGA AGCTTCACAC 1200  
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 CGAGGCGCTT CGGACAGAGG TCACCTCAA GATGTTCCAG AAGACGAGGA CTGGGTCTCT 1380  
 TCACATCCGG CGGGGGGAG TGGGTATATA CCAGGTGCAG CTGCGGGCCC TTGAGCACGT 1440

5	GGATGGGACG CACGTGTGCC AGCTGCCGGA GGACAGAAG GGCAACATCC ATCTGAAACC 1500
	TTCTTTCTCC GACGGCTCA AGATGGAGCG GGGCATCATC TGTGATGTGT GCACCTGCGA 1560
	GCTGCAAAAA GAGGTGCGGT CAGCTCGCTG CAGCTTCAAC GGAGACTTCG TGTGCGGACA 1620
	GTGTGTGTGC AGCGAGGGCT GGAGTGGCCA GACCTGCAAC TGCTCCACCG GCTCTCTGAG 1680
	TGACATTTCAG CCTTGCCTGC GGGAGGGGCGA GGACAAGCCG TGCTCCGGCC GTGGGGAGTG 1740
	CCAGTGGCGG CACTGTGTGT GCTACGGCGA AGGCCGCTAC GAGGGTCAGT TCTGCGAGTA 1800
	TGACAACTTC CAGTGTCCCC GCACTTCGCG GTTCTGTGCG AATGACCGAG GACGCTGCTC 1860
	CATGGGCCAG TGTGTGTGTG AGCCTGGTTG GACAGGCCCA AGCTGTGACT GTCCCCCTAG 1920
10	CAATGCCACC TGCATCGACA GCAATGGGGG CATCTGTAAAT GGACGTGGCC ACTGTGAGTG 1980
	TGGCGCTGCG CACTGCCACC AGCAGTTCGT CTACACGGAC ACCATCTGCG AGATCAACTA 2040
	CTCGCGGATC CACCGGGGCC TCTGCGAGGA CCTACGCTCC TGCGTGCAGT GCCAGGCGTG 2100
	GGGACCGGCG GAGAAAGAGG GCGCAGCTGT TGAGGAATGC AACTTCAAGG TCAAGATGGT 2160
	GGACGAGCTT AAGAGAGCCG AGGAGGTGGT GGTGCGCTGC TCCTTCCGGG ACGAGGATGA 2220
15	CGACTGCACC TACAGCTACA CCATGGAAGG TGACCGCGCC CCTGGGCCCA ACAGCACTGT 2280
	CCTGGTGCAC AAGAAGAAGG ACTGCCCTCC GGGCTCCTTC TGGTGGCTCA TCCCCCTGCT 2340
	CCTCTCTGTC CTGCGGCTCC TGGCCCTGCT ACTGCTGCTA TGTGGAAGT ACTGTGCTTG 2400
	CTGCAAGGCC TGCTTGGCAC TTCTCCCGTG CTGCAACCGA GGTCAATGG TGGGCTTTAA 2460
	GGAAAGCTCT CATATGCTCG GGGAGAACCT GATGGCTCTT GACCACTTGG ACACGCCCAT 2520
20	GCTGCGCAGC GGGAACTTCA AGGGCCGTGA CGTGGTCCCG TGGAAAGTCA CCAACAACAT 2580
	GCAGCGGGCT GCGTTTGCCA CTCATGCCGC CAGCATCAAC CCCACAGAGC TGGTGCCTTA 2640
	CGGGCTGTCC TTGCGGCTGG CCGCGCTTTG CACCGAGAAC CTGCTGAAGC CTGACACTCG 2700
	GGAGTGGGCC CAGCTGCGCC AGGAGGTGGA GGAGAACCTG AACGAGGTCT ACAGGCAGAT 2760
	CTCGGTGTTA CACAAGCTCC AGCAGACCAA GTTCCGGCAG CAGCCCAATG CCGGAAAAAA 2820
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	GCTGAAGCTT ACAGAGAAGC AGGTGGAACA GAGGGCTTTC CACGACCTCA AGGTGGCCCC 2940
	CGGCTACTAC ACCCTCACTG CAGACCAGGA CGCCCGGGGC ATGTGTGAGT TCCAGGAGGG 3000
	CGTGGAGCTG GTGGAGCTAC GGGTGGCCCT CTTTATCCGG CCTGAGGATG ACACGAGGAA 3060
	GCAGCTGTCT GTGGAGGCCA TCGACGTGCC CGCAGGCAC TGCCACCTCG GCGCGCCCT 3120
30	GGTAAACATC ACCATCATCA AGGAGCAAGC CAGAGACGTG GTGTCTTTG AGCAGCCTGA 3180
	GTCTCTGCTC AGCGCGGGGG ACCAGGTGGC CCGCATCCCT GTCATCCGGC GTGTCTTGGA 3240
	CGCGCGGAAG TCCAGGCTCT CTTACCGCAC ACAGGATGGC ACCCGCGCAG GCAACCGGGA 3300
	CTACATCCCC GTGGAGGGTG AGCTGTCTGT CCAGCCTGGG GAGGCTTGA AAGAGCTGCA 3360
	GGTGAAGCTC CTGGAGCTGC AAGAAGTTGA CTCCTCTCTG CGGGGCGGCC AGGTCCGCGC 3420
35	TTTCCACGTC CAGCTCAGCA ACCCTAAGTT TGGGGCCAC CTGGGCCAGC CCCACTCCAC 3480
	CACCATCATC ATCAGGAGCC CAGATGAACT GGACCGGAGC TTCACGAGTC AGATGTTGTC 3540
	ATCACAGCCA CCCCCTCAGC GCGACCTGGG CGCCCCGCGC AACCCCAATG CTAAGGCCGC 3600
	TGGGTCCAGG AAGATCCATT TCAACTGGCT GCCCCTCTCT GGCAAGCCAA TGGGGTACAG 3660
	GGTAAAGTCA TGATTCAGG GCGACTCCGA ATCCGAAGCC CACCTGCTCG ACAGCAAGGT 3720
40	GCCCTCAGTG GAGCTCACCA ACCTGTATCC GTATTGCGAC TATGAGATGA AGGTGTGGGC 3780
	CTACGGGGCT CAGGGCGAGG GACCTACAG CTCCTGTGGT TCCTGCGCGA CCCACCAGGA 3840
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	CCTGTCTAAC GTGATCAAC GACCTATTGG GCCATGAAG AAGTGTCTGG TTGCAACCC 4020
45	TAAGAACCGG ATGTGCTTA TTGAGAACCT TCGGAGTCC CAGCCCTACC GCTACACGGT 4080
	GAAGCGCGGC AACGGGGCGG GCTGGGGGCC TGAGCGGGAG GGCATCATCA ACCTGGCCAC 4140
	CCAGCCCAAG AGGCCCATGT CCATCCCAT CATCCCTGAC ATCCCTATCG TGGACGCCCA 4200
	GAGCGGGGAG GACTACGACA GCTTCTTAT GTACAGCGAT GAGCTTCTAC GCTCTCCATC 4260
	GGGCGAGCAG AGGCCAGCG TCTCCGATGA CACTGGCTGC GGCTGGAAGT TCGAGCCCT 4320
50	GCTGGGGGAG GAGCTGGACC TCGGGCGGCT CAOGTGGCGG CTGCCCCCGG AGCTCATCCC 4380
	GCGCCTGTGG GCCAGCAGCG GGGCTCTCTC CGACGCGGAG GCCCCCAGG CCCCCCGGAC 4440
	GACGGCGGCG CGGGCGGGAA GGGCGGCGAG CGTGGCCGCG AGTGGGACAC CGGGGCCCCC 4500
	CGGAGAGCAC CTGGTGAATG GCCGGATGGA CTTTGCCTTC CCGGGCAGCA CCAACTCCCT 4560
	GCACAGGATG ACCACGACCA GTGCTGCTGC CTATGGCACC CACCTGAGCC CACACGTGCC 4620
	CCACCGGCTG CTAAGCAGAT CCTCCACCCT CACACGGGAC TACAACCTAC TGACCGGCTC 4680
55	AGAACACTCA CACTCGACCA CACTGCCAG GGACTACTCC ACCCTCACTC CGTCTCTCTC 4740
	CCAGACTCT GCGCTGACTC CTGGTGTGCC CGACACGCCC ACCCGCCTGG TGTCTCTGTC 4800
	CCTGGGGCCC ACATCTCTCA GAGTGAGCTG CGAGGAGCCG CGGTGCGAGC GGCGCTGCA 4860
	GGGCTACAGT GTGGAGTACC AGCTGCTGAA CGGCGGTGAG CTGCATCGGC TCAACATCC 4920
	CAACCTGCCC CAGACCTCGG TGGTGGTGGG AGACTCTCTG CCAACCACT CTAAGTGT 4980
60	CGCGTGGCG GCGCAGAGCC AGGAAGGCTG GGGCGGAGAG CGTGAGGCTG TCATCACCAT 5040
	TGAATCCAG GTGCACCCCG AGAGCCACT GTGTCCCTG CCAGGCTCG CTTCACTTT 5100
	GAGCACTCCC AGTGCCTCAG GCCCGCTGGT GTTCACTGCC CTGAGCCAG ACTGCTGCA 5160
	GCTGAGCTGG GAGCGGCCAC GGAGGCCCAA TGGGGATATC GTGCGCTACC TGGTGAACCTG 5220
65	TGAGATGGCC CAGGAGGAG GGCCAGCCAC CGCATTCCGG GTGGATGGAG ACAGCCCGA 5280
	GAGCGGCTG ACCGTGCCGG GCCTCAGCGA GAACGTGCCC TACAAGTTCA AGGTGCAGGC 5340
	CAGGACCACT GAGGGCTTCG GGCCAGAGCG CGAGGGCATC ATCACCATAG AGTCCAGGA 5400
	TGGAGGACCC TTCCCGCAGC TGGGCGAGCG TGCGGGGCTC TTCCAGCACC CGCTGCAAG 5460
	CGAGTACAGC AGCATCACCA CCAACCACAC CAGCGCCACC GAGCCCTTCC TAGTGGATGG 5520
70	GCTGACCTCG GGGGCCAGC ACCTGGAGGC AGCGGCTCC CTCACCGGCG ATGTGACCCA 5580
	GGAGTTTGTG AGCCGGACAC TGACCCAGC CGGAACCTTT AGCACCCACA TGGACCAACA 5640
	GTCTTTCCAA ACTTGACGCG ACCCTGCCCC ACCCGCGCCA TGTCCACTA GGGTCTCTCC 5700
	CGACTCTCTT CCGCGAGCCT CCTCAGCTAC TCATCTCTTG CACCCCTGGG GGGCCAGCCC 5760
	ACCGCATGTC ACAGAGCAGG GGCTAGGTGT CTCTGGGAG GAGTGAAGGG GGCAAGGTC 5820
75	GTCTCTGTGT GGGCCAAACC TATTGTAAAC CAAAGAGCTG GGAGCAGCAC AAGGACCCAG 5880
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	AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 5994

Seq ID NO: C92 DNA Sequence  
 Nucleic Acid Accession #: NM\_023915  
 Coding sequence: 250..1326

1 11 21 31 41 51  
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 CCCACGGCTC AATCGTCCCC AAGTGTTCCT TGACACGCAT CTTTGCTTAC AGTGCAATCAC 240  
 5 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300  
 CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCCTTAC 360  
 AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTTTG GGCAAGCATC 420  
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480  
 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCATTTOGA 540  
 10 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600  
 TCAGTTTGTG TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660  
 GATCGCTATC TGAAGGTGGT CAAGCCATTG GGGGACTCTC GGATGTACAG CATAACCTTC 720  
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 ATCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840  
 15 CCTTGGGGG TCAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTGTGGCC 900  
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960  
 AGGCAATTCA TAAGTCAGGT AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020  
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATCC TTTTACTTTT 1080  
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 20 ATTACACTTT TCTGTCTGCT GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG 1200  
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 TTCATTATCC TTAATAAAAA AA 1402

25 Seq ID NO: C93 DNA Sequence  
 Nucleic Acid Accession #: NM\_020789.1  
 Coding sequence: 208..3699

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 35 GGGCTGGGTG AGCAGGCCAG CTGGGCTATG GTGTGGTGCC TCGGCTCGGC CGTCTCAGC 240  
 TGGTTCATCA GCCAGGGGGC TGACGGTCTGA GGAAGCGCTG AGGTGGTATC GGTGGTGGGC 300  
 CGGGCTGAGG AGAGTGTGGT GCTGGGCTGT GACCTGCTGC CCCCGGCCGG CGGCCCCCCC 360  
 CTGATGTCA TCGAGTGGCT GCGCTTTGGA TTCTGCTTC CCATCTTCAT CCAGTTCGGC 420  
 CTCTACTCTC CCGAATTGA CCTGATTAC GTGGGAGGAG TCGGCTGCA GAAGGGGGCC 480  
 40 TCTCTCCAGA TTGAGGCTCT CCGGCTGGA GACCAGGGCT GGTACGAGTG CCGGCTGTTT 540  
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 GTCAATTAC CCCTCAATT CCAGGAGACA CCTCTGCTG TGTGGGAAGT GCAGGAAGCT 660  
 GAGCCTGTGA CCTGCGTGTG TGTGGCCGCT GGCAGCCCCC TGCTCATGT GACGTGAAG 720  
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 45 CGGATCGCC GGGTAGAGCG AGGCAGCTCT GGGGTCTACA CCTGCCAAGC CTCAGCACT 840  
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 50 CAGCCTGATG ATGCCGGCTG CTACACCTGT GTGCCAGCA ATGCCCTCT GCATCCACCC 1140  
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 55 CCTGTGACCC GCGTGTGCT CAAGGCTCCC CCAGCTTTTA TAGAGCGGCC CAAGGAAGAA 1440  
 TATTTCCAG AAGTAGGGCG GGAGCTGCT ATCCCTGCT CCGCCCAAGG GGACCTCTCT 1500  
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 60 CCTCATGTTG TCACCAATGT GTCCGTGGTG GCTTTGCCCA AGGTTGCCAA TGTCTCTG 1740  
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 65 ACCACGCCAG CTGACCCCGG GCTTCCCCCA ACAGAGATAC OGCTCCCTCT GTCCCTCCG 2040  
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 70 AGCAACAGCG CCAAGTCTC CACTCCGGT GTGAGGTCT ACCTTCGCG CACGAGCTG 2340  
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 GTGGCGCTCC TGTGAGCAT CCTGGCCGCG TGCTCTCTGA ACGGCGCAG GGTCTGCCGC 2460  
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 75 GGATCCCGAG TCCCAGCCT GCGCCAGAGT CTGCTCTGG GGGATCCTGC CGGAACCTCC 2640  
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 GGCCCAAGAG GCGCTTTGT GATGGGGGCC ACTGTGGCGG CCCCCAGGA AAGGTGAGC 2760  
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 80 CCCCCTCCAG CAGCCCCACC CAGTCCCTTG CCAGGTCTG GACCCCTGCT CCACTACCTG 2940  
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 GCTGGGGCCA CTGCAAGGCC CCCTTACACA GCGCTGGCTG ACTGGACACT GAGGAGCGG 3180  
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 TGGGACTCAG AATTCCTCGG GGACATGGAA TTGCTGGAGA CTTCGACCT GGGCTTGGCC 3480  
 5 AGCTCCCGGC TCAGACCTGA AGCTGAGACA GAGCTAGGTG TGAAGACTCC AGAGGAGGGC 3540  
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 GAATTCCTGG CCTTCGGCGG CCGCCGAGAT GCTACTAGGG CTGGCTACC AGCCTATCGA 3660  
 CAGCCAGTCC CCCACCCCGA ACAGGCCACT CTGCTGTGAA CATCCCTAAT GTGAGGCTGT 3720  
 10 GAAAAGGCAT ATGGACCTGC AAAGGAGGCC CCCAACCAGA CAGACCTAGT TTCAAACGAG 3780  
 GGCACCTGCC CTGCTGCCCT CTTTGGTGCC CAGGCACAGA CCTGATAGT GGGTTTGGGT 3840  
 CACCTTGGTA TGGAAATGAT GTGCTGACCC CTTAGGTGAG TCTGGGGATT GGAACAGGGA 3900  
 TCTTAGGTCT GCCTCTCTCT CTCTCTCTCT CTCTCTCTCT GTGTGTGTGT 3960  
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 15 AAAA 4024

Seq ID NO: C94 DNA Sequence  
 Nucleic Acid Accession #: NM\_006875  
 Coding sequence: 186..1190

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 25 CCGCGGGTTC CAGCCCTGCG GGGCTTAGCG GGTTCAGTGG GCTCAATCTG CCGAGCGCCA 180  
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 CGCCAGGAGG CAAGGATCGG GAAGCGTTCG AGGCCGAGTA TCGACTCGGC CCCCTCCTGG 300  
 GTAAGGGGGG CTTTGGCACC GTCTTCGAG GACACCGCCT CACAGATCGA CTCAGGTGG 360  
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 30 CATGCCCACT CGAAGTCGCA CTGCTATGGA AAGTGGGTGC AGGTGGTGGG CACCTGGCG 480  
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 CAAGCCGCTG CTTCCTTGGC CAAGTAGTGG CAGCCATCCA GCACTGCCAT TCCCGTGGAG 660  
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 35 AACTCATTTA TTTTGGTTCT GGTGCCCTGC TTCATGATGA ACCCTACACT GACTTTGATG 780  
 GGACAAGGAT GTACAGCCCC CAGAGTGGGA TCTCTCGACA CCACTACCAT GCACTCCCGG 840  
 CCACTGTCTG GTCACTGGGC ATCCTCTCTC ATGACATGGT GTGTGGGAC ATTCCCTTTG 900  
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 40 CGTGTGCCCT AATCGCGCGG TGCTGGCCCG CCAAACTTC TCCCGACCC TCACTGGAAG 1020  
 AGATCTCTGT GGACCCCTGG ATGCAACAC CAGCCGAGGA TGTTACCCCT CAACCCCTCC 1080  
 AAAGGAGGCC CTGCCCCCTT GGCTGGTCC TTGCTACCCT AAGCCTGGCC TGGCCTGGCC 1140  
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 GTTGACTTGG TTTTACAGGT CATTACCACT CATTAAAGTC CAGTATTACT AAGGTAAGGG 1260  
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 45 CAAGAGGCC TTCCTCCAG AACCTGTGGT CCCTGATT 60  
 CTCATTTTGC TAAGGAAGTT TATTTTGGTG AAGTTGTTC CATTTTGAGC CCGGGACTC 1440  
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 TCATATGCTT TTACTTGGGC AAGGGTGTCT TCCTTCCAAT ACCCCAGTAG CTTTATTTT 1560  
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 50 TCAGCCACGG ATTTTATTAT TTGGGGGAGG TAATGCCCTG TTGTACCCC AAGCCTTCTT 1680  
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 55 CTGAGCCGGG ATGTGCAAT TACTAAATG TAAATAATCA CGTATTGTGG GGAGGGGAGT 1980  
 TCCAAGTGTG CCCCTCTTTT TTTTCTGCCC TGGATTATTT AAAAAGCCAT GTGTGGAAC 2040  
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Seq ID NO: C95 DNA Sequence  
 Nucleic Acid Accession #: NM\_002510.1  
 Coding sequence: 92..1774

60 1 11 21 31 41 51  
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 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGGCGCCAAA CGATTTCATG ATGTGCTGGG 180  
 CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAATAGGCT GGTCTTCTGA 240  
 TGAATAATGAC TGGAAATGAA AACTCTACCC AGTGTGGAAG CGGGGAGACA TGAGGTGGAA 300  
 70 AAATCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTGACC AGTGAATCAC CAGCCCTCGT 360  
 GGGCTCAAAAT ATAACATTG CGGTGAACCT GATATTCCTT AGATGCCAAA AGGAAGATGC 420  
 CAATGGCAAC ATAGTCTATG AGAAGAATG CAGAAATGAG GCTGGTTTAT CTGCTGATCC 480  
 ATATGTTTAC AACTGGACAG CATGGTCAGA GGACAGTGAC GGGGAAATG GCACCGGCCA 540  
 AAGCCATCAT AACGTCTTCC CTGATGGGAA ACCTTTTCTT CACCAACCCG GATGGAGAAG 600  
 75 ATGGAATTTT ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT TGGGACGATG 660  
 TTCAGTGAGA GTTTCTGTGA ACACAGCCAA TGTGACACTT GGGCTCTCAAC TCATGGAAGT 720  
 GACTGTGTAC AGAAGACATG GACGGGCATA TGTTCCTATC GCACAAGTGA AAGATGTGTA 780  
 CGTGGTAACA GATCAGATTG CTGTGTTTGT GACTATGTTT CAGAAGAACG ATCGAAATTC 840  
 ATCCGAGCAA ACCTTCTTCC AAGATCTCCC CATTATGTTT GATGTCCTGA TTCATGATCC 900  
 80 TAGCCACTTC CTCATTTATT CTACCAITAA CTACAAGTGG AGCTTCGGGG ATAATACTGG 960  
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 AATTGTAGAG GGAATCTTAG AGGTTAACAT CATCCAGATG ACAGACGTCC TGATGCCGGT 1260

5	GCCATGGCCT	GAAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
	GGAGTCTCTG	ACCATCATTT	CTGACCCAC	CTGCGAGATC	ACCCAGAACA	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCCCT	1500
	GATTTCTGTT	CTGTACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAACA	GTGCCCTGAT	1560
	CTCCGTTGGC	TGCTTGGCCA	TATTTGTAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAATAGTCC	TGGGAATGTG	GTGAGAAGCA	AAGGCCTGAG	1680
	TGTCTTTCTC	AACCGTGCAA	AAGCGGTGT	CTTCCCGGGA	AACCAGGAAA	AGGATCCGCT	1740
10	ACTCAAAAC	CAAGAAATTA	AAGGAGTTTC	TAAATTTTCG	ACCTTGTTC	TGAAGCTCAC	1800
	TTTTCACTGC	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTT	TTCTTAAAGA	1860
	TTATTGTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGT	TAAATGTCAAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACTTATA	AAGTCTTAGG	2040
15	TAAGTAGTAG	GATAGAAACA	CTGTGTCCCG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
	AGCCTAACCC	AGGTTAACTG	CAAGAAGAGG	CGGGATACCT	TCAGCTTTCC	ATGTAAGTGT	2160
	ATGCATAAAG	CCAATTGATG	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
	TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTGACTCTA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
20	TGACAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCAT	2400
	GGACATTTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460
	ATTTCCAAAT	TTTTGTATAG	TGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGTGC	CCTGTTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTCCAC	TCTGTTTGTA	2580
	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTTCTTT	TCTCTCTTC	CTGAAAAATA	2640
25	AAGTGTGGGA	AGAGACAAAA	AAAAAAA				2669

Seq ID NO: C96 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1-4247

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35	ACAGGAGCAC	TGAATCAAAA	AAATTGGGGA	AAGAAATATC	CAACATGTAA	TAGCCCAAAA	180
	CAATCTCCTA	TCAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
	AAATTTCAAG	GTTGGGATAA	AACATCATTG	GAAAAACAT	TCATTCTATA	CAGTGGGAAA	300
	ACAGTGGAAA	TTAATCTCAC	TAATGACTAC	CGTGTGAGCG	GAGGAGTTTC	AGAAATGGTG	360
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40	GAGCATAGTT	TAGAAGGACA	AAAATTTCCA	CTTGAGATGC	AAATCTACTG	CTTTGATGCA	480
	GACCGATTIT	CAAGTTTTGA	GGAAGCAGTC	AAAGGAAAAG	GGAAGTTAAG	AGCTTTATCC	540
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	GAAAGTGTTA	GTGTTTTTGG	GGAAGCAGCT	GCTTTAGATC	CATTCTACT	GTGAAACCTT	660
	CTGCCAAACT	CAACTGACAA	GTATTACATT	TACAATGGCT	CATTGACATC	TCCTCCCTGC	720
45	ACAGACACAG	TTGACTGGAT	TGTTTTTAAA	GATACAGTTA	GCATCTCTGA	AAGCCAGTTG	780
	GCTGTTTTTT	GTGAAGTTCT	TACAATGCAA	CAATCTGGTT	ATGTCATGCT	GATGGACTAC	840
	TTACAAAACA	ATTTTCGAGA	GCAACAGTAC	AAGTTCTCTA	GACAGGTGTT	TTCTCTATAC	900
	ACTGGAAGG	AAGAGATTCA	TGAAGCAGTT	TGTAGTTTCA	AACCAGAAAA	TGTTTCAAGCT	960
	GACCCAGAGA	ATATACCCAG	CCTTCTTGT	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
50	ACCATGATTG	AGAAGTTTGC	AGTTTGTGAC	CAGCAGTTGG	ATGAGAGGGA	CCAAACCAAG	1080
	CATGAATTTT	TGACAGATGG	CTATCAAGAC	TTGGGTGCTA	TTCTCAATAA	TTTGCTACCC	1140
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	ATCATTACCC	AGCACCCCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
10	CATAATGCC	AACTGGTGGT	TATGATTCTT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAAAATAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGST	CACCTTTATG	4140
	GCTGAAGAAC	NCAAAATGTCT	ATCTAATGAG	GAAAAACTTA	TAATTCAGGA	CTTTATCTTA	4200
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAAGTGTCC	TAAATGGCCA	4260
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACCTATAA	GTGTTATAAA	AGAAGAAGCT	4320
15	GCCATAGGG	ATGGCCCTAT	GATTGTTTCT	GATGAGCATG	GAGGAGTGAC	GGCAGGAAC	4380
	TTCTGTGCTC	TGACAAACCTT	TATGCACCAA	CTAGAAAAAG	AAAATTCCTG	GGATGTTTAC	4440
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	ACCTCTCTGG	CAGATTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
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	AGTAACTTTC	ATGACATAGG	ATTCTGCCGC	CAAAATTTATA	TCATTAACAA	TGTTGCTCTT	4800
	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	4860
	TTCTCACTAG	GGAATTTGGG	TATTTTCTTC	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	4920
25	ATAGAGGTTA	GGAATTCCAA	ACTACAGAAA	ATGTTTGTTT	TTAGTGTCAA	ATTTTGTAGCT	4980
	GTATTTGTAG	CAATTATCAG	GTTTGCTAGA	AAATAAATCT	TTAATACAGT	AGCCTGTAAA	5040
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	AATAATCTGT	TACTTATGT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	5160
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30	TAGTTTAATG	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTGTA	CATTGTATTG	5280
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	ATACCTTCAT	TTTGAAGAAA	GTTTTATGA	GAATAACACC	TTACCAACAA	TTGTTCAAAT	5400
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Coding sequence: 1..3340

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	AAATTTCAGG	GTGGGATAA	AACATCATTC	GAAAACACAT	TCATTATATA	CACCTGGGAA	300
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	TTTAAAGCAA	GCAAGATAAC	TTTTCACTGG	GGAAAAATGA	ATATGTCTATC	TGATGGATCA	420
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	ACTGGAAGAG	AGAGATTCCA	TGAAGCAGTT	TGTAGTTTCA	AACCAGAAAA	TGTTCAAGCT	960
	GACCCAGAGA	ATTATACCAG	CCTTCTTGT	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
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	AGCGACCAAC	TGATTGTGGA	CATGCCCTACT	GATAATCCTG	AGGCCAGTAA	TAGTAGCCAT	1260
	GAGTCTCGTA	TTGTTCTAGC	TGAGGGGTTG	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	1320
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75	CTTGCTTATT	ATACTGTGAG	GAATTTTACT	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	2040
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	AAGCCCATG	CAGTGGGGCC	TGTTGTGCTC	CACCTGAGTG	CTGGAGTTGG	AAGAACAGGC	2220
	ACATATATTG	TGCTAGACAG	TATGTTGACG	CAGATTCAAC	ACGAAGGAAC	TGTCACATA	2280
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	GCAGCGCTAA	AGCAATGCAA	CAGGGAAAAG	AATCGAACTT	CTTCTATCAT	CCCTGTGGAA	2580
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	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	2820
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	CTTGTAGACA	CAAGGCAGGA	AGAGAATCCA	TCTACCTCTC	TGGACAGTAA	TGGTGACGCA	3300
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Nucleic Acid Accession #: Eos sequence  
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Coding sequence: 77..1372

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Seq ID NO: C113 DNA Sequence  
Nucleic Acid Accession #: XM\_087254.1  
Coding sequence: 47..2332

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Coding sequence: 138..1820

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70	CGGACTTTCG	CTCCCTGGAT	GCCAAGACCT	CTAGCCGCTT	GGGCGTCTTC	ACCGTGGGCT	420
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 Nucleic Acid Accession #: NM\_002203.2  
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Seq ID NO: C124 DNA Sequence  
Nucleic Acid Accession #: NM\_031460  
Coding sequence: 103..1101

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Coding sequence: 18..1763

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TGGCGCGGCA GCACAAGTCC AAAATGAACA ACCAGACTAA AACGCTGGAC TGCCTGATGG 1500
CGGCCCTCAT CCGCGCGGTG GAGATCTTCA TGGTGAAGAT CTTTATGCTG CTGGTGGTGG 1560
GGATCACCAAG CGGAGTGTGG ATTTGGACCT CCAAGACTCT GCAGTCTCGG CAGCAGGTGT 1620
CGAGCGGTAG GTTAAAGAA GAGAGCCGGA GAAACCGCGC CAGCGTGATC ACCAGCGGTG 1680
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CCCATCTGCC CACCTGCGTG TGAACAGGGC TGGAGGGGAG GGCACAGGGG CGCCCGGAGC 1800
TAAGATGTGG TGCTTTTCTT GGTGTGTGTT TTCTTTCTTC TTCTTCTTTT TTTTTTTTTT 1860
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ACACTGAAG GAAAAATGTA CTAAAGGGT TTTGTTTTGT TTTGGTTTTT CAGCGAAGGG 1980
AAGCTCTCC AGTGAAGTAG CCTCTGTGT AACTAATTG TGGTAAAGTA GTTGATTGAT 2040
CCCTCAGAG AAAACTTTT TTTAGAGCCC TCGTAAATA TACATCTGTG TATTGAGTTG 2100
GGCTTTGCTA CCCATTTACA AATAAGAGGA CAGATAACTG CTTTGCAAT TCAAGACCT 2160
CCCTTGGGTT AACAAATGAG CCATCCCGAG GGGCCACCCC CAGGAAGGCC ACAGTGTCTG 2220
GGGCGATCCC TGCAGAGGAA AGACAGGACC CGGGGCCCGC CTCACACCCC AGTGGATTG 2280
GAGTTGCTTA AAATAGACTC TGGCCTTCA CAATAGTCTC TCTGCAAGAC AGAAACCTCC 2340
ATCAAACTG AACTTTGTGA ACTCAACGA TGTGCAATC ATTTTCTTCT CTTTCTTGA 2400
AAATAAAAG AGAAACAAGT ATTTTGCTAT ATATAAGAC AACAAAGAA ATCTCCTAAC 2460
AAAAGAACTA AGAGGCCGAG CCCTCAGAAA CCCTTCAGTG CTACATTTTG TGGCTTTTTA 2520
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GGGAGAAGGA TCATTCAAAA GTTACCCAAA GGGCTTATG ACTCTTCTA TTGTTAAACA 2640
AATGATTAG AACAACAGAT CAGGAAGCAC TAGGTTGGCA GAGACACTT GTCTAGTGA 2700
TTCTCTTCA AGTGCCAGGA AAGAGTGGT TCTGCGTGTG TATATTGTA ATATATGATA 2760
TTTTTCATGC TCCACTATTT TATTAATAAT AAAATATGTT CTTTAAAAAA A 2811

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50 Seq ID NO: C127 DNA Sequence  
Nucleic Acid Accession #: NM\_005761.1  
Coding sequence: 250..4956

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65  
70  
75  
80

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1 11 21 31 41 51
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GGATGGGGCG CGCGCGGGAG CCGAGGCGCG CGCAGGAACC GCGCGCGCGG CGCGCGCGGT 180
CTCGGTGCCC GCGCGCGCTGA GCGCGCGTGC CGCGCGCGCG CCTTGCCTGG GGGCGGCGCC 240
CCGACGCCCA TGGAGGTCTC CCGGAGGAAG GCGCGCGCGC GCGCGCGCGG CCGCGCGAGG 300
CCACTGCCCC TGCTGCGCTA TCTGCTGGCA CTGGCGGCTC CCGCGCGGGG CGCGGACGAG 360
CCCGTGTGGC GGTGCGAGCA AGCCATCGGA GCCATCGCGG CGAGCCAGGA GGAAGCGGTG 420
TTTGTGGGGA GCGGCGAGTG CCGGAGCCAG CTGGACTACA GCCTGGAGCA CAGCCTCTCG 480
CGCCTGTACC GGAACCAAGC GGGCAACTGC ACAGAGCCGG TCTCGTGGC GCGCCCGCGG 540
CGGCGCGCGG CCGGAGAGCT CTTCAGCAAG CTGCTGCTGC CCTACCGCGA GGGGGCGGGC 600
GGCTCGGGGG GGTGCTGCTC CACCGGCTGG ACCTTGGACC GGGGGCGCTG CGAGGTGCGG 660
CCCTTGGGCA ACTTGAAGCG CAACTCCCTG CGCAACGGCA CGAGGTGGT GTGCTGCCAC 720
CGCAGGGGCT CGAGCGCGCG CGTGGTGTAC CGCGCGGGCC GGAACAACCG CTGTGACCTG 780
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CAGGCATCCC TCGACTGCGG CCGAGCGCAC CCGCGCTGCT CCTCTCTCC 1140
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GATCAACCTG AAAGAGTCCA ACCAATCGCA TCATCTACCT TGATCCATTC CGACCTGACA 1380
TCCGTTTATG GCACCGTGGT AATGAACAGG ACTGTTTAT TCTTGGGGAC TGGAGATGGC 1440
CAGTTACTTA AGTTATTCTT TGGTGAGAAT TTGACTTCAA ATTGTCCAGA GGTATCTAT 1500
GAAATTAAAG AAGAGACACC TGTTTTCTAC AAACCTCGTT CTGATCTCTG GAAGAATATC 1560
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CATAAATCCT GTTCGAGTG TTTAAGAGCC ACAGACCCCT ACTGCGGTTG GTGCCATTG 1680
CTACAAAGGT GCACTTTTCA AGGAGATTGT GTACATTGAG AGAACTTAGA AAACCTGGCT 1740
GATATTTCGT CTGGAGCAAA AAAGTGCCCT AAAATTCAGA TAATTGGAAG CAGTAAAGAA 1800

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AAGACTACAG TGAATATGGT GGGAAAGCTTC TCTCCAAGAC ACTCAAAGTG CATGGTGAAG 1860  
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 45 AGCAGAGCTC CATTGCTAT AAAATACTTT TTTGACTTTT TGGACGCCA GGCTGAAAA 4440  
 AAAAAATCA CAGATCTGGA CGTGTACAT ATTTGAAAA CAAACAGCCT TCCCTTCTGC 4500  
 TTTGCGGTAA ACATCTTGAA GAACCTCAG TTTGTCTTTG ACATTAAGAA GACACCACT 4560  
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Seq ID NO: C128 DNA Sequence  
 Nucleic Acid Accession #: NM\_002185.1  
 Coding sequence: 23..1402

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 AGAACTGGAT GACTACTCAT TCTCATGCTA TAGCCAGTTG GAAGTGAATG GATCGCAGCA 180  
 TTCACTGACC TGTGCTTTTG AGGACCCAGA TGTCAACACC ACCAATCTGG AATTTGAAAT 240  
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 70 CATCGAGACA AAGAAATCTT TACTGATTGG AAAGAGCAAT ATATGTGTGA AGGTGGAGGA 360  
 AAAGAGTCTA ACCTGCAAAA AAATAGACCT AACCACTATA GTTAAACCTG AGGCTCCTTT 420  
 TGACCTGAGT GTCATCTATC GGAAGGAGGC CAATGACTTT GTGGTGACAT TTAATACATC 480  
 ACATCTGCAA AAGAGTATG TAAAGTTTTT AATGCATGAT GTAGCTTACC GCCAGGAAAA 540  
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 75 AAAGCTCCAA CCGCAGCAA TGTATGAGAT TAAAGTTGGA TCCATCCCTG ATCACTATTT 660  
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Seq ID NO: C129 DNA Sequence  
 Nucleic Acid Accession #: NM\_002722.1  
 Coding sequence: 15..302

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 GCGTGGCTCT GTTACTACAG CCACTGCTGG GTGCCAGGG AGCCCCACTG GAGCCAGTGT 120  
 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCAGTA TGCAGCTGAT CTCGCTAGAT 180  
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAAGACA CAAAGAGGAC ACGCTGGCCT 240  
 TCTGGGAGTG GGGTCCCGG CATGCTGCTG TCCCAGGGA GCTCAGCCCG CTGGACTTAT 300  
 20 AATGCCACTT TCTGCTCTCT ACGACTCCAT GAGCAGCGCC AGCCCAGCTC TCCCCTCTGC 360  
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Seq ID NO: C130 DNA Sequence  
 Nucleic Acid Accession #: NM\_032545.1  
 Coding sequence: 47..718

1 11 21 31 41 51  
 30 AAACGTATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA 60  
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 35 CGCGGGGCGG CGCTGCTGCA GGAACGGCGG TACCTGGGTG CTGGGAGCT TCTGCGTGTG 360  
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 40 CCACGCTCAG GGGCCGAGCG CCGGGGGCGC GCCAGCCTG CTACTCTTGC TCCCTGCGC 600  
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 CGTCCTCCAG CGGAGCGCGC GCCCTGCGG AAGGCGGGA CTGCGGCATC GCCTTTAATT 720  
 TTCTATGTTG TAAATAATAG ATGTGTTAG TTACCGTAA GCTGAAGCAC TGGGTGAATA 780  
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 AAAAAA 846

Seq ID NO: C131 DNA Sequence  
 Nucleic Acid Accession #: NM\_006533.1  
 Coding sequence: 72..467

1 11 21 31 41 51  
 50 AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60  
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 TCTCCGACC TGTGTGTCAG GGTGGTCTTA TGGCCAAAGT GGTGACCGG AAGCTGTGTG 180  
 55 CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240  
 CCGACTGCGG ATTCTCTGAC ATTACCGGG GCCAAGTGTG GTATGTCTTC TCCAAGCTGA 300  
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 CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAAACCTG 420  
 60 GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480  
 CTGGCCTGCG CGTTTCCCTT CCTTGGGTTT ATGCCAAATAC AATCAGCCCA GTGCAAAC 538

Seq ID NO: C132 DNA Sequence  
 Nucleic Acid Accession #: AB064272  
 Coding sequence: 1..708

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 65 ATGACACAAG TCACAGAAAA GTCCACAGAA CACCCAGAAA AGACCACGTC AACCCAGAG 60  
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 70 GGGAAAAACA CACCACTCCC AGAAAAGCCT ACAGAAAACC TGGGGAACAC CACACTGACC 180  
 ACTGAGACCA TAAAGGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240  
 ACAAGACTTA TAAACCTTTC AGTCAAGTTC ACAGAGAGCA AATCTCTCAC TACTACCTCT 300  
 TCTCATCTAA ATAAAACTGA AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCCTCAT 360  
 75 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAGCCA CAGGAAACGA GAGCCATCCA 420  
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 TCATTCCCTG CATGGGCCAT AGTTATTGTG GTCCCTGGTG CTGTGATTCT CCTCTGGTG 540  
 TTCCTGGGCC TGATCTTCTT GGTCTCCTAT ATGATGCGGA CACGCGCCAC ACTAACCCAG 600  
 AACACCCAGT ACAATGATGC AGAGGATGAG GGTGCCCCCA ATTCTTACCC GGTCTACCTG 660  
 80 ATGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA 708

Seq ID NO: C133 DNA Sequence  
 Nucleic Acid Accession #: NM\_080870.1  
 Coding sequence: 3..710

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	AAGGGAAAAA	CACACCAGTC	CCAGAAAAGC	CTACAGAAAA	CCTGGGGAAAC	ACCACACTGA	180
	CCACTGAGAC	CATAAAAGCC	CCAGTAAAGT	CCACAGAAAA	CCCAGAAAAA	ACAGCAGCAG	240
	TCACAAAGAC	TATAAAACCT	TCAGTCAAGG	TCACAGGAGA	CAAACTCTCT	ACTACTACCT	300
10	CTTCTCATCT	AAATAAAACT	GAAGTTACTC	ATCAGGTGCC	CACTGGTTCT	TTCAACCTCA	360
	TTACATCTAG	AAAGAGCTG	AGTTCTATCA	CATCAGAAGC	CACAGGAAAC	GAGAGCCATC	420
	CATACCTCAA	TAAAGATGGC	TCACAGAAAG	GTATCCACGC	TGACACAGATG	GGAGAGAATG	480
	ATTCTATCCC	TGCAATGGCC	ATAGTTATTT	TGGTCTCGGT	GGCTGTGATT	CTCCTCCTGG	540
	TGTTCTCTGG	CCTGATCTTC	TTGGTCTCCT	ATATGATGCG	GACACGCCGC	ACACTAACCC	600
15	AGAACACCCA	GTACAATGAT	GCAGAGGATG	AGGGTGGCCC	CAATTCTCTAC	CCGGTCTACC	660
	TGATGGAGCA	GCAGAACTTT	GGCATGGGCC	AGATCCCTTC	CCCAOGGTGA	TCTTGGAGTA	720
	GGCGCCACGC	CCTGCTCTT	CCATGCTCTG	CCCCTTTCTT	GGATGAGGAA	CCGGACTCAC	780
	AATTTCTATT	TCGGGAGCTA	CAGGAAGGGC	AGAGAATACT	GACGGTTACC	AGTATTAAAC	840
	CTTCACTGT	TCTTGAACCT	GGTTGGGGAA	TGAGGTGATA	AGCAAGGAGG	GTGTAAGTTT	900
20	AGGGGACAAA	GAAGAAAGAA	TGAATAATAC	GAGCAGACAT	TCTCTGTAGA	AGGTAATGGT	960
	CTGAGAATGA	AAGAGTGT	GATGGACATG	TTGTGGGGCC	ACCAATGCAG	AACACTGCAC	1020
	TGAGTCTTAA	AGGAAGGACA	GGAGCCTTAT	AGGCAATGCC	CCAGACTGAC	TTGTGAGTGG	1080
	GGTTTATGGG	GAAAGGGAGG	GACTGAGGGC	AGAGTCTCTG	GGTTTCAGGA	CAGCATTATG	1140
	TTAATTCTGC	TCACTATTAC	TTAAGAGTTT	GTGTGTAAC	AGGCTCATCT	CTGAGTTCTC	1200
25	AGGACCCCTG	CCCCCACC	CATTTTTTTA	ATGAAAAAAA	AAAACAAAAA	AAACGGATCC	1260
	AAGAAGAAAA	GAGAATTAT	TTCTTCTCCT	ACTCTCTCCA	TGCCCTGGAG	AAAAAAAGT	1320
	CCAGAAGAAA	TCATAAATAT	CTCTCATCTA	CATGGTTGCT	TCTCTTCTCT	CCCAAAATCC	1380
	TTAGTTTTCC	TAAATGTCTA	CAGTGGACGC	CCTGTTGGTT	TGGCTTGCTG	GGTTGTGGGT	1440
	GGACACGCAA	GGAGGGGATT	TTTATTTGGC	CAGCAGTCTC	ACCCACTGAT	CTCCACCCCA	1500
30	GACCTTCCTT	GATGGGTGTC	TCAGCATTTA	TTTTCTCTGTC	TCTTCCACCA	AAAGCCAGCT	1560
	GTAGCTTTAT	CTCGTAAAG	TTACCCATCT	TCTCTACTGT	CCCAATCTC	TCTCTCCCA	1620
	CCTTCACCCC	AGATTCAAGT	TTTCTCTCTT	GTAGGCCATT	CATCTGTGTG	TGTTTTCTGG	1680
	ATTTCTCTCT	TCTCTTCTTA	TGGCCATTTC	ACCTTATTAC	TGATTGGGTA	GAGGGGGAAA	1740
35	AGGAGAATGA	TGATGATAGT	TTCTTCTGTT	CTATTGACCT	TTTTTATAAT	AAAGTATAAC	1800
	ATGTT						1805

Seq ID NO: C134 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..10674

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	GGGGCCCCCG	GGAGTATCCC	CGCGCCGCC	GCTCCTGGCG	ACGAAGCGGC	GGGGAGCAGA	180
	GTGGAGCGGC	TGGGCCAGGC	GTTCCGGCGA	CGCGTGC	TGCTGCGGGA	GCTCAGCGAG	240
	CGCTCGGAGC	TGTTCTTCTT	GGTGGATGAT	TCGTCCAGCG	TGGGCGGAAGT	CAACTTCCGC	300
	AGCGAGCTCA	TGTTCTCTCG	CAAGCTGCTG	TCCGACTTCC	CGGTGGTGCC	CAGGCGCACG	360
50	CGGCTGGCCA	TCGTGACCTT	CTGTCCTCAAG	AACCTACGTG	TGCCCGCGCT	CGATTACATC	420
	TCACCCCGCC	CGCGCGGCCA	GCACAAGTGC	CGCTGCTCCT	TCCAAGAGAT	CCCTGCCATC	480
	TCCTACCGAG	GTGGCGGCAC	CTACACCAAG	GGCGCCTTCC	AGCAGCCGCG	GCAAAATCTT	540
	CTTCATGCTA	GAGAAAACCT	AACAAAAGTT	GTATTTCTCA	TCATCTGATG	ATATTCCAAT	600
	GGGGGAGACC	CTAGACCAAT	TGCAGCGTCA	CTCGAGAGAT	CAGGAGTGGA	GATCTTCACT	660
55	TTTGGCATAT	GGCAAGGGAA	CATTCAGAG	CTGAATGACA	TGGCTTCCAC	CCCAAGGAG	720
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Seq ID NO: C135 DNA Sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..390

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Seq ID NO: C136 DNA Sequence

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Coding sequence: 126..1745

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Seq ID NO: C137 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1761

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AGAGATACCT CTTTATTGTG CAAAGCTGCC ATCCATGCAG GAATAATTGC TGATGAACCTA 780
GGTGGCCAGA TTCTGTGCTC TCAGCGCAAA GGGATCAGTC GATATGAAGG GATTCTGGCC 840
AATGGTGTTC TTAGCAGGGA TGGTTCCCTG TCAGACAAGC GATTCTGTGT TACCTCCAAT 900
GGTTGCAGCA GATCCTTGAG TTTTGAACCT GACGGGCAAA TCAGAGCTTC TTCTCTATGG 960
CAGTCGGTCA ATGAGAGTGG AGACCAAGTT CACTGGTCTC CTGGCCAAAG CCGACTTCAG 1020
GACCAAGGCC CATCATGGGC TTCGGGCGAC AGTAGCAACA ACCACAAACC ACGAGAGTGG 1080
CTGGAGATCG ATTTGGGGGA GAAAAAGAAA ATAACAGGAA TTAGGACCAC AGGATCTACA 1140
CAGTCGAAGT TCACTTTTGA TGTTAAGAGT TTTGTGATGA ACTTCAAAAA CAATAATTCT 1200
AAGTGAAGA CCTATAAAGG AATTGTGAAT AATGAAGAAA AGGTGTTTCA GGGTAATCTT 1260
AACTTTCCGG ACCCAGTGCA AAACAATTTC ATCCCTCCCA TCGTGCCGCA ATATGTGCGG 1320
GTTGTCCCCC AGACATGGCA CCAGAGGATA GCCTTGAAGG TGGAGCTCAT TGGTTGCCAG 1380
ATTACCAAGG TGAATGATTG ATTGGTGTGG CGCAAGACAA GTCAAAGCAC CAGTGTTCAT 1440
ACTAAGAAAG AAGATGAGAC AATCACAAGG CCCATCCCTT CGGAAGAAAC ATCCACAGGA 1500
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ATGGGAGTGG ACATTCCTGT TAGAAAGAAG AAGAAGAAAG GAAGTCCGTA TGGATCAGCA 1620
GAGGCTCAGA AAACAGACTG TTGGAAGCAG ATTAAATATC CCTTTGCCAG ACATCAGTCA 1680
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ACAAGTGATA TGGCAGGTTA A 1761

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Seq ID NO: C138 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2310

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TTGGATATCG AATCCAGAGC CTGTGCTTCT GACTATCTTC TCTTCACCAG CTCTTCAGAT 300
CAATATGGAA TGCAGAAGGA GGAGGAGACA GAAGTGCTTT GTCTTTTCACT GGCCTGGGCT 360
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TATTTGAAGA CAGAATACAG CAAATTCTGC CCAGCTGGTT GTAGAGACGT AGCAGGAGAC 660
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CATGCAGGAA TAATGTCTGA TGAACATAGT GGCCAGATCA GTGTGCTTCA GCGCAAGAGG 780
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AAGACAAGTC AAAGCACCCG TGTTCAACT AAGAAAGAAG ATGAGACAAT CACAAGGCC 1440  
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CAGATGATCT CACAAAGGGA GAATCTGGGA CCTGATGAGG GCAAAATACC TTTTAAAGGC 1560  
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GAGGCGAGGG TGAGCACCGA TGCCGGGGGC CACTATGACT GCCCGCAGCG GCCCGGCCGC 1920  
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CGGCAGTGGC TGCGCGCCCA CACGTTCTCT GCGCAGAGCG GCTACCGCGT CCCAGGGCCC 2040  
CAGCCCGGCC ACAACACTC CCTCTCCTCG GGCGCTTCT CCCCCTAGC GGGTGTGGGC 2100  
GCCCAGGACG GAGACTATCA AAGGCCACAC AGCGCACAGC CTGCGGACAG GGGCTACGAC 2160  
CGGCCCAAAG CTGTACAGCG CCTGCCACC GAAAGCGGGC ACCCTGACTC TCAGAAGCCC 2220  
CCAAACGATC CCGGACGAG TGACAGTAT TCTGCCCCCA GAGACTGCCT CACACCCCTC 2280  
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Seq ID NO: C139 DNA Sequence  
Nucleic Acid Accession #: NM\_004616.2  
Coding sequence: 180..893

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GACAAGCCTG TAACGAATAG TTAATTCAC GGCACTCTGA TTCCTAATCC TTTTCCGAAA 180  
TGGCAGGTGT GAGTGCCCTG ATAAATATT CTATGTTAC CTCAACTTC TTGTTCTGGC 240  
TATGTGGTAT CTTGATCCTA GCATTAGCAA TATGGGTACG AGTAAGCAAT GACTCTCAAG 300  
CAATTTTGG GTTGAAGAT GTAGGCTCTA GCTCTACGT TGCTGTGGAC ATATTGATTG 360  
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GTGCTGTCAT GCTTCTGTGT TTTTTCATAG GCTTCTTCT GATCCTGCTC CTGCAGGTGG 480  
CGACAGGTAT CCTAGGAGCT GTTTTCAAAT CTAAGTCTGA TCGATTGTG AATGAACTC 540  
TCTATGAAAA CACAAGCTT TTGAGCGCCA CAGGGGAAAG TGAAAAACAA TTCCAGGAAG 600  
CCATAATTGT GTTCAAGAA GAGTTTAAAT GCTGCGGTTT GGTCAATGGA GCTGCTGATT 660  
GGGGAATAA TTTTCAACAC TATCCTGAAT TATGTGCCCT TCTAGATAAG CAGAGACCAT 720  
GCCAAGCTA TAATGGAATA CAAAGTTTACA AAGAGACCTG TATTTCTTTC ATAAAAGACT 780  
TCTTGGCAAA AAATTGTATT ATAGTTATTG GAATATCAT TGGACTGGCA GTTATTGAGA 840  
TACTGGGTTT GGTGTTTCT ATGTCCTGT ATTGCCAGAT CGGGAACAAA TGAATCTGTG 900  
GATGATCAAA CCTATCGTCA GTCAAAACCC TTTAAATGT TGCTTTGGCT TTGTAAATTT 960  
AAATATGTAA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TAAAATGTG TCGGCTAGCT 1020  
AGACCACAGA TATCTTCTAG ACATATTGAA CACATTTAAG ATTTGAGGGA TATAAGGGA 1080  
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Seq ID NO: C140 DNA Sequence  
Nucleic Acid Accession #: NM\_004617.2  
Coding sequence: 232..840

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ATTGAATTGG AGACAATTAC AAGGACTCTC TGGCCAAAAA CCTTGAAGA GGCCCGTGA 180  
AGGAGGCAGT GAGGAGCTTT TGATTGCTGA CCTGTGTCGT ACCACCCAG AATGTGCACT 240  
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GCTAACATCC TGTTATTTT TCTTGGAGGA AAAGTGATAG ATGACAACGA CCACCTTTCC 360  
CAAGAGATCT GGTTTTTCGG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTTCCCTGCG 420  
CTGGTGTCT TGCGCCTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCAA CGAGGCTGTG 480  
GGGAAGCGAT TTGCGATGTT CACCTCCAGC ATATTGCTG TGTTGGGATT CTTGGGAGCT 540  
GGATACTCGT TTATCATCTC AGCCATTTC AACAACAAGG GTCTTAAATG CCTCATGGCC 600  
AATAGTACAT GGGGCTACCC CTTCCACGAC GGGGATTATC TCAATGATGA GGCCTTATGG 660  
AACAAAGTGC GAGAGCCTCT CAATGTGGTT CCTTGGAAATC TGACCTCTT CTCCATCCTG 720  
CTGCTGTAG GAGGAATCCA GATGGTTCTC TGCGCCATCC AGGTGGTCAA TGGCCTCCTG 780  
GGGACCTCT GTGGGGACTG CCACTGTTGT GGCTGCTGTG GGGAGATGG ACCCGTTTAA 840  
ACCTCCGAGA TGAGTGCTCT AGACTCTACA GCATGACGAC TACATTTCT TTTCAATAAA 900  
CTTCTCTCT TCTTGAATTT ATTAATTCCT ATCTGCTTCC TAGCTGATAA AGCTTAGAAA 960  
AGGCAGTTAT TCTTCTTTC CAACAGCCTT TGCTCGAGTT AGAATTTGT TATTTTCAA 1020  
TAAAAATAG TTTGGCCACT TAACAAATTT GATTATATAA TCTTCAAAT TAGTTCCTTT 1080  
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Seq ID NO: C141 DNA Sequence  
Nucleic Acid Accession #: NM\_002381.2

Coding sequence: 64..1524

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   CTGCTGCTGC TGCCCTCCGC CGCCCCCGAC CCGTGGGCCC GCGCGGGCTT CCGGAGGCTG 180
   GAGACCCGAG GTCCCGGGGG CAGCCCTGGA CGCGCCCTCT CTCCTGCGGC TCCCGACGGC 240
   GCGCCGCTT CCGGGACCAG CGAGCCTGGC CGCGCCCGCG GTGCAGGTGT TTGCAAGAGC 300
10 AGACCCCTGG ACCTGGTGT TATCATTGAT AGTTCTCGTA GCGTACGGCC CCGGAATTTC 360
   ACCAAGTGA AAACCTTTGT TCCCGGATA ATCGACACTC TGGACATTGG GCCAGCCGAC 420
   ACGCGGGTGG CAGTGGTGAA CTATGCTAGC ACTGTGAAGA TCGAGTTCCA ACTCCAGGCC 480
   TACACAGATA AGCAGTCCCT GAAGCAGGCT GTGGGTGAA TCACACCTCT GTCAACAGGC 540
   ACCATGTGAG GCTAGCCAT CCAGACGACA ATGGACGAG CCTTCACAGT GGAGGCGAGG 600
15 GCTCGAGAGC CCTCTTCTAA CATCCCTAAG GTGCCCATCA TTGTTACAGA TGGGAGGCC 660
   CAGGACCAAG TGAATGAAGT GGCGGCTCGG GCCCAAGCAT CTGGTATTGA GCTCTATGCT 720
   GTGGGCGTGG ACCGGGCGAG CATGGCGTCC CTCAAGATGA TGGCCAGTGA GCCCTTAGAG 780
   GAGCATGTCT TCTACGTGGA GACCTATGGG GTCAATTGAG AACTTTCCTC TAGATTCCAG 840
   GAAACCTCTT GTGCGCTGGA CCCTGTGTGT CTTGGAACAC ACCAGTGCCA GCACGTCTGC 900
20 ATCAGTGATG GGAAGGCGAA GCACCACTGT GAGTGTAGCC AAGGATACAC CTTGAATGCC 960
   GACAAGAAAA CGTGTTCAGC TCTTGATAGG TGTGCTCTTA ACACCCACGG ATGTGAGCAC 1020
   ATCTGTGTA ATGACAGAA TGGCTCTTAT CATTTGTAGT GCTATGAAGG TTATACCTTG 1080
   AATGAAGACA AGCAAACTTG TTCAGCTCAA GATAAATGTG CTTTGGGTAC CCATGGGTGT 1140
   CAGCACATTT GTGTGAATGA CAGAACAGGG TCCCATCATT GTGAATGCTA TGAGGGCTAC 1200
25 ACTCTGAATG CAGATAAAAA AACATGTTCA GTCCGTGACA AGTGTGCCCT AGGCTCTCAT 1260
   GGTGCGCAGC ACATTTGTGT GAGTGTAGGG GCCGCATCCT ACCACTGTGA TTGCTATCCT 1320
   GGTACACCTT TAAATGAGGA CAAGAAAAA TGTTCAGCCA CTGAGGAAGC ACGAAGACTT 1380
   GTTTCACCTG AAGATGCTTG TGGATGTGAA GCTACACTGG CATTCCAGGA CAAGGTGAGC 1440
   TCGTATCTTC AAGAGCTGAA CACTAACTT GATGACATT TGGAGAAGTT GAAATATAAT 1500
30 GAATATGGAC AAATACATCG TTAATTTGCT CCAATTTCTC ACCTGAAAAA GTGACAGCT 1560
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   TAATTTGCCA TTATCTGTAT TAATGCTTGA ATATTACTGG ATAAATTTGA TGAAGATCTT 1680
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   CTTTAGTGTC TCTAAGTTAT GACTGTGAAA TGATTGGTAG GAAATAGAAT GAAAGTTTA 1800
35 GTGTTCTTTT ATCTACTAAT TGAGCCATTT AATTTTAA TGTTTATATT AGATAACCAT 1860
   ATTCACAATG GAAACTTTAG GTCTAGTTTC TTTTGATAGT ATTTATAATA TAAATCAATC 1920
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   TGAATGTAT TTTGAACCTG TTAACACTTT TGTTTTTTGT CTTATTTTGT TGGAGTATA 2040
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   ATCGACAAA TCTAATGTTG TCTTTTAAAT GTTAGTGATC CACCTGCCTC AGCCTCCCAA 2340
   AGTGCTGGGA TTACAGGCTT GAAAGTCAA CTTTTTTTTA CTTATATATT TGATACATAT 2400
45 AATTCCTTTG GCTTTGAATG TTGCAACTTT GAGAACAATA CAGTCTTTTA AATTTTGAC 2460
   TGCTCAATTC TGTTTTTCGT TTGATTTGTC TTTAATATAA TAAAGTTAT TACCTTTACA 2520
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Seq ID NO: C142 DNA Sequence  
Nucleic Acid Accession #: NM\_016639.1  
Coding sequence: 40..429

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   AAGTGCAATG ACTGCGGCTC TTGCAAGGCG CGACCGCACA GCGACTTCTG CTTGGGCTGC 240
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   CTGACCTTCG TGCTGGGGCT GCTTCTGCGC TTTTGGTCTG GGAGACGATG CGCGAGGAGA 360
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65 TTCTAGAGCC AGTCTCTGCC TCCAGACGCG GCGGGAGGCC AAGTCTCTCC AACCACAAGG 540
   GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTGAGG GAACCTTCCA 600
   AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
   ACAAAACAGC TGACACTGAC TAAGGAACTG CAGCATTGCG ACAGGGGAGG GGGGTGCCCT 720
   CCTTCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGCA GACTTGACAC TAGGCCCCAC 780
70 TCACTCAGAT GTCTGAAAT TCCACCAAGG GGGTCACCTT GGGGGGTTAG GGACCTATT 840
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Seq ID NO: C143 DNA Sequence  
Nucleic Acid Accession #: NM\_001819  
Coding sequence: 113..2146

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   AACGCTGCTT CTCAGCCTCC TGGAGCGCGT GGGGCTGGCG GCTGTCAATT CCATGCCAGT 180
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Seq ID NO: C144 DNA Sequence  
Nucleic Acid Accession #: XM\_093082.1  
Coding sequence: 93...1988

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TTGGGGCTCT AGCAGCTGTT CTTAGCACCA GTCACTGGCT CACTGAAGTG GAATTTAGTG 240
AGACAAACT GGAAGCTTCA GCTTTGAAAT TGCTCTATGG AGGCTTAAAA GATCCAAATT 300
GCAAAATACA GAAGCTCAAC TTGCAGTTT CTATTCTGT AACCGCTGCA AAACCTCCAG 360
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TTGCTGCTGC AAAGGATTGT GGGAGTCTTA AGTCTTCTC ATCAGAAAGG CTGAAGTGGG 540
CAGGAAGACT TGAGGAGTG GAGGAGGTT TGGGGTTGGG GGTGCTTGTA CAGCCCGGTG 600
ACCCAGCATC TCAGGGTGGG GGGCAITGTG AAAACTATGG GTCITTTAGA GACTTGGTGG 660
ACTTAGAAGT CAAGCGAGAA CCAAGCCTGA GAAAAGTGG TATGGATCTC CAGAGACCCA 720
CCCTACAAGT TGTCTCTCTT TGCAAAATCT TCTCCCTCAA ACTATTTCTC TTTATTGCAT 780
TGCTTAATTC TCTGTGTGAG GTTAGTGTGG TGCAAGTGAC CATCCAGAC GGTTTGTTGA 840
AOGTGAAGT TGATCTAAT GTCACTCTCA TCTGCATCTA CACCACCACT GTGGGCTCCC 900
GAGAACAGCT TTCCATCCAG TGTCTTTCT TCCATAAGAA GGAGATGGAG CCAATTTCTT 960
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GAGAAGCCA AGCAATGCCA AGAGAAGACG CTACCCAAC AGAAGTAACT CTACCATCTT 1740
CCATTATGAG GACTGGCCCT GATACCATCC AAGAACCAGA CTATGAGCCA AAGCCTACTC 1800
AGGAGCCTGC CCCAGGCTC GCCCAGGAT CAGAGCCTAT GGCAGTGCCT GACCTTGACA 1860
TOGAGCTGGA GCTGGAGCCA GAAACGCAGT CGGAATTGGA GCCAGAGCCA GAGCCAGAGC 1920
CAGAGTCAGA GCCTGGGGTT GTAGTTGAGC CCTTAAGTGA AGATGAAAAG GGAGTGGTTA 1980
AGGCATAG

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Seq ID NO: C145 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1242

1 11 21 31 41 51



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ATGGTGTTCG	CATTTTGGAA	GGTCTTTCTG	ATCCTAAGCT	GCCTTGACAG	TCAGGTTAGT	60
GTGGTGCAAG	TGACCATCCC	AGACGGTTTC	GTGAACGTGA	CTGTTGGATC	TAATGTCACT	120
CTCATCTGCA	TCTACACCAC	CACGTGGGCC	TCCCGAGAAC	AGCTTTCCAT	CCAGTGGTCT	180
TTCTTCCATA	AGAAGGAGAT	GGAGCCCAAT	TCTTCTCCTT	GGGAGGAGGG	GAAGTGGCCA	240
GATGTTGAGG	CTGTGAAGGG	CACCTTTGAT	GGACAGCAGG	CTGAACCTCA	GATTTACTTT	300
TCTCAAGGTG	GACAACTGTG	AGCCATCGGG	CAATTTAAAG	ATCGAATTAC	AGGGTCCAAC	360
GATCCAGGTA	ATGCATCTAT	CACATCTCTG	CATATGCAGC	CAGCAGACAG	TGGAATTTAC	420
ATCTCGCATG	TTAACAAACC	CCCAGACTTT	CTCGGCCAAA	ACCAAGGCAT	CCTCAACGTC	480
AGTGTGTTAG	TGAACCTTTC	TAAGCCCTTT	TGTAGCGTTC	AAGGAAGACC	AGAACTGGC	540
CACACTATTT	CCCTTTCTGT	TCTCTCTGCG	CTTGGAAACAC	CTTCCCCTGT	GTACTACTGG	600
CATAAACTTG	AGGGAAGAGA	CATCGTGCCA	GTGAAAGAAA	ACTTCAACCC	AACCACCGGG	660
ATTTTGGTCA	TTGAAATCT	GACAAATTTT	GAACAAGGTT	ATTACCAGTG	TACTGCCATC	720
AACAGACTTG	GCAATAGTTC	CTGCGAAATC	GATCTCACTT	CTTCACATCC	AGAAGTTGGA	780
ATCATTGTTG	GGGCTTGTAT	TGGTAGCCTG	GTAGGTGCGG	CCATCATCAT	CTCTGTTGTG	840
TGCTTCGCAA	GGAAATAGGC	AAAAGCAAAG	GCAAAAGAAA	GAAATCTTAA	GACCATCGCG	900
GAACCTTGAGC	CAATGACAAA	GATAAACCCA	AGGGGAGAAA	GCGAAGCAAT	GCCAGAGAGAA	960
GACGCTAGCC	AAGTAGAAGT	AACTCTACCA	TCTTCCATTC	ATGAGACTGG	CCCTGATACC	1020
ATCCAAGAAC	CAGACTATGA	GCCAAAGCCT	ACTCAGGAGC	CTGCCCCAGA	GCTTGCCCCA	1080
GGATCAGAGC	CTATGGCAGT	GCCTGACCTT	GACATCGAGC	TGGAGCTGGA	GCCAGAAACG	1140
CAGTCGGAAT	TGGAGCCAGA	GCCAGAGCCA	GAGCCAGAGT	CAGAGCCTGG	GGTTGTAGTT	1200
GAGCCCTTAA	GTGAAGATGA	AAAGGGAGTG	GTAAAGGCAT	AG		1242

Seq ID NO: C146 DNA Sequence

Nucleic Acid Accession #: NM\_003020.1

Coding sequence: 29..664

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CGCTCCTCGG	GCTGCCCTTC	GGTTGACAAAT	GGTCTCCAGG	ATGGTCTCTA	CCATGCTATC	60
TGGCCTACTG	TTTGGGCTGG	CATCTGGATG	GACTCCAGCA	TTTGCTTACA	GCCCCCGGAC	120
CCCTGACCGG	GTCTCAGAAG	CAGATATCCA	GAGGCTGCTT	CATGGTCTTA	TGGAGCAATT	180
GGGCATGGCC	AGGCCCCGAG	TGGAATATCC	AGCTCACCAG	GCCATGAATC	TTGTGGGCCCC	240
CCAGAGCATT	GAGGTGGGAG	CTCATGAAGG	ACTTCAGCAT	TTGGGTCTCT	TTGGCAACAT	300
CCCCAACATC	GTGGCAGAGT	TGACTGGAGA	CAACATTCCT	AAGGACTTTA	GTGAGSATCA	360
GGGTATCCCA	GACCCCTCCAA	ATCCCTGTCC	TGTTGGAAAA	ACAGATGATG	GATGTCTAGA	420
AAACACCCCT	GACACTGCAG	AGTTTCAGTC	AGAGTTCACG	TTGCACCAGC	ATCTCTTTGA	480
TCGGGAACAT	GACTATCCAG	GCTTGGGCAA	GTGGAACAAG	AAACTCCTTT	ACGAGAAGAT	540
GAAGGGAGGA	GAGAGACGAA	AGCGGAGGAG	TGTCAATCCA	TATCTACAAG	GACAGAGACT	600
GGATAATGTT	GTTCGAAGA	AGTCTGTCCC	CCATTTTTC	GATGAGGATA	AGGATCCAGA	660
GTAAAGAGAA	GATGCTAGAC	GAAAAACCCAC	ATTACCTGTT	AGGCCTCAGC	ATGGCTTAGT	720
TGCACTGTGA	AATGGAGTCC	CTGTGAATGA	CAGCATGTTT	CTTACATAGA	TAATTATGGA	780
TACAAAGCAG	CTGTATGTAT	ATAGTGTATT	GTCTTCACAC	CGATGATTCT	GCTTTTGTCT	840
AAATTAGAAAT	AAGAGCTTTT	TTGTTTCTTG	GGTTTTTAAA	ATGTGAATCT	GCAATGATCA	900
TAAAAATTAA	AATGTGAATG	TCAACAATAA	AAAGCAAGAC	TATGAAAGGC	TCAGATTTC	960
TGCAGTTTAA	AATGGTGTCT	GAGGTTGTAC	TATTTTGGCC	AAGTCTGTAG	AAAGCTGTCT	1020
TTTGATTTTG	ATTATGTAGT	TCATCCAGCC	CTTGGGCATT	GTTATACACC	AGTAAAGAAG	1080
GCTGTACTCA	AGAGGAGGAG	CTGACACATT	TCATTGGCT	GCGTCTTAAT	AAACATGAAT	1140
GCAAGCATTG	GC					1152

Seq ID NO: C147 DNA Sequence

Nucleic Acid Accession #: NM\_024021.2

Coding sequence: 144..806

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AACTTCTCTG	CAATGGTTT	CAATATATGC	AGATGTCTCG	ATATAGGAAT	GAAATTACGT	60
CTTTGGAAAC	ACTTAAATAA	GTCAATATA	CTTGGAGCTT	TAAAAATTAA	AAGGAGAGAG	120
ATTCCAGCAC	CTTTTCTGCT	GCCATGACAA	CCATGCAAGG	AATGGAACAG	GCCATGCCAG	180
GGGCTGGCCC	TGGTGTGCCC	CAGCTGGGAA	ACATGGCTGT	CATACATTCA	CATCTGTGGA	240
AAGGATTGCA	AGAGAAGTTC	TTGAAGGGAG	AAACCCAAAGT	CCTTGGGGTT	GTGCAGATTG	300
TGACTGCCCT	GATGAGCCCT	AGCATGGGAA	TAACAAATGAT	GTGTATGGCA	TCTAATACTT	360
ATGGAAGTAA	CCCTATTTC	GTGTATATCG	GGTACACAAT	TTGGGGTCTA	GTAATGTTTA	420
TTATTTTCAG	ATCCTTGTC	ATTGCAGCAG	GAATTAGAAC	TACAAAAGGC	CTGGTCCGAG	480
GTAGTCTAGG	AATGAATATC	ACCAGCTCTG	TACTGGCTGC	ATCAGGGATC	TTAATCAACA	540
CATTTAGCTT	GGGTTTTTAT	TCATTCCATC	ACCCTTACTG	TAACTACTAT	GGCAACTCAA	600
ATAATTGTCA	TGGGACTATG	TCCATCTTAA	TGGGTCTGGA	TGGCATGGTG	CTCCTCTTAA	660
GTGTGCTGGA	ATTCTGCATT	GCTGTGTCCC	TCTCTGCCTT	TGGATGTAAA	GTGCTCTGTT	720
GTACCCCTGG	TGGGTTGTG	TTAATTCTGC	CATCACAATC	TCACATGGCA	GAAACAGCAT	780
CTCCACACCC	ACTTAATGAG	GTTTGAAGGC	ACCAAAAGAT	CAACAGACAA	ATGCTCCAGA	840
AATCTATGCT	GACTGTGACA	CAAGAGCCCT	ACATGAGAAA	TTACCAAGAT	CCAACCTCGA	900
TACTGTATGA	CTTGTGTGTA	TTATTATTAT	ATGTAATCCA	ATTATGAATC	GTGTGTGAT	960
AGAGAGATTA	TAAATTCAAA	ATTATGTTCT	CATTTTTC	CCTGGAACCT	AATAACTCAT	1020
TTCACTGGCT	CTTATCGAG	AGTACTAGAA	GTTAAATTAA	TAAATAATGC	ATTAAATGAG	1080
GCAACAGCAC	TTGAAAGTTT	TTCAATCATC	ATAAGAATCT	TATATAAAGG	CATTACATTG	1140
GCAAAATAGG	TTTGAAGACA	GAAGAGCAAA	AAAAAGATAT	TGTTAAAAATG	AGGCCTCCAT	1200
GCAAAACACA	TACTTCCCTC	CCATTATTAT	AACCTTTTTT	TTCTCCTACC	TATGGGGACC	1260
AAAGTCTTTT	TTCTTCCAGG	AAGTGGAGAT	GCAATGGCCAT	CTCCCCCTCC	CTTTTCTCTT	1320
CTCTGCTTTT	TCTTTCCCCA	TAGAAAGTAC	CTTGAAGTAG	CACAGTCCGT	CCTTGCAATG	1380
GCACAGGCTA	TCATTGAGT	AAAAGTATAC	ATGGAGTAAA	AATCATATTA	AGCATCAGAT	1440
TCAACTTATA	TTTTCTATT	CATCTTCTTC	CTTCCCCTTC	TCCACCTTTC	TACTGGGCAT	1500
AATTATATCT	TAATCATATA	TGGAAATGTG	CAACATATGG	TATTTGTTAA	ATACGTTTGT	1560
TTTTATTGCA	GAGCAAAAT	AAATCAAAT	AGAAGCAATA	AAAAAATAAA	AAAAAATAAA	1619

Seq ID NO: C148 DNA Sequence  
Nucleic Acid Accession #: NM\_002091.1  
Coding sequence: 56..502

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AGTCTCTGCT	CTTCCCAGCC	TCTCCGGCGC	GCTCCAAGGG	CTTCCCGTCG	GGACCATGCG	60
CGGCAGTGAG	CTCCCCGCTGG	TCTGCTGGC	GCTGGTCTCTC	TGCCTAGCGC	CCCGGGGGCG	120
AGCGGTCCCG	CTGCTCTCGG	GCGGAGGGAC	CGTGTCTGACC	AAGATGTACC	CGCGCGGCAA	180
CCACTGGGCG	GTGGGGCACT	TAATGGGGAA	AAAGAGCACA	GGGGAGTCTT	CTTCTGTTTC	240
TGAGAGAGGG	AGCCTGAAGC	AGCAGCTGAG	AGAGTACATC	AGGTGGGAAG	AAGCTGCAAG	300
GAATTGTCTG	GGTCTCATAG	AAGCAAAGGA	GAACAGAAAC	CACCAGCCAC	CTCAACCCAA	360
GGCCTTGGGC	AATCAGCAGC	CTTCGTGGGA	TTCAGAGGAT	AGCAGCAACT	TCAAAGATGT	420
AGTTTCAAAA	GGCAAAGTTG	GTAGACTCTC	TGCTCCAGGT	TCTCAACGTG	AAGGAAGGAA	480
CCCCCAGCTG	AACCAGCAAT	GATAATGATG	GCCTCTCTCA	AAAGAGAAAA	ACAAAACCCC	540
TAAGAGACTG	AGTTCTGCAA	GCATCAGTTC	TACGGATCAT	CAACAAGATT	TCCTTGTGCA	600
AAATATTGTA	CTATTCTGTA	TCTTTCATCC	TTGACTAAAT	TCGTGATTTT	CAAGCAGCAT	660
CTTCTGGTTT	AAACTGTGTT	GCTGTGAACA	ATTGTGAAAA	AGAGTCTTCC	AATTAATGCT	720
TTTTTATATC	TAGGCTACCT	GTTGGTTAGA	TTCAAGGCCC	CGAGCTGTGA	CCATTACAAA	780
TAAAAGCTTA	AACACAT					797

Seq ID NO: C149 DNA Sequence  
Nucleic Acid Accession #: NM\_012261.1  
Coding sequence: 203..1045

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1	11	21	31	41	51	
GATTGTCTCT	GCCAGCAGCT	GTCGGTGCCG	CGCTCGACAC	CGAGTCTCTAG	CTAGGCGCTC	60
ACAGAATACG	CGCTCCCTCC	CTCCCCCTTC	TCTGTCCCCC	GCCTCTGCGT	CACCCCGGCC	120
CACTCCAGCG	GGCACTTTGA	GGGATTCCCT	CTCTGGCGCG	CTCTGCAGCA	GCAACAGCCG	180
CCTCATCTGG	GGCACTGCGA	GTATGGATCT	CCAAGGAAGA	GGGGTCCCCA	GCATCGACAG	240
ACTTCGAGTT	CTCTGTATGT	TGTTCCATAC	AATGGCTCAA	ATCATGGCAG	AACAAGAAGT	300
GGAAAATCTC	TCAGGCCTTT	CCACTAACCC	TGAAAAAGAT	ATATTGTGGG	TGCGGGAAAA	360
TGGGACGACG	TGTCTCATGG	CAGAGTTTGC	AGCCAAATTT	ATTGTACCTT	ATGATGTGTG	420
GGCCAGCAAC	TAGCTAGATC	TGATCACAGA	ACAGGCCGAT	ATCGCATTGA	CCCGGGGAGC	480
TGAGGTGAAG	GGCCGCTGTG	GCCACAGCCA	GTCGGAGCTG	CAAGTGTCTT	GGGTGGATCG	540
CGCATATGCA	CTCAAAATGC	TCITTTGTAA	GGAAAGCCAC	AACATGTCCA	AGGGACCTGA	600
GGCGACTTGG	AGGCTGAGCA	AAGTGCAGTT	TGTCTAGCAC	TCCTCGGAGA	AAACCCACTT	660
CAAGAGCGCA	GTCAGTGCTG	GGAGGACAC	AGCCAACTCG	CACCACTCTT	CTGCCTTGGT	720
CACCCCGCTG	GGGAAGTCC	ATGAGTGTCA	AGCTCAACAA	ACCATTTTCA	TGGCCTCTAG	780
TGATCCGCGA	AAGACGGTCA	CCATGATCCT	GTCTGCGGTC	CACATCCAAC	CTTTTGACAT	840
TATCTCAGAT	TTTGTCTTCA	GTGAAGAGCA	TAAATGCCCA	GTGGATGAGC	GGGAGCAACT	900
GGAAAGAAAC	TTGCCCTGTA	TTTGGGGGCT	CATCTTGGGC	CTCGTCATCA	TGTAACACT	960
ATCCAGTTAC	CAGTCCACCC	ACAAAATGAC	TGCCAAACAG	GTGCAGATCC	CTCGGGAGAC	1020
ATCCCAAGTAT	AAGCAGATGG	GCTAGAGGCC	GTTAGGCAGG	CACCCCTTAT	TCTGTCTCCC	1080
CAAACCTGAG	CAGTAGAAG	AACAAAAGCA	CTTTTCCATC	TTGTACACGA	GATACACCAA	1140
CTAGCTGACA	ATCAAAACAG	CCTGGGTATC	TGAGGCTTGC	TTGGCTTGTG	TCCATGCTTA	1200
AACCCACGGA	AGGGGGAGAC	TCITTCGGAT	TTGTAGGGTG	AAATGCAAT	TATTCTCTCC	1260
ATGCTGGGGA	GGAGGGGAGG	AGGGTCTCAG	ACAGCTTTCC	TGCTCATGCT	GGCTTGGCTT	1320
TGACTCTCCA	AAGAGCAATA	AATGCCACTT	GGAGCTGTAT	CTGGCCCCAA	AGTTTAGGGA	1380
TTGAARACAT	GCTTCTTTGA	GGAGGAAACC	CCTTTAGGTT	CAGAAGAATA	TGGGTGCTT	1440
TGCTCCCTTG	GACACAGCTG	GCTTATCCTA	TACAGTTGTC	AATGCACACA	GAATACAAAC	1500
TCATGCTCCC	TGCAGCAAGA	CCCCTGAAAG	TGATTATGTC	TTCTGGCTGG	CATTCTGCAT	1560
GTTTAGTGAT	TGTTCTGGGA	ATGTTTCACT	GCTACCCGCA	TCCAGCGACT	GCAGCACCAG	1620
AAAACGACTA	TGTTAACTAT	GCAGAGTTGT	TTGACTTTCT	TCCTGTGCCA	GGTCCAAGTC	1680
GGGGGACCTG	AAGAATCAAT	CTGTGTGAGT	CTGTTTTTCA	AAATGAAATA	AAACACACTA	1740
TTCTCTGGC						1749

Seq ID NO: C150 DNA Sequence  
Nucleic Acid Accession #: NM\_003226.1  
Coding sequence: 2..226

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1	11	21	31	41	51	
GATGCTGGGG	CTGGTCTCGG	CCTTGCTGTC	CTCCAGCTCT	GCTGAGGAGT	ACGTGGGCCT	60
GTCTGCAAA	CAGTGTGCGG	TGCCGGCCAA	GGACAGGGTG	GACTGCGGCT	ACCCCATGTT	120
CACCCCAAG	GAGTGCARCA	ACCGGGGCTG	CTGCTTTGAC	TCCAGGATCC	CTGGAGTGCC	180
TTGGTGTTC	AAGCCCTTGA	CTAGGAAGAC	AGAATGCACC	TTCTGAGGCA	CCTCCAGCTG	240
CCCCTGGGAT	GCAGGCTGAG	CACCTTGCC	CGGCTGTGAT	TGCTGCCAGG	CAGTGTTCAT	300
CTCAGTTTTT	CTGTCCCTTT	GCTCCCGGCA	AGCTTTCTGC	TGAAAGTTCA	TATCTGGAGC	360
CTGATGCTCT	AACGAATAAA	GGTCCCATGC	TCCACCCG			398

Seq ID NO: C151 DNA Sequence  
Nucleic Acid Accession #: NM\_002993.1  
Coding sequence: 64..408

75  
80

1	11	21	31	41	51	
GGCACGAGCC	AGTCTCCGCG	CCTCCACCCA	GCTCAGGAAC	CCGGAACCC	TCTCTTGACC	60
ACTATGAGCC	TCCCGTCCAG	CCGCGCGGCC	CGTGTCCCGG	GTCTTCCGGG	CTCCTTGTGC	120
CGCTGCTCG	CGCTGCTGCT	CTGCTGACG	CCGCGGGGCG	CCCTCCCGAG	CGCTGGTCTT	180
GTCTCTGCTG	TGCTGACAGA	GCTGCGTTGC	ACTTGTGTTT	CGCTTACGCT	GAGAGTAAAC	240

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CCCCAAACGA TTGGTAAACT GCAGGTGTTC CCGCAGGCC CGCAGTGCTC CAAGGTGGAA 300
GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
AAGAAAGTCA TCCAGAAAT TTTGGACAGT GGAACAAGA AAAACTGAGT AACAAAAAAG 420
ACCATGCATC ATAAATATGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
CAGTAAGAAT AAGAAGGAAG GGTGGTTTT TTTCCATTT CTACATGGAT TCCCTACTTT 540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCITTGG 660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCITTCAATG AATATTGAAT 720
TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCITTCCGAA AAGGCTGTGG 780
ATTTCTGTATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTTCTT 840
ACTCACTCTT CTATATAAAT AGGAAATATT TTAGTTCTGT TTTCTGGGG AATATTGTAC 900
TCTTTACCTT AGGATGCTAT TTAAGTTGTA CTGTATTAGA AACTGGGTG TGTCTATCCG 960
TTATCTGTGC AGAATATATT TCCTTATTC GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
CTAATATATT CTCTTCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
CATGATTATC TCATTAACCT TTGATTTTGT ATGCTATTTT TTCCTATAG GATGACTATA 1140
ATTTCTGGTA CTAAATATAC ACTTTAGATA GATGAAGAAG CCAAAAAACA GATAAATTCC 1200
TGATTGCTAA TTTACATAGA AATGTATTCT CTGGTTTTT TAAATAAAG CAAAATTAAAC 1260
AATGATCTGT GCTCTGCAA GTTTTGAAAA TATATTGAA CAATTTGAAT ATAAATTCAT 1320
CATTTAGTCC TCAAAATATA TACAGCAATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
AAATTGCATC TTTATTTTTT CCGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500
TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAAANA AAAAAA 1547
  
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 Seq ID NO: C152 DNA Sequence  
 Nucleic Acid Accession #: NM\_005242.2  
 Coding sequence: 148..1341

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1 11 21 31 41 51
CGGCCCCGCC TGGGAGGCG CGCAGCAGAG GCTCCGATTC GGGGCAGGTG AGAGGCTGAC 60
TTTCTCTCGG TGCCTCCAGT GGAGCTCTGA GTTTCGAATC GGTGCGCGCG GATTCGCCGC 120
GCGCCCGGCG TCGGGGCTTC CAGGAGGATG CGGAGCCCCA GCGCGCGGTG GCTGCTGGGG 180
GCCGCCATCC TGCTAGCAGC CTCCTCTCC TGCAGTGSCA CCATCCAAGG AACCAATAGA 240
TCCCTCTAAG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCACGT CACTGGAAAA 300
GGAGTTACAG TTGAAACAGT CTTTCTGTG GATGAGTTT TGCATCTGT CCTCAGTGA 360
AAACTGACCA CGGTCTTCTT TCCAATTGTC TACCAATTG TGTGTTGGT GGGTTTGCCA 420
AGTAACGCCA TGGCCCTGTG GGTCTTTCTT TTCCGAACA AGAAGAAGCA CCCTGCTGTG 480
ATTACATGCG CCAATCTGGC CTGGCTGAC CTCCTCTCTG TCATCTGTT CCCTTGAAG 540
ATTGCCTATC ACATACATGC CAACACTGG ATTTATGGGG AAGCTCTTTG TAATGTGCTT 600
ATTGGCTTTT TCTATGGCAA CATGTACTGT TCCATTCTCT TCATGACCTG CCTCAGTGTG 660
CAGAGGTATT GGGTCATCGT GAACCCCATG GGGCACTCCA GGAAGAAGGC AAACATTGCC 720
ATTGGCATCT CCTGGCAAT ATGGCTGCTG ATCTGCTGG TCACCATCCC TTTGTATGTC 780
GTGAAGCAGA CCATCTTCAT TCCTGCCCTG AACATCAGCA CTGTCTATGA TGTGTTGCTT 840
GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCTCT CTCTGGCCAT TGGGGTCTTT 900
CTGTTCCAGC CCTTCTCTAC AGCCTCTGCC TATGTGCTGA TGATCAGAAAT GCTGCGATCT 960
TCTGCCATGG ATGAAACATC AGAGAAGAAA AGGAAGAGGG CCATCAAATG CATGTGCACT 1020
GTCTGCGCCA TGTAACCTGT CTGCTTCACT CCTAGTAACC TTCTGCTTGT GGTGATTAT 1080
TTCTGATTA AGAGCCAGGG CCAGAGCCAT GTCTATGCC TGTACATTGT AGCCCTCTGC 1140
CTCTCTACCC TTAACAGCTG CATCGACCCC TTTGTCTATT ACTTTGTTTC ACATGATTTT 1200
AGGGATCATG CAAAGAAGCG TCTCCTTTG CGAAGTGTCC GCAGTGAAA GCAGATGCAA 1260
GTATCCCTCA CCTCAAAGAA ACACTCCAGG AAATCCAGCT CTTACTCTTC AAGTTCAACC 1320
ACTGTTAAGA CCTCTATTG AGTTTCCAG GTCCCTCAGAT GGAATTGCA CAGTAGGATG 1380
TGGAACCTGT TTAATGTTAT GAGGACGTGT CTGTTATTTC CTAATCAAAA AGGTCTCACC 1440
ACATACCACC G 1451
  
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60  
 Seq ID NO: C153 DNA Sequence  
 Nucleic Acid Accession #: NM\_003469.2  
 Coding sequence: 92..1945

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1 11 21 31 41 51
GAAACGGCCC GAGAAGCTCG CCCGAGAAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60
CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG 120
AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAATAAT TCCAAAAGTT 240
TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCOGAC AACAGCTCA 300
TAAGGAAGAA AGCAGCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360
AAAAGAAAT GCGGATGAAA GCCACTTGCC CGAGAGGGAT TCACGTAGTG AAGAAGACTG 420
GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA 480
AGAAATAAAG CCTATGCGCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540
TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA 600
TGAAGAGAA TCCAGGGATA ACCCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
TACTCTCTAA AGCCTTGCTA CATTGGAATC TGTCTTCAA GAGCTGGGGA AACTGACAGG 720
ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTATA CGGATGATGA 780
AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTGGGG GAGAAGACTG 840
GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900
GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960
CCAGGAAGAA GATCTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020
AAATGGCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
AAATGGGGAA AGGGCCACCA GGCTTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGGAA GACTTAATTG AGATGCTCAA 1200
AACTGGGGAG AAGCCGAATG GATCAGTGA ACOGGAGCGG GAGCTTGACC TTCCTGTTGA 1260
CCTAGATGAC ATCTCAGAGG CTGACTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320
  
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5 CTCCAAGAGT GGCTACCCCTA AAACACCTGG TCGTGCTGGG ACTGAGGCC TACCAGACGG 1380  
 GCTCAGTGTG GAGGATATTT TAAATCTTT AGGGATGGAG AGTGACAGCA ATCAGAAAAC 1440  
 GTCGTATTTT CCCAATCCAT ATAACCAGGA GAAAGTTCTG CCAAGGCTCC CTATGGTGC 1500  
 TGGAAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCACATG TTGAAAACAG 1560  
 10 ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620  
 GATGCTAGTT AATATCCCTG AGATCATTTA TTCAAACCAA GTGAAGCGAG TTCTGGTCA 1680  
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAAGAGCA 1740  
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC 1800  
 TGTGGGGCCC CGAAGAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860  
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920  
 TAAGAGAGCA ATGGAAAATA TGTAAAGCTGC TTTCAATTAAT TACCTACTT TCATTCTCC 1980  
 CACCCCAAGC AATCCCAAC ATTTCTCTTC AGTGTGTGA CTCTATCCT GTTAAACATG 2040  
 15 TAATATCTTT AATGATGTA CAGGCAGATG AAACCAAGTC ACTGGGAGT CTGCTTCATT 2100  
 TCCTCTGAGC TGTATCTTG TGTATGGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160  
 ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTAATAG TATATCTAAT 2220  
 GGCTGGGCA TTGTTGATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280  
 TTTTAAATAT TTATGAATT ATTTGTATC TGTCTGTAGC GTTTGTGGA GTACTGGACC 2340  
 AAAAAATAA AGCATTATAA ATATA 2365

20 Seq ID NO: C154 DNA Sequence  
 Nucleic Acid Accession #: NM\_030955  
 Coding sequence: 327..5108

25 1 11 21 31 41 51  
 GAATTCGGGG AGCGGGGGGG CTGCGAGGCC GCGGGGCATG CGGGAGGCGG AGGGGTGGGA 60  
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 CCTTTTAGGA GGAGGGAGGG GGAAGAGGTG TCTAGCTAAT TTCTGCTTAA AAAAGCACAG 180  
 30 GAGATCGCGG GTACAGCTTTG CAGTCGCTGC CTCTCGCGC CTGACCATGC ACCCTGTCAT 240  
 CTTCCTGCTG GGCACAGCGG AGCGCTTTAT TTCTGGAGCT GAGGGCTAAA ACTTTTTCAT 300  
 CTTTCTCTCT CCTCAACATC TGAATCATGC CATGTGCCCA GAGGAGCTGG CTTCGAAACC 360  
 TTTCCGTGGT GGCTCAGCTC CTAACTTTG GGGCGCTTTG CTATGGGAGA CAGCCTCAGC 420  
 CAGGCCCGGT TCGCTTCCCG GACAGGAGGC AAGAGCATTT TATCAGGGC CTGCCAGAA 480  
 35 ACCACGTGGT GGGTCCAGTC CGAGTAGATG CCAGTGGGCA TTTTGTGTC TATGGCTTGC 540  
 ACTATCCCAT CACGAGCAGC AGGAGGAAGA GAGATTGGA TGGCTCAGAG GACTGGGTGT 600  
 ACTACAGAA TTTCTACGAG GAGAAGGACC TGTTTTAA CTGACGGTC AATCAAGGAT 660  
 TTTCTTCCAA TAGCTACATC ATGGAGAAGA GATATGGGAA CCTCTCCCAT GTTAAAGTGA 720  
 TGGCTTCTCT TGCCCTCCCTC TGCCATCTCA GTGGCACGGT TCTACAGCAG GGCAACAGAG 780  
 40 TTGGGAGCGC AGCCCTCAGT GCCTGCCATG GACTGACTGG ATTTTCCAA CTACCATATG 840  
 GAGACTTTTT CATTTGAACC GTGAAGAAGC ATCCACTGGT TGAGGGAGGG TACCACCCGC 900  
 ACATCGTTTA CAGGAGGCAG AAAGTTCCAG AAACCAAGGA GCCAACCTGT GGATTAAAGG 960  
 ACAGTGTAA CATCTCCAGC AAGCAAGAGC TATGGCGGGA GAAGTGGGAG AGGCACAACT 1020  
 TGCCAGAGT AAGCCTCTCT CGCGTGTCCA TCAGCAAGGA GAGATGGGTG GAGACACTGG 1080  
 45 TGGTGGCGGA CACAAGATG ATTGAATACC ATGGAGTGA GAATGTGGAG TCCTACATCC 1140  
 TCACCATCAT GAACATGGTC ACTGGGTGTG TCCATAACCC AAGCATGGC AATGCAATTC 1200  
 ACATTGTTGT GGTTCGGCTC ATTCTACTCG AAGAAGAAGA GCAAGGACTG AAAATAGTTC 1260  
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 GTGACTGCAA TCTGTTCAT CACGACGTGG CTGTCTTCT CACCAGAAAG GACATCTGTG 1380  
 50 CTGTTTCAA TGCCCTCTGC GAGACCCCTG GCCTGTCTCA CCTTCCAGGA ATGTGTGAGC 1440  
 CTCACCCGAG TTGTAACATC AATGAAGATT CCGGACTCCC TCTGGCTTTC ACAATTGCC 1500  
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 TGGGAGAGCA TCCGTACATC ATGTCCCGCC AGCTCCAGTA CGATCCCATC COGCTGACAT 1620  
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 55 TTGATGACAT ACCTAAAGAG AAGGCTTGA AGTCCAAGGT CATTGCCCC GGAGTGATCT 1740  
 ATGATGTTCA CCACCATGTC CAGCTACAAT ATGGACCCAA TGCTACCTTC TGCCAGGAAG 1800  
 TAGAAAACGT CTGCAGACA CTGTGGTGTCT CGTGAAGGG CTTTGTCTGC TCTAAGCTGG 1860  
 ACCTGTCTGC AGATGGAATC CAATGTGGTG AGAAGAAGTG GTGTATGGCA GGCAAGTGCA 1920  
 TCACAGTGGG GAAGAAACCA GAGAGCATTC CTGGAGGCTG GGGCCGCTGG TCACCTGGT 1980  
 60 CCCACTGTTC CAGGACCTGT GGGGCTGGAG TCCAGAGCGC AGAGAGGCTC TGCAACAAAC 2040  
 CCGAGCCAAA GTTTGAGGG AAATATTGCA CTGGAGAAAG AAAACGCTAT CGCTTGTGCA 2100  
 ACGTCCACCC CTGTCGCTCA GAGGCACCAA CATTTGGCA GATGAGTGC AGTGAATTTG 2160  
 ACATGTTCC CTACAAGAT GAATCTACC ACTGTTTCC CATTTTAAAC CCAGCACATC 2220  
 CTTGTGAGCT CTACTGCGA CCCATAGATG GCCAGTTTC TGAGAAAATG CTGGATGCTG 2280  
 65 TCATTGATGG TACCCCTTGC TTTGAAGCG GCAACAGCAG AAATGTCTGT ATTAATGGCA 2340  
 TATGTAAGAT GGTGCTGT GACTATGAGA TCGATTCCAA TGCCACCGAG GATGCTGCG 2400  
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 70 ACCTGAATGG AGGGTTTATT ATCCAGTGA ACGGGAATA TAAGCTGGCA GGGACTGTCT 2640  
 TTCAGTATGA CAGGAAAGGA GACCTGGAAA AGCTGATGGC CACAGGTCCC ACCAATGAGT 2700  
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 75 AGAAGGGCG CGGGATGGTG AAAGCTACAT TCTGTGACCC AGAAACACAG CCCAATGGGA 2940  
 GACAGAAGAA GTGCCATGAA AAGGCTTGT CACCCAGGTG GTGGGAGGG GAGTGGGAAG 3000  
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 80 GGAATGAGTG TTTGTTTCC TGTGTTGGTG GAGTGGGAT TCGCAGTGTG ACATGTGCCA 3240  
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 TCCAGCAATG CCTTCTAGC CGGAGAGTTC TGAAACCAA CAAAGGCACT ATTTCCAATG 3360  
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 CCACACCCAC AGGCGCTGAG TCTATGAGCA CAAGCACTCC AGCAATCAG AGCCCTAGTC 3480  
 CTACCAACGC CTCCAAAGAA GGAGACCTGG GTGGGAAACA GTGGCAAGAT AGCTCAACCC 3540

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 5 GCAACCTTAT CACTTGGCCT GTGACTCCAT TTTACAATAC CTTGACCAAA GGTCCAGAAA 3780  
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 TCAGCACAGT AATGGAAGGA CTGCTCCCA GCCAAAGGCC CACTACTTCC GAAACTGGGA 4020  
 10 CACCCAGAGT TGAGGGGATG GTTACTGAAA AGCCAGCCAA CACTCTGCTC CCTCTGGGAG 4080  
 GAGACCACCA GCCAGAACC TCAGGAAAGA CGGCAACCG TAACCACCTG AAACCTCCAA 4140  
 ACAACATGAA CCAACAAAA AGTTCTGAAC CAGTCTGAC TGAGGAGGAT GCAACAAGTC 4200  
 TGATTACTGA GGGCTTTTGT CTAATGCTCT CCAATTACAA GCAGCTCACA AACGGCCACG 4260  
 GCTCTGCACA CTGGATCGTC GGAACCTGGA GCGAGTGCTC CACCACATGT GGCCTGGGGG 4320  
 15 CCTACTGAAA AAGGGTGGAG TGCACCAACC AGATGGATTG TGACTGTGCG GCCATCCAGA 4380  
 GAGCTGACCC TGCAAAAAGA TGCCACCTCC GTCCCTGTGC TGGCTGAAA GTGGGAAAT 4440  
 GGAGCAAGT CTCCAGAAAC TGGAGTGGGG GCTTCAAGAT ACGCGAGATT CAGTGCCTGG 4500  
 ACAGCCGGAG CCACCCGAAC CTGAGGCCAT TTCACTGCCA GTTCTGGGCC GGCATTCTCT 4560  
 CCCCATGGAG CATGAGCTGT AACCCGGAGC CCTGTGAGGC GTGGCAGGTG GAGCCTTGGA 4620  
 20 GCCAGTGCTC CAGGTCTCTG GAGGTGGAG TTCAGGAGAG AGGAGTGTC TGTCACAGGAG 4680  
 GCCTCTGTGA TTGACAAAA AGACCCACAT CCACCATGTC TTGCAATGAG CACCTGTGCT 4740  
 GTCACTGGGC CTGCGGAAC TGGGACCTGT GTTCCACTTC CTGTGGAGGT GGCTTTTCAGA 4800  
 AGAGGATTGT CCAATGTGTG CCCTCAGAGG GCAATAAAAC TGAAGACCAA GACCAATGTC 4860  
 TATGTGATCA CAAACCCAGA CTTCCAGAA TCACAAAAATG CAACCAAGAG GCCTGCAAGA 4920  
 25 AAAGTGCCGA TTTACTTTGC ACTAAGGACA AACTGTGAGC CAGTTTCTGC CAGACACTGA 4980  
 AAGCCATGAA GAAATGTTCT GTGCCACCAG TGAGGGCTGA GTGCTGCTTC TCGTGTCCCC 5040  
 AGACACACAT CACACACACC CAAAGGCAAA GAAGGCAACG GTTGCTCCAA AAGTCAAAAG 5100  
 AACTCTAAGC CAAA 5115

Seq ID NO: C155 DNA Sequence  
 Nucleic Acid Accession #: NM\_001062.1  
 Coding sequence: 76..1380

1 11 21 31 41 51  
 35 | | | | |  
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 TACACTGTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT 120  
 TCTTTTATTC CAGGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180  
 CTAAACCTC TGTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240  
 40 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGTAT GCAAAGATG 300  
 ATCCAACAAA TCAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAAOCTG AGGAAACCTT AATATATGAT 420  
 TACCACCTGA CTGACAAGCT AGAAAAATAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480  
 CACAATGGCA CTCCCTGAC TAACCTACTC CAGCTCAGCC TGGACGTTTT GGCCTGTGT 540  
 45 CTGTTCATG GGAACACTC AACCGCGAA GTTGTCAACC ACTTCACTCC TGAAAAATAA 600  
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660  
 AACTGTGTGA AGAAGAGTCT AATAAATGG CAGATCAAG CAGATGAAGG CAGTTTAAAG 720  
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAAT 780  
 GGTCTCATCT GAAACACATT TAGCAGGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840  
 50 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCACGGAA 900  
 ATTTCTCAG GAGCATTGAG TAATCCAAAC GCTGCAGCCC AGGCTTACC TGGCCTGATG 960  
 GGAAAGACCT TCTTGGATAT TAACAAGAG TCTTCTTGG TCTCTGCTTC AGGTAACCTC 1020  
 AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080  
 GTCAATTACT CTGTGAGAA CAATGAAACA TATTTACCA ATGTCACTGT GCTAAATGGT 1140  
 55 TCTGTCTTCC TCACTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200  
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260  
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320  
 GGTAGTTAGC TTGTGCGCAA TGGAGAAAAC TTGGAGGTTG GCTGGAGCAA ATACTAATAA 1380  
 GCCCAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCATG TTTATTGTCC 1440  
 60 TTATGCCCTC TTCTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500  
 TTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC 1537

Seq ID NO: C156 DNA Sequence  
 Nucleic Acid Accession #: NM\_004591  
 Coding sequence: 59..349

1 11 21 31 41 51  
 65 | | | | |  
 CACTCCAAA GAACCTGGTA CTCAACACTG AGCAGATCTG TTCCTTGAGC TAAAAACCAT 60  
 GTGCTGTACC AAGAGTTTGC TCCGGCTGTC TTTGATGTC GTGCTGTAC TCACCTCTG 120  
 70 CGGGAATCA GAAGCAGCAA GCAACTTTGA CTGCTGTCTT GGATACACAG ACOGTATTCT 180  
 TCATCTTAAA TTTATTGTGG GCTTCACACG GCAGCTGGCC AATGAAGGCT GTGACATCAA 240  
 TGCTATCATC TTTACACAA AGAAAAAGTT GTCTGTGTGC GCAATCCAA AACAGACTTG 300  
 GGTGAAATAT ATTGTGGCTC TCCTCAGTAA AAAAGTCAAG AACATGTAAG AACTGTGGCT 360  
 75 TTTCTGGAAT GGAATTGGAC ATAGCCCAAG AACAGAAAGA ACCTTGCTGG GGTGGAGGT 420  
 TTCCTTGCA CATCATGGAG GGTTTAGTGC TTATCTAATT TGTGCTCAC TGGACTTGTC 480  
 CAATTAAATGA AGTTGATTCA TATTGCATCA TAGTTTGCTT TGTTAAGCA TCACATTAAA 540  
 GTTAACTGT ATTTATGTTT ATTTATAGCT GTAGGTTTTC TGTGTTTACG TATTTAATAC 600  
 TAAITTTCCA TAAGCTATTT TGGTTTAGTG CAAAGTATAA AATTATATT GGGGGGGAAT 660  
 80 AAGATTATAT GCACTTTCTT GCAAGCAACA AGCTATTTT TAAAAAATC ATTTAACATT 720  
 CTTTGTGTTA TATTGTTTTG TCTCCTAAAT TGTGTGAATT GCATTATAAA ATAAGAAAAA 780  
 CATTAAATAG ACAAATATT 799

Seq ID NO: C157 DNA Sequence  
 Nucleic Acid Accession #: NM\_013271.1

Coding sequence: 27..809

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1      11      21      31      41      51
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CCGGGGCGGT CGGCTTTTGG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCGCGCG 120
TCTGCGCGCG GCGGTAAG GAACCCGCGC GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
AGACTGGCGC TCCTCGCGCG TTCCGGCGGT CAGTGCCCG AGGTGAGGCG GCGGGGCGCG 240
TGCAGGAGCT GCGCGGGCG CTGCGGCATC TGCTGGAGGC CGAACGTGAG GAGCGGGCGC 300
GGGCGGAGGC GCAGGAGGCT GAGGATCAGC AGGCGGCGGT CCTGGCGCAG CTGCTGCGCG 360
TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GAGCGACGAC CCGGACGCGC 420
CTGAGGCGCA GCTGCTGCG GCTCTGTCC GCGCCGCGCT TGACCTGCGC GCGCTAGCAG 480
CCGAGCTTGT CCGCGCGGCC GTCCCGCGCG CGGCGCTCG ACCCGGGCCC CCGTCTACG 540
ACGACGGCCC CCGGGGCCCC GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGGGG AAGCGCGGAC TCCGAGGGGG 660
TGGCAGCCCG GCGCGGCGCT CGCCGTGCGC CGGACCACTA TGTGGGCTCT GAGCTGCCCC 720
CTGAGGCGGT GCTGGGGCG CTGCTGCGTG TGAACGCGCT AGACCCCGC GCGCCCCAGG 780
TGCTGTCAGC CCGGCTCTTG CCACCTGAG CACTGCGCG ATCCGCTGCA CCTGGGACC 840
CAGAAGTGCC CCGCCCATCC CGCCACCAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900
TTACCCCGCG CAGCCAGCCC TCTCACCGCA GGATCCCTAC CCCCTGGCCC ACAATAACAT 960
GATCTGAGC
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Seq ID NO: C158 DNA Sequence  
Nucleic Acid Accession #: NM\_002245.2  
Coding sequence: 183..1193

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1      11      21      31      41      51
30     |      |      |      |      |
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GCGGGCGGGA GCCAGGCCCG GCGGGGGGCG GGGGCGGGCG GGCCAGAAGA GCGCGCGGGC 120
CGCGCTCCGG CCGGCTGCGC CGCTTGGCCT TGGCTTTGGC TTGGCGCGCG GCGGTGGAGA 180
AGATGCTGCA GTCCCTGGCC GGCAGCTCGT CGCTGCGCCT GGTGGAGCGG CACCGCTCGG 240
CCTGTGCTTT CGGCTTCTTG GTGCTGGGCT ACTTGCTCTA CCTGGTCTTC GCGCGAGTGG 300
TCTTCTCTCT GGTGGAGCTG CCCTATGAGG ACCTGCTGCG CCAGGAGCTG CGCAAGCTGA 360
AGCGAGCTGT CTGGGAGGAG CACGAGTGCC TGTCTGAGCA GCAGCTGGAG CAGTTCTCTG 420
GCGGGTGCTT GAGGGCCAGC AACTACGCGC TGTGCGTGCT CAGCAACGCC TCGGGCAACT 480
GGAAGTGGGA CTTCACCTCC GCGCTCTTCT TCGCCAGCAC CGTGCTCTCC ACCACAGGTT 540
ATGGCCACAC CGTGCCCTTG TCAGATGGAG GTAAGGCCCT CTGCATCATC TACTCGTCA 600
TTGGCATTCC CTTCACCTTC CTGTTCTCTA CCGCTGTGGT CCAGCGCATC ACCGTGCAAG 660
TCACCCGCGAG GCGGCTCTCT TACTTCCACA TCCGCTGGGG CTCTCCAAG CAGGTGGTGG 720
CCATGCTCCA TGGCGTGCTC CTGGGTTTG TCACTGTGTC CTGCTTCTTC TTCTATCCCG 780
CCGCTGTCTT CTAGTCTCTG GAGGATGACT GGAATCTTCT GGAATCTTCT TATTTTGT 840
TTATTTCCCT GAGCACCATG GCGCTGGGG ATTATGTGCC TGGGAAGGC TACAATCAA 900
AATTCAGAGA GCTCTATAAG ATTGGGATCA CGTGTACCT GCTACTTGGC CTATTTGCCA 960
TGTTGGTAGT TCTGGAAACC TTCTGTGAAC TCCATGAGCT GAAAAAATTC AGAAAAATGT 1020
TCTATGTGAA GAAGGACAAG GACGAGGATC AGGTGCACAT CATAGAGCAT GACCAACTGT 1080
CCTTCTCTCT GATCACAGAC CAGGACGCTG GCATGAAAGA GGACCAAGAG CAAATGAGC 1140
CTTTTGTGGC CACCCAGTCA TCTGCTGCG TGGATGGCCC TGCAACCAT TGAGCGTAGG 1200
ATTGTTGCA TTATGCTAGA GCACCAGGT CAGGTGCA GGAAGAGGCT TAAGTATGTT 1260
CATTTTATC AGAATGCAAA AGCGAAAATT ATGTCATTT AAGAAATAGC TACTGTTTGC 1320
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TCTGACCTT ACATAGGAGG AGAATACTTG AAGCAGTATG CTGCTGTGGT TAGAAGCAGA 1500
TTTTATCTT TAACTGGAA ACTTTGGGT TTGCATTTAG ATCATTTAGC TGATGGCTAA 1560
ATAGCAAAAT TTATATTAG AAGCAAAAAA AAAAAGCATA GAGATGTGTT TTATAAATAG 1620
GTTTATGTT ACTGGTTTGC ATGTACCCAC CCAAAATGAT TATTTTGGGA GAATCTAAGT 1680
CAAACTCACT ATTATATAG CATAGGTAAC CATTAACATG GTACATATAA AGTATAAATA 1740
TGTTTATAT CTGTACATAT GGTTTAGGTC ACCAGATCCT AGTGTAGTTC TGAATAAAG 1800
ACTATAGATA TTTTGTCTCT TTTGATTCTT CTTTATACTA AAGAATCCAG AGTGTCTACA 1860
ATAAATAAG GGAATAAATA AACTTGAGAG TGAATAACCA T 1901
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Seq ID NO: C159 DNA Sequence  
Nucleic Acid Accession #: NM\_005472.1  
Coding sequence: 93..404

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CCGAGTCTTC CCCCACCTCA ATCCCTGTGT CTATGGAGAC TACCAATGGA ACGGAGACCT 120
GGTATGAGAG CCTGCATGCC GTGCTGAAGG CTCTAAATGC CACTCTTCAC AGCAATTTGC 180
TCTGCGCGCC AGGGCCAGGG CTGGGGCCAG ACAACAGAGC TGAAGAGAGG CGGGCCAGCC 240
TAACCTGGCG TGATGACAA TCCTACATGT ACATTCTCTT TGTCATGTTT CTATTTGCTG 300
TAACTGTGGC CAGCCTCATC CTGGGATACA CCGCTCCCG CAAAGTGGAC AAGCGTAGTG 360
ACCCCTATCA TGTGTATATC AAGAACCCTG TGTCTATGAT CTAACACGAG AGGGCTGGGA 420
CGGTGGAAGA CCAAGACACC TGGGGATTGC GTCTGGGGCC TCCAGAACTC TGCTGTGGAC 480
TGATCAGGT CT
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Seq ID NO: C160 DNA Sequence  
Nucleic Acid Accession #: NM\_005245.1  
Coding sequence: 187..13959

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1      11      21      31      41      51
80     |      |      |      |      |
CTGGGCGGCC GGGCGGGGG AGAGGGCGCG GGAGCGGCTC GTGCGGCGAG TACCATGCGG 60
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	ACGCGCGAGC	CGCGCGAGGC	CCCGCGAGGC	CCGTCCCTGC	TCGGGGGCGC	GCTGAGACGG	120
	CGGGTGAGCT	CCACGAGAGC	GGCGCGGCCA	CTTCGGGGCA	ACTTTGCGAT	TCCCGACAGT	180
	TAAGCAATGG	GGAGACATTT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCAACATTTT	240
5	GGAGACAGTG	ATGGCAGCCA	ACGACTTGAA	CAGACTCTCT	TGCAGTTTAC	ACACCTCGAG	300
	TACAACGTCA	CGGTGCAGGA	GAACCTCTGA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAAGTAAGGT	ACAAAATTGT	TTCCGAGAGC	420
	AGTGAAGAAC	TGTTCAAAGC	TGAAGAGTAC	ATTCTCGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
10	ATAGTGAAG	CACTTGAAAA	AAATACTAAT	GTGGAGGCGC	GAACAAAGGT	CAGGGTGCAG	600
	GTGCTGGATA	CAATGACTT	GAGACCGTTA	TTCTCACCCA	CCTCATACAG	CGTTTCTTTA	660
	CCTGAAAAACA	CAGCTATAAG	GACCAGTATC	GCAAGAGTCA	GGCCACCGGA	TGCAGACATA	720
	GGAAACCAAG	GGGAATTTTA	CTACAGTTT	AAAGATCGAA	CAGATATGTT	TGCTATTTCAC	780
	CCAACCAAGT	GTGTGATAGT	GTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
15	GAGATGGAAA	TCTCGCTGTC	GGACCGTGCC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
	AGCATGGCCA	AGCTAACCGT	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	GCAGTGACAT	TGTACCCATC	AGAACTGGAC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGACTCGC	ATCAGGGTGC	CAATGGTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTAGAAC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
20	GCCATCGGTG	ACATTGATTG	GGACAGTCAT	CCITTCCGGCT	ACAATCTCAC	ACTACAGGCT	1200
	AAAGATAAAG	GAACCTCGCC	CCAGTTCTCT	TCTGTTAAAG	TCATTCAAGT	GACTTCTCCA	1260
	CAGTTCAAAG	CCGGGCCAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGCTCTCT	CCAACACACC	TGTGGTCATG	GTAAGGGCCA	TTCTGCTCTA	TTCCCATTTG	1380
	AGGTATGTTT	TTAAAGGAGC	ACCTGGAAAA	GCTAAATTCA	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTTAGAAC	AGTTAAAGAA	CAGCAGGCAG	CCCATTITGA	ACTTGAAGTA	1500
	ACACACAGTG	ACAGAAAAGC	GTCCACCAAG	GTCTTGGTGA	AAGTCTTAGG	TGCAAAATAGC	1560
	AATCCCCCTG	AATTTACCCA	GACAGCGTAC	AAAGCTGCTT	TGATGAGAA	CGTGCCCAT	1620
	GGTACTACTA	TGATGAGCCT	GAGTGCCGTA	GACCCGTATG	AGGGTGAGAA	TGGGTACGTG	1680
	ACATACAGTA	TGCAAAATTT	AAATCATGTG	CCGTTTGCGA	TTGACCATTT	CACTGGTGCC	1740
30	GTGAGTACGT	CAGAAAACCT	GGACTACGAA	CTGATGCCCT	GGGTTTATAC	TCTGAGGATT	1800
	CGTGACATCAG	ACTGGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCCPTGC	TACATTAAT	1860
	CTCAATAACT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTGTGA	AGGGACAATT	1920
	CCAGAGATGC	TAGGCGTGGG	AGAGCAAAAT	ACCAGCTGTT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAGTTGG	TACAGTATCA	GATTGAAGCT	GGAAATGAAC	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCAACTCGG	GGGTATTGTC	ATTAAGCGA	TCGCTAATGG	ATGGCTTAGG	TGCAAAAGTG	2100
	TCTTTCCACA	GTCGTAGAAT	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCATTATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAAG	CTGGTAAACT	TGCAGTGTGA	AGAGACTGGT	2220
	GTGCCCCAAA	TGCTGGCAGA	GAACTCCTG	CAGGCAAAAT	AATTACACAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTTCTTCCA	TTCTCACTCT	GTCAATGCTC	ACATACCGCA	GTTTAGAAGC	2340
40	ACTCTTCCGA	CTGTATTTC	GGTAAAGGAA	AACACGCTG	TGGTTCCAG	TGTAATTTTC	2400
	ATGAACCTCA	CTGACCTTGA	CAGTGGCTTC	AATGGAAAAC	TGGTCTATGC	TGTTCTCGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCTCTTGACC	GTGAAAACAC	AGACAAATAC	ACCCTGAATA	TTACCGTCTA	TGACCTTGGG	2580
	ATACCCCTGA	AGGCTGGCTG	GGCTCTTCTA	CATGTGCTGG	TTGTGATGTC	CAATGATAAT	2640
45	CCACCCGAGT	TTTTACAGGA	GAGCTATTTT	GTGGAAGTGA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAAATCA	TCCAGGTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACGG	ACACGTGACG	2760
	TACTCAATTC	TTACAGACAC	AGACACATTT	TCAATTGACA	GCGTGACGGG	TGTTGTTAAC	2820
	ATCGCAGGCC	CTCTGGATCG	AGAGCTGCAG	CATGAGCACT	CCTTAAAGAT	TGAGGGCCAGG	2880
	GACCAAGCCA	GAGGAGAGCC	TCAGCTGTTC	TCCACTGTGG	TTGTGAAAGT	ATCACTAGAA	2940
50	GATGTTAATG	ACAAACCCAC	TACATTTATT	CCACCTAATT	ATCGTGTGAA	AGTCCGAGAG	3000
	GATCTTCCAG	AAGGAACCGT	CATCATGTGG	TTAGAAAGCC	ACGATCTGTA	TTTAGGTGAG	3060
	TCCTGGTCAGG	TGAGATACAG	CCTTCTGGAC	CACGGAGAAG	GAACCTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAAGAAGCA	AGTGTATAAT	3180
	CTCACTGTGA	GGGCTGAAAG	CAAGGGAAAG	CCAATTTCTC	TGCTTCTTAC	TTGCTATGTT	3240
55	GAAGTTGAGG	TGGTTGATGT	GAATGAGAAC	CTGACCCAC	CCGTGTTTTC	CAGCTTTGTG	3300
	GAAGAGGGGA	CAGTGAAAGA	AGATGCACCT	GTGGTTTCAT	TGGTAATGAC	GGTGCGGCT	3360
	CATGATGAGG	ACGCGGAGAG	AGATGGGGAG	ATCCGATACT	CCATTAGAGA	TGGCTCTGGC	3420
	GTGTGTGTTT	TCAAAATAGG	TGAAGAGACA	GGTGTCTAG	AGACGTGAGA	TGCACTGGAC	3480
	CGTGAATCGA	CCTCCCATTA	TTGGCTAACA	CTCTTTGCAA	CGATCAGGG	TGCTGTCCCT	3540
60	CTTTCTATGT	TCATAGAGAT	CTACATAGAG	GTGAGGATG	TCAATGACAA	TGCACCAACG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAATAAT	CTCCTAAAGA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTTGA	TCCAGATTGG	AGCTCTAATG	ACAAGCTCAT	GTACAAAATT	3720
	ACAAGTGGA	ATCCACAAGG	ATTCTTTTCA	ATACATCTTA	AAACAGGTCT	CATCACAATT	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACATGATGA	GTCCCCCAA	ATCAACCAT	GCAAGAGTCA	TTGTGAAAT	CCTTGATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTCTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACGG	GAGCGCTCT	ATCGGCTCAT	AGCCACCGAC	4020
	AAGGATGAGG	GCCCAATGAC	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTTC	TGCAACCGAA	AACCTGGAGT	GTITGTTCCA	AGAGGTTTTC	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAGTT	GACAATGGTC	GCCCTCAAAA	GTCTCAACCC	4200
	ACCAAGCTCC	ATATTGAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTCATT	4260
	GAAGAATCAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CGSTGCTCA	CATGATTGGA	4320
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75	GCAGAACAGA	AGTCARAATA	CAACCTCACA	GTGAGGCTCA	CAGATGGAAC	CACCACTATC	4500
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	AGTGCTGTGG	ATCAGGATGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
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	GTGCGCTGAA	AACGCAACTT	TGCAAGGATT	GTGGTCAATG	TCAGCGACAC	GAATGAACAC	4860
	GCCCGTGGT	TCACCGCTTC	CTCCTACAAA	GGGCGGGTTT	ATGAATCGGC	AGCCGTTGGC	4920
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	TACTCGATCG	AGTCAGGAAA	TATTGGAAAT	ATTGGAAAT	CTTTTATGAT	TGATCTGCTG	5040
	TTGGCTCTCA	TTAAACTGTC	CAAGGAATTA	GATCGAAGTA	ACCAAGCGGA	GTATGATTTA	5100

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	CTTAGTGAAA	CTGTGAGCAT	TGGGAGTTTC	GTTGGGATGG	TTACAGCCCA	TAGTCAATCA	5280
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5	TCTGGAACATA	TCATCACTCA	GAAGGCCCTG	GACTTTGAAA	CTTTGCCCAT	TTACACATTG	5400
	ATAATACAAG	GAACATAACAT	GGCTGGTTTG	TCCACTAATA	CAACGGTTCT	AGTTCACTTG	5460
	CAGGATGAGA	ATGACAACGC	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
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10	GCAGCTGATG	CTGATAAAGA	CTCAATGCT	TTGCTTGAT	ATCACATTGT	TGAACCATCT	5640
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	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAGAATCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
	TACTCCATCA	CCGAAGGCCA	CATCGGGGAG	AAGTTTCTTA	TGGACTACAA	GACTGGTGCT	6000
	CTCACTGTCC	AGCAACAAC	TCAGTTAAGA	AGCGCTACG	AGCTAACCGT	TAGAGCTTCC	6060
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	GAACATTAG	CTGTCAATTAC	TGCTATTGGG	AGTCCAATCA	ATGAGCCTTT	GTITTTATCAC	6240
20	ATCCTCAACC	CAGATCGCAG	ATTTAAAAATA	AGCCGCACCT	CAGGGGTTCT	GTCAACCACT	6300
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	GAACATAAGC	CTTCTGCAGT	GGCCCAAGTT	GTCTGTAAGG	TCATTGTAGA	AGACCAAAAT	6420
	GATAATAGCT	CGGCTGTTGT	CAACCTTCCC	TACTACGCCG	TGTTAAAGT	GGACACTGAG	6480
25	GTGGGCCATG	TCATTGCGTA	TGTCACTGCT	GTAGACAGAG	ACAGTGGCAG	AAACGGGGAA	6540
	GTGCATTACT	ACCTCAAGGA	ACATCATGAA	CACCTTCAAA	TTGGACCTTT	GGGTGAAATT	6600
	TCACGTAAAA	AGCAATTGTA	GCTTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCAAAAGATG	GAGGGAACCC	GGCCTTTTCA	CGGGAAGTTA	TGCTTCCGAT	CACGTGCTAG	6720
	AATAAAGCCA	TGCTGTGTTT	TGAAAAACCT	TTCTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
	CAGGTGCACA	GGCCTGTGGT	CCACGTGCAG	GCTAACAGCC	CGGAAGGCCCT	GAAAGTGTTC	6840
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	ATCAATGTCA	TAGCTCTCTT	GGACTTTGAG	GGCCACCCGG	CATATAAGCT	GAGCATACGC	6960
	GCAACTGACT	CCTTGACGGG	CGCTCATGCT	GAAGTATTTG	TGGACATCAT	AGTAGACGAC	7020
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80 Seq ID NO: C161 DNA Sequence  
Nucleic Acid Accession #: NM\_014220.1  
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	GCTGGGTATT	TTGGAGTCAT	GTTTTTCTG	AACATTGCCA	TGTTCAATTG	GGTAATGGTG	1200
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15	AACCTGGCGA	GTGTGGTTAG	CTTGACCTTT	CTGTGGGCA	TGACATGGGG	TTTTGCATTG	1320
	TTTGGCTGGG	GACCTTAA	TATCCCTTTC	ATGTACCTCT	TCTCCATCTT	CAATTCAATTA	1380
	CAAGGCTTAT	TTATATTTCAT	CTTCCACTGT	GCTATGAAGG	AGAATGTTCA	GAACACAGTG	1440
	CGGCGGCATC	TCTGCTGTGG	TAGATTTGGG	TTAGCAGATA	ACTCAGATTG	GAGTAAGACA	1500
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20	ATTGGTTCCA	ACTCAACCTA	TCTTACATCC	AAATCTAAAT	CCAGCTCTAC	CACCTATTTC	1620
	AAAAGGAATA	GCCACACAGA	TAATGTCTCC	TATGAGCATT	CCTTCAACAA	AAGTGGATCA	1680
	CTCAGACAGT	GCTTCCATGG	ACAAGTCTCT	GTCAAACCTG	GCCCCATGCT	ATGGAGATCA	1740
	AAACATCAATC	ATCCCTGTCC	ATCAGGTCAT	TGATAAGGTC	AAGGGTTATT	GCAATGCTCA	1800
25	TTCAAGCAAC	TTCTATAAAA	ATATTATCAT	GTCAAGACCC	TTCAAGCCCA	GCACAAAGTT	1860
	TTAATGTCTT	TAAGAAAAAG	AAATCAATCT	GCAGAAATGT	GAAGATTGTC	AAGCAGTGTA	1920
	AACTGCAACT	AGTGATGTAA	ATGTGCTATT	ACCTAGGTAA	CTGCATATAT	ATAAGGAATG	1980
	TATTTTGTGA	AGAAGGCTTT	TGTGAAATTC	AGAATTTTTC	TTTTTAATAT	ATTTCTTCCA	2040
	TGGAAGAGTT	GTCATCACTA	AAACTTCAGT	ACTGAGAGTA	ACATGACTCA	GTAGCCACAG	2100
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	TGTCCTTGCT	TTGGAGACTT	TAAGACATT	CCTAAAGCAC	AAATAAAGC	CTCGTATTTC	2340
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35	CAAAATAATT	TATGAAGAGC	TGGGTCTGCA	ATAGCTAGTC	TAAAACTAC	TTGTGTGTCA	2460
	GTCTCTCGT	TATAGTATAT	AAGAGCCTGA	GSAGGTCTGG	CAAGATAGAT	GGTGATTAT	2520
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	AGACTATTCT	GAGTAATGCT	TGCTTGCTAA	TGAATGTATA	GGAGACCACA	TTGTAATTGT	2640
40	TCTTAGAGTA	TGGAGTCCAT	GCACTTTCTT	AGAAATCGGT	CTCAGTGAT	GCTGTGCTTT	2700
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	GATAAGAAAA	GGAGACATTC	TGGCAAAGCC	AATCTGCTTA	AAGGCAAGT	CCAGAACCTG	2820
	GAACCTAGAG	GCCTTTCTCT	CTGCACGAAA	AACAGGAGT	TTGCAGTCTG	AGATATGGGA	2880
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45	GAAGCTATT	GCTGTGCTCC	AGCAGATGAT	GAGATAATGA	GGTAGTGGGT	TTTTTATTAC	3000
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Nucleic Acid Accession #: NM\_000574.1  
Coding sequence: 66..1211

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	CCCCAGATGT	ACCTAATGCC	CAGCCAGCTT	TGGAAGGCGG	TACAAGTTTT	CCCGAGGATA	240
	CTGTAATAAC	GTACAATGT	GAAGAAAGCT	TTGTGAAAT	TCTTGGCGAG	AAGGACTCAG	300
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	AGGTGCCAAC	AAGGCTAAAT	TCTGCATCCC	TCAAACAGCC	TTATATCACT	CAGAATTATT	420
60	TTCCAGTCGG	TACTGTTGTG	GAATATGAGT	GCGGTCCAGG	TTACAGAAGA	GAACCTTCTC	480
	TATCACCAAA	ACTAATCTGC	CTTCAGAAAT	TAAATGGTTC	CACAGCAGTC	GAATTTGTGA	540
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70	CTACCAAGT	AAATGTTCCA	ACTACAGAAG	TCTCACCAC	TTCTCAGAAA	ACCACCACAA	1020
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80	CCACTTATA	AGGAATATA	AAATGAAAA	CATTATTGG	ATATCAAAG	CAATAAAAA	1620
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	AATCTTCGTT	TGTTGCAACA	ATAGAGTTTG	GAAAAAGCCT	TGAAAGGTTG	TCTTCTTTGA	1860
	CTTAATGTCT	TAAAGATAT	CCAGAGATAC	TACAATATTA	ACATAAGAAA	AGATTATATA	1920

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 GT 2102

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 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2651

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 CTGCTCCCGA ATCCCTCGCC CAGTCTCCGC TTCCTGGAGG AGTTAGCTCT TCGGGGAAAC 300  
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Seq ID NO: C168 DNA Sequence  
 Nucleic Acid Accession #: NM\_003667.2  
 Coding sequence: 49..2772

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	TTAACTCACT	TAAAATTAA	AGGAATCAT	GCCTTACAGA	GCTTGATATC	ATCTGAAAC	1440
	TTTCAGAAC	TCAAGTTAT	AGAAATGCCT	TATGCTTACC	AGTGCTGTGC	ATTTGGAGTG	1500
	TGTGAGAATG	CCTATAAGAT	TTCTAATCAA	TGGAATAAAG	GTGACACACG	CAGTATGGAC	1560
	GACCTTCATA	AGAAAGATGC	TGGAATGTTT	CAGGCTCAAG	ATGAACGTGA	CCTTGAAGAT	1620
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5  
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GGTGCCTACT CAAAGAGTGT CCACTATTGA TTGTATTATG CTGCTCACTG ATCCTTCTGC 3120  
ATAATTAAAA TAAATATGTC TAAAGGGTTA GTAGACAAAA TGTAGTCTTT TTGTATATTA 3180  
GGCCAAGTGC AATTGACTTC CCTTTTTTAA TGTTCATGA CCACCCATTG ATTGTATTAT 3240  
AACCACITAC AGTTGCTTAT ATTTTGTGTT TTAACCTTGG TTTCTTAACA TTTAGAATAT 3300  
TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG 3342

Seq ID NO: C170 DNA Sequence  
Nucleic Acid Accession #: NM\_000582  
Coding sequence: 88..990

10  
1 11 21 31 41 51  
15 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60  
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GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG 180  
CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240  
CAGAATCTCC TAGCCGCCA GACCCCTTCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300  
20 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360  
AOCGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420  
TCTGATGAAT CTGATGAAC TGTCTACTGAT TTTCCACCG ACCTGCCAGC AACCGAAGTT 480  
TTCATCCAGT TTGTCCTCCAG AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540  
GGACTGAGGT CAAATCTTAA GAAGTTTCGC AGAAGTGAACA TCCAGTACCC TGATGCTACA 600  
25 GAGGAGGACA TCACCTCACA CATGGAAGC GAGGAGTTGA ATGGTGACATA CAAGGCCATC 660  
CCCGTTGCCC AGGACCTGAA CGGCCCTTCT GATTGGGACA GCCGTGGGAA GACAGATTAT 720  
GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780  
TATAAGCGGA AAGCCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA 840  
CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTTT ACAGCCATGA AGATATGCTG 900  
30 GTTGTAGACC CCAAAAGTAA GGAAGAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA 960  
TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCATTTTGC 1020  
ATTTAGTCAA AAGAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080  
CTCAGTTTAT TGGTTGAATG TGTATCTAT TTAGTCTGGA AATAACTAAT GTGTTTGATA 1140  
ATTAGTTTAG TTTGTGGCTT CATGGAACCT CCCTGTAAAC TAAAGGCTTC AGGGTTATGT 1200  
35 CTATGTTTAT TCTATAGAAG AAATGCAAC TATCACTGTA TTTAATATT TGTATTCTC 1260  
TCATGAATAG AATTTATGTG AGAAGCAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320  
ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380  
TATCTTTTGG TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAAAT TGGTGGTGTG 1440  
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40 GCCTAAAAAA AAAAAAAA AAAA 1524

Seq ID NO: C171 DNA Sequence  
Nucleic Acid Accession #: NM\_002821  
Coding sequence: 150..3362

45 1 11 21 31 41 51  
AATCCCGGCC TCGGGAGGCC TCGGGGTCGG GCTCCGGCTG CGGCTGCTGC TGCGGCGCCC 60  
GGGCTCCGGT GCGTCCGCTT CCTGTGCCCG CCGCGGAGCA GTCTGCGGCC CGCGGTGGCC 120  
CTCAGCTCC TTTTCTGAG CCGCGCGGCA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC 180  
50 CCGCGCGGTT GCGTCTGCTC AGCGTCTGCG TGCTGCCGCT GCTGGGCGGT ACCCAGACAG 240  
CATGTGCTT CATCAAGCAG CGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300  
TTGCTGTGA GGTGTAGGCT CCGGGCCCGG TACATGTGTA TGGCTGCTC GATGGGGCCC 360  
CTGTCCAGGA CACGGAGCGG CGTTTGGCCC AGGCGAGCAG CTTGAGCTTT GCAGCTGTGG 420  
AOCGGCTGCA GACTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480  
55 AAGCCCGCAG TGCCTCAACA TCAATGGAT TGAGGCGAGT CTTGTGGTCC 540  
TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGTTCACA CTTGTTGCCC 600  
ACATTGATGG GCACCTCCG CCCACCTACC AATGGTCCG AGATGGGACC CCGCTTCTTG 660  
ATGGTCAGAG CAACACACACA GTCCAGCAGC AGGAGCGGAA CCTGAGCTTC CGGCCAGCTG 720  
GTCTGAGCA TAGTGGGCTG TATTCTGCT GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780  
60 GCAGCCAGAA CTTCACTCTG AGCATGTCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840  
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AGCCACCCCC GAGCCTGCGG TGGCTCTTTG AGGATGAGC TCCCATCACT AACCGCAGTC 960  
GCCGCCACCA CCTCGCAGAG GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020  
TCCGCCACCG CCGTCAAGGG ATCTACCGCT GCATTGGCCA GGGGCGAGAG GGGCCACCCA 1080  
65 TCATCTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTAGGCCAC 1140  
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AGCCACGCGT GTGCTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260  
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GCCACGCGGC CAACCTGGCT GGTCAAGCGA GACAGGATGT CAACATCACT GTGGCCACTG 1380  
70 TGCCCTCTCT GCTGAAGAAG CCCCAGACA GCCAGCTGGA GGAGGGCAAA CCGCGCTACT 1440  
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TCATCTCAGA GGACTCACGG TTCGAGGTCT TCAAGAATGG GACCTTGCGC ATCAACAGCG 1560  
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AGGCGCAAGC CCGTGTCCAA GTGCTGAAA AGCTCAAGTT CACACCAACA CCCCAGCCAC 1680  
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75 AGCCCTACTT TAAGTGGGAA OGGCAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA 1800  
ACGCTGGGAC CTTGCAATTT GCCCGGTGA CTGAGATGA CGCTGGCAAC TACACTTGCA 1860  
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TTATCACTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980  
TGCTGAGCCA GGCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAAGGC AAGGACCGCA 2040  
80 TCTGTGACCC CACCAAGCTT GACCCAGGA TGACATCTT CCAGAAATGGC TCCTGTGTGA 2100  
TCCATGACGT GGCCCTGAG GACTCAGGCC GCTACACCTG CATTGCAGGC AACAGCTGCA 2160  
ACATCAGCA CAGGAGGCC CCCCTCTATG TCGTGACAA GCCTGTGCCG GAGGAGTCGG 2220  
AGGGCCCTCG CAGCCCTCCC CCTACAAGA TGATCCAGAC CATTGGGTTG TGGTGGGTG 2280  
CCGCTGTGCG CTACATCATT GCCGTGCTGG GCCTCATGTT CTACTGCAAG AAGCGCTGCA 2340



5	AAGCCAAGCG	GCTGCAGAAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCTTT	GCAGAAACGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGCCCCCGCG	CCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCACCGGTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCCTGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAGCTGAA	CCAGCCCAAC	GTGGTGGCGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCTCT	AGGATTTCCA	2820
10	AGAGCAAGGA	TGAAAAATTG	AAGTCAAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTAGGC	ATGGAGCACC	TGTCCAAACA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACCTGCTG	GTCACTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACCTCCG	CCAGGCCTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCCTGG	3120
	CCTTGGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
15	CAGATGATG	ATGCTGGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCTC	CAGCCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCTGGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
	CAGCATGATG	GGCAAGATCC	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
20	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCTCTA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCTTGCCAC	3600
	CTCTTCTCTG	ATCAGGGACA	GTGTGGGTGC	CACAGTAAAC	CCCAATTCTT	GGCCTTCAAC	3660
	TTCTCCCTCT	GACCGGGTCC	AACCTCGCCA	CTCATCTGCC	AACCTTGCCCT	GGGAGGGGCT	3720
	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTTAATA	TTCTCAAGTT	CTGGGCACAC	3780
25	AGGGTTAATG	AGTCTCTTTC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAAG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCCAAGTCTT	3900
	CCCCACCCCT	CTCTCTCTTC	CTCATCTTAA	GTGCCCTGGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAAC	GCCCTTTTTC	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
30	GCCATCCTTA	CCCCACACTT	TTATTTGTGT	CGTTTTTGT	TTGTTTTGTT	TTTTTGTGTT	4140
	TGTTTTGTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTTA		4187

Seq ID NO: C172 DNA Sequence

Nucleic Acid Accession #: NM\_002309.2

Coding sequence: 65..673

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	TGGGGCGGGG	AGCCCCCTCC	CCATCACCCC	TGTCAACGCC	ACCTGTGCCA	TACGCCACCC	180
	ATGTCAACAC	AACCTCATGA	ACCAGATCAG	GAGCCAACTG	GCACAGCTCA	ATGGCACTGC	240
	CAATGCCCTC	TTTATTCTCT	ATTACACAGC	CCAGGGGGAG	CCGTTCCCCA	ACAACTGGGA	300
45	CAGCTATGTT	GGCCCAACG	TGAAGGACTT	CCCGCCCTTC	CACGCCAACG	GCACGGAGAA	360
	GGCCAAGCTG	GTGGAGCTGT	ACCGCATAGT	CGTGTAACCT	GGCACTCTCC	TGGGCAACAT	420
	CACCGGGGAC	CAGAAGATCC	TCAACCCAG	TGCCCTCAGC	CTCCACAGCA	AGCTCAAGCG	480
	CACCGCCGAC	ATCCTGGCAG	GCCCTCTTAG	CAACGTGCTG	TGCCGCTGT	GCACCAAGTA	540
	CCAAGTGGGC	CATGTGGACG	TGACCTACGG	CCCTGACACC	TCGGGTAAAG	ATGCTTTCCA	600
50	GAAGAGAGAG	CTGGGCTGTC	AACCTCTGGG	GAAGTATAAG	CAGATCATCG	CCGTGTGGGC	660
	CAGGCGCTTC	TAGCAGGAGG	TCTTGAAGTG	TGCTGTGAAC	CGAGGGATCT	CAGGAGTTGG	720
	GTCCAGATGT	GGGGCGCTGT	CCAAGGGTGG	CTGGGGCCCA	GGGCATCGCT	AAACCCAAAT	780
	GGGGCTCTCT	GGCAGACCCC	GAGGGTGCCCT	GGCCAGTCCA	CTCCACTCTG	GGCTGGGCTG	840
	TGATGAAGCT	GAGCAGAGTG	GAAACTTCCA	TAGGGAGGGA	GCTAGAAGAA	GGTGCCCTCT	900
55	CCTCTGGGAG	ATTGTGGACT	GGGGAGCGTG	GGCTGGACTT	CTGCCTCTAC	TTGTCCCTTT	960
	GGCCCTCTGC	TCACTTTTGT	CAGTGAACAA	ACTACACAAG	TCATCTACAA	GAGCCCTGAC	1020
	CACAGGGTGA	GACAGCAGGG	CCCAGGGGAG	TGGACCAAGC	CCAGCAAAAT	TATCACCATC	1080
	TGTGCTCTTG	CTGCCCTTTA	GGTTGGGACT	TAGGTGGGCC	AGAGGGGCTA	GGATCCCAAA	1140
	GGACTCCTTG	TCCCTTAGAA	GTTTGATGAG	TGGAAGATAG	AGAGGGGCTC	CTGGGATGGA	1200
60	AGGCTGTCTT	CTTTTGAGGA	TGATCAGAGA	ACTTGGGCAT	AGGAACAATC	TGGCAGAAGT	1260
	TTCCAGAAGG	AGGTCACTTG	GCATTCAAGC	TCTTGGGGAG	GCAGAGAAGC	CACCTTCAGG	1320
	CCTGGGAAGG	AAGACACTGG	GAGGAGGAGA	GGCCTGGAAA	GCTTTGGTAG	GTTCTTCGTT	1380
	CTCTTCCCGG	TGATCTTCCC	TGCAGCCTGG	GATGGCCAGG	GTCTGATGGC	TGGACCTGCA	1440
	GCAGGGGTTT	GTGGAGGTGG	GTAGGGCAGG	GGCAGGTTGC	TAAGTCAGGT	GCAGAGGTTT	1500
65	TGAGGGACCC	AGGCTCTTCC	TCTGGGTAAA	GGTCTGTAA	AAGGGGCTGG	GGTAGCTCAG	1560
	AGTAGCAGCT	CACATCTGAG	GCCCTGGGAG	GTCTTGTGAG	GTCAACACAG	GGTACTTGAG	1620
	GGGGACTGGA	GGCGTCTCT	GGTCCCCAGG	GCAAGGGAA	AGCAGAACTT	AGGGTCAGGG	1680
	TCTCAGGGAA	CCCTGAGCTC	CAAGCGTGCT	GTGCGTCTGA	CCTGGCATGA	TTTCTATTTA	1740
	TTATGATATC	CTATTTATAT	TAACCTTATTG	GTGCTTTCAG	TGGCCAAAGT	AATTCCTCTT	1800
70	TTCCCTGGTCC	CTACTCAACA	AAATATGATG	ATGGCTCCCC	ACACAAGCGC	CAGGGCCAGG	1860
	GCTTAGCAGG	GCCTGTCTCT	GAAGTCGACA	ATGTTACAAG	TGGAATAAGC	TTACGGGTGA	1920
	AGCTCAGAGA	AGGTCGGGAT	CTGAGAGAAT	GGGGAGGCCT	GAGTGGGAGT	GGGGGGCCTT	1980
	GCTCAACCCC	CATCCCCTAC	TGTGACTTGC	TTTAGCGTGT	CAGGGTCCAG	GCTGCAGGGG	2040
	CTGGGCCAAT	TTGTGGAGAG	GCCCGGTGCC	TTTCTGTCTT	GCTTCCAGGG	GGCTGGTTCA	2100
75	CACGTGTTCT	GGGGGCCCCA	GCATTGTGTT	GTGAGGGGCA	CTGTTCTCTG	CAGATATTGT	2160
	GCCCCCTGGA	GCAGTGGGCA	AGACAGTCCT	TGTGGCCAC	CCTGTCTCTG	TTTCTGTGTC	2220
	CCATGCTGCG	CTCTGAAATA	GCGCCCTGGA	ACAACCTCTG	CCCTGCACCC	AGCATGTCTC	2280
	GACACAGCAG	GGAAGCTCCT	CCTGTGGCCC	GGACACCCAT	AGACGGTGGG	GGGGGCTTGG	2340
	CTGGGCCAGA	CCCCAGGAAG	GTGGGGTAGA	CTGGGGGAT	CAGCTGCCCA	TTGCTCCCAA	2400
80	GAGGAGGAGA	GGGAGGCTGC	AGAGCCCTGG	GACTCAGACC	AGGAAGCTGT	GGGCCCTCTT	2460
	GCTCCACCCC	CATCCCCTCT	CCACCCATGT	CTGGGCTCCC	AGGCAGGGAA	CCCGATCTCT	2520
	TCCTTTGTGC	TGGGGCCAGG	CGAGTGGAGA	AAOCCCTCTC	AGTCTGAGAG	CAGGGGAGGG	2580
	AAGGAGGCAG	CAGAGTTGGG	GCAGCTGCTC	AGAGCAGTGT	TCTGCTTCTT	TCTCAAAACC	2640
	TGAGCGGGCT	GCCCGCTCTC	AAGTTCTCTC	GACAAGATGA	TGGTACTAAT	TATGGTACTT	2700
	TTCACTCACT	TTGCACCTTT	CCCTGTGCTG	CTCTAAGCAC	TTTACTCTGA	TGGCGCGTGG	2760

	GCAGTGTGCA	GGCAGGTCTCT	GAGGCCTGGG	GTTGGGGTGG	AGGGTGC	CCGGAGTTGT	2820
	CCATCTGTCC	ATCCCAACAG	CAAGACGAGG	ATGTGGCTGT	TGAGATGTGG	GCCACACTCA	2880
	CCCTTGTCCA	GGATGCAGGG	ACTGCCCTCT	CCTTCTGTCT	TCATCCGGCT	TAGCTTGGGG	2940
5	CTGGCTGCTC	TCCCCAGGA	TGGGCTTGA	GAAAGACAAA	CTTGTCTGGA	AACCAGAGTT	3000
	GCTGATTCCA	CCCGGGGGGC	CGGGCTGACT	CGCCCATCAC	CTCATCTCCC	TGTGGACTTG	3060
	GGAGCTCTGT	GCCAGGCCCA	CCTTGGGGCC	CTGGCTCTGA	GTGGCTCTCC	CACCCAGCCT	3120
	GGACTTGGCC	CCATGGGACC	CATCCTCAGT	GCTCCCTCCA	GATCCCGTCC	GGCAGCTTGG	3180
	CGTCCACCCT	GCACAGCATC	ACTGAATCAC	AGAGCCTTTG	CGTGAACAG	CTCTGCCAGG	3240
	CCGGAGCTGT	GTTTTCTCTT	CCCTTTTAT	CTGCTGGTGT	GGACCACACC	TGGGCTTGGC	3300
10	CGGAGGAAGA	GAGAGTTTAC	CAAGAGAGAT	GTCTCCGGGC	CCTTATTAT	TATTTAAACA	3360
	TTTTTTTAAA	AAGCACTGCT	AGTTTACTTG	TCTCTCCTCC	CCATCGTCCC	CATCGTCTC	3420
	CTTGCTCCGT	ACTTGGGGCA	CTTCCACCCT	GACCCAGCCA	GTCCAGCTCT	GCCTTGGCGG	3480
	CTCTCCAGAG	TAGACATAGT	GTGTGGGGTT	GGAGCTCTGG	CACCCGGGGA	GGTAGCATTT	3540
	CCCTGCAGAT	GGTACAGATG	TTCTGCCTT	AGAGTCATCT	CTAGTTCCCC	ACCTCAATCC	3600
15	CGGCATCCAG	CCTTCAGTCT	CGCCACGCTG	CTAGCTCCGT	GGGCCACCGC	TGCGGCTTGA	3660
	GAGGTTTCCC	TCCTTCTCTT	CACTGAAAA	GCACATGGCC	TGGGTGACA	AATTCCTCTT	3720
	TGATGAATGT	ACCGTGTGGG	GATGTTTCAT	ACTGACAGAT	TATTTTATAT	TATTCATGT	3780
	CATATTTAAA	ATATTTTATTT	TTTATACCAA	ATGAATCACT	TTTTTTTTTA	AGAAAAAAA	3840
20	GAGAAATGAA	TAAAGAACT	ACTCTTCG				3868

Seq ID NO: C173 DNA Sequence  
Nucleic Acid Accession #: XM\_097508  
Coding sequence: 44..2788

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30	CACAGAGCTT	CAGCCTGGCC	TCTTCCACCA	CCTGCGCTTC	TTGGAGGAGC	TGCGTCTCTC	180
	TGGGAACCAT	CTCTCACACA	TCCCAGGACA	AGCATTCTCT	GGTCTCTACA	GCCTGAAAT	240
	CCTGATGCTG	CAGAACATTC	AGCTGGGAGG	AATCCCCGCA	GAGGCGCTGT	GGGAGCTGCC	300
	GAGCCTGCAG	TCGCTGCGCC	TAGATGCCAA	CCTCATCTCC	CTGGTCCCGG	AGAGGAGCTT	360
	TGAGGGGCTG	TCCTCCCTCC	GCCACCTCTG	GCTGGACGAC	AATGCATCA	CGGAGATCCC	420
	TGTCAAGGCC	CTCAACAACC	TCCCTGCCCT	CGAGGCCATG	ACCCTGGCCC	TCAACCGCAT	480
35	CAGCCACATC	CCCGCTACG	CGTTCCAGAA	TCTCACCAGC	CTTGTGGTGC	TGCATTGACA	540
	TAAACAACGC	ATCCAGCATC	TGGGGAACCA	CAGCTTCGAG	GGGCTGCACA	ATCTGGAGAC	600
	ACTAGACCTG	AATTATAACA	AGCTGCAGGA	GTTCCTGTG	GCCATCCGGA	CCCTGGGCG	660
	ACTGCAGGAA	CTGGGGTTCC	ATAACAACAA	CATCAAGGCC	ATCCCAGAAA	AGGCCTTCAT	720
	GGGGAACCTT	CTGCTACAGA	CGATACACTT	TTATGATAAC	CCAATCCAGT	TTGTGGGAAG	780
40	ATCGGCACTC	CAGTACCTGC	CTAAACTCCA	CACACTATCT	CTGAATGGTG	CCATGGACAT	840
	CCAGGAGTTT	CCAGATCTCA	AAGGCACCAC	CAGCCTGGAG	ATCCTGACCC	TGACCGCGGC	900
	AGGCATCCGG	CTGCTCCCAT	CGGGGATGTG	CCAACAGCTG	CCCAGGCTCC	GAGTCTTGGA	960
	ACTGTCTCAC	AATCAAAATG	AGGAGCTGCC	CAGCGTCGAC	AGGTGTGAGA	AATTGGAGGA	1020
	AATCGGCTCC	CAACAACAAC	GCATCTGGGA	AATTGGAGCT	GACACCTTCA	GCCAGCTGAG	1080
45	CTCCCTGCAA	GCCTTGGATG	TTAGCTGGAA	CGCCATCCGG	TCCATCCACC	CCGAGGCTTT	1140
	CTCCACCTTG	CATCTCCCTG	TCAAGCTGGA	CCTGACAGAC	AACCAGCTGA	CCACACTGCC	1200
	CCTGGCTGGA	CTTGGGGGCT	TGATGCACT	GAAGCTCAAA	GGGAACCTTG	CTCTCTCCCA	1260
	GGCCTTCTCC	AAGGACAGTT	TCCCAAAACT	GAGGATCCTG	GAGGTGCCCT	ATGCCATACCA	1320
	GTGCTGTCCC	TATGGGATGT	GTGCCAGCTT	CTTCAAGGCC	TCTGGGCACT	GGGAGGCTGA	1380
50	AGACCTTCAC	CTTGATGATG	AGGAGTCTTC	AAAAAGGCC	CTGGGCTTCC	TTGCCAGACA	1440
	AGCAGAGAAC	CACATATGAC	AGGACCTGGA	TGAGCTCCAG	CTGGAGATGG	AGGACTCAAA	1500
	GCCACACCCC	AGTGTCAGT	GTAGCCCTAC	TCCAGGCCCC	TTCAAGCCCT	GTGAGTACCT	1560
	CTTTGAAAGC	TGGGGCATCC	GCCTGGCCGT	GTGGGCCATC	GTGTTGCTCT	CCGTGCTCTG	1620
	CAATGGACTG	GTGCTGTGTA	CCGTGTTCGC	TGGGGGCCCT	GTCCCTCTGC	CCCCGGTCAA	1680
55	GTTTGTGGTA	GGTGGGATGG	CAGGCGCCAA	CACCTTGACT	GGCATTCTCT	GTGGCCTTCT	1740
	AGCCTCAGTC	GATGCCCTGA	CTTTTGTGTA	GTCTCTGAG	TACGGAGCCC	GCTGGGAGAC	1800
	GGGGCTAGGC	TGCCGGGCCA	CTGGCTTCTT	GGCAGTACTT	GGGTGGGAGG	CATCGGTGCT	1860
	GCTGCTCACT	TGGGCGGAG	TGCAGTGAG	CGTCTCGTCT	TCTGTGTGTC	GGGCTATGG	1920
	GAAGTCCCCC	TCCCTGGGCA	GCCTTCGAGC	AGGGGTCTTA	GGCTGCTTGG	CATGGGAGG	1980
60	CTGGGCGGCC	GGCTGGCCCC	TGGCCTCAGT	GGGAGAATAC	GGGGCTTCCC	CATCTGCTCT	2040
	GGCCTACGCG	CCACTGTAGG	GTGAGCCAGC	AGCCCTGGGC	TTCAACGTTG	CCCTGGTGAT	2100
	GATGAATCTC	TTCTGTTTCC	TGGTCTGTGC	CGGTGCTTAC	ATCAAACTGT	ACTGTGACCT	2160
	GCGCGGGGGC	GACTTTGAGG	CGGTGTGGGA	CTGGGCAATG	GTGAGGCAGC	TGGGCTGGCT	2220
	CATCTTCGCA	GACGGGCTCC	TCTACTGTCC	CGTGGCCTTC	CTCAGCTTTG	CCTCCATGCT	2280
65	GGGCTCTTTC	CCTGTCAOGC	CCGAGGCGGT	CAAGTCTGTC	CTGCTGGTGG	TGCTGCCCTC	2340
	GGCTGCTTGC	CTCAACCCAC	TGCTGTACCT	GCTCTTCAAC	CCCCACTTCC	GGGATGACCT	2400
	TGGGCGGCTT	CGGCCCCGCG	CAGGGGACTC	AGGGCCCTTA	GCCTATGCTG	CGGCGGGGGA	2460
	GCTGGAGAAG	AGCTCCTGTG	ATTCTACCCA	GGCCCTGGTA	GCCTTCTCTG	ATGTGGATCT	2520
	CATTCTGAA	GCTTCTGAAG	CTGGGCGGCC	CCCTGGGCTG	GAGACCTATG	GCTTCCCTCT	2580
70	AGTGACCTCT	ATCTCTGTGC	AGCAGCCAGG	GGCCCCCAGG	CTGGAGGGCA	GCCATTGTGT	2640
	AGAGCCAGAG	GGGAACCACT	TTGGGAACCC	CCAACCTTCC	ATGGATGGAG	AATGCTGCTG	2700
	GAGGGCAGAG	GGATCTACGC	CAGCAGTGG	AGGCTTGTCA	GGGGGTGGCG	GCTTTCAGCC	2760
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	TCTTCCCTTT	CCTCTCTCCC	CCTCGGTGAA	TGATGGCTGC	TTCTAAAACA	AATACAACCA	2880
75	AAACTCAGCA	GTGTGATCTA	TAGCAGGATG	GCCCACTCCC	TGGCTCCACT	GATCACCTCT	2940
	CTCCTGTGAC	CATCAACCAAC	GGGTGCTCT	TGGCCTGGCT	TTCCCTTGGC	CTTCTCAGC	3000
	TTCACTTGA	TACTGGGCTT	CTTCTTGTCT	ATGTCTGAAG	CTGTGGACCA	GAGACCTGGA	3060
	CTTTGTCTG	CTTAAGGGAA	ATGAGGGAAG	TAAAGACAGT	GAAGGGGTGG	AGGGTTGATC	3120
	AGGGCAGCT	GGACAGGGAG	ACCTCACAGA	GAAAGGCTTG	GAAGGTGATT	TCCGTTGTGA	3180
80	CTCATGGATA	GGATACAAAA	TGTGTTCCAT	GTACCATTA	TCTTGACATA	TGCCATGCAT	3240
	AAAGACTTCC	TATTAATAA	AGCTTTGGAA	GAG			3273

Seq ID NO: C174 DNA Sequence  
Nucleic Acid Accession #: NM\_130849

Coding sequence: 101..2044

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   GGAGCTGGGG CTGCTTCTGG CTGTGCTGGT GGTGACGGCG ACGCGTCCC CGCTGCTGG 180
   TCTGCTGAGC CTGCTCACTT CTGGCCAGGG CGCTCTGGAT CAAGAGGCTC TGGGCGGCCT 240
   GTTAAATAGC CTGCGGAGCC GTGTGCACTG CACCAACGGG CCGTGTGGAA AGTGCTGTCT 300
10  TGTGGAGGAC GCCCTGGGCC TGGGCGAGCC TGAGGGGTCA GGGCTGCCCC CGGGCCCGGT 360
   CCTGGAGGCC AGGTACGTCG CCGGCTCAG TGCCGCGGCC GTCTGTACC TCAGCAACCC 420
   CGAGGGGACC TGTGAGGACA CTCGGGCTGG CCTCTGGGCC TCTCATGCAG ACCACTCCT 480
   GGCCTTGCTC GAGAGCCCCA AGGCCCTGAC CCGGGGCTG AGCTGGCTGC TGCAGAGGAT 540
   GCAGGCGCGG GCTCGCGGCC AGACCCCAAA GAOGGCTGC GTAGATATCC CTCAGCTGCT 600
15  GGAGGAGGGG GTGGGGGGGG GGGCTCCGGG CAGTGTGGC GGCCTCCTGG CTGCCCTGCT 660
   GGACCATGTC AGGAGCGGGT CTGTCTTCCA CGCTTGCGG AGCCTCAGT ACTTCGTGGA 720
   CTTTGTGTTT CAGCAGCACA GCAGCGAGGT CCCTATGACG CTGGCCGAGC TGTACGCTT 780
   GATGCAAGGC CTGGGGGTGG GCAGGGAGGC CCACAGTGAC CACAGTCATC GGCACAGGG 840
   AGCCAGCAGC CGGACCCCTG TGCCCTCAT CAGCTCCAGC AACAGCTCCA GTGTGTGGGA 900
20  CAOGGTATGC CGGACCTGCA GGGACGTGAT GGCTGCATAT GGACTGTGCG AACAGGCTGG 960
   GGTGACCCCG GAGGCGCTGG CCAACTGAG CCCTGCCCTG CTCCAACAGC AGCTGAGTGG 1020
   AGCCTGCACC TCCAGTCCA GGGCCCCCGT CCAGGACCAG CTCAGCCAGT CAGAGAGTA 1080
   TCTGTAGGCG TCCCTGGCCA CGCTGCTCAT CTGCTCTGCG GCGGTCTTTG GCCTCCTGCT 1140
   GCTGACCTGC ACTGGCTGCA GGGGGGTGCG CCACTACATC CTGCAGACCT TCCTGAGCCT 1200
25  GGCACTGGGT GCACTCACTG GGGACGCTGT CCGTGCATCT AGCCCCAAGG TGTGGGGCT 1260
   GCATACACAC AGCGAAGAGG GCCTCAGCCC ACAGCCCAAC TGGCGCTCC TGGTATGCT 1320
   GGC CGGGCTC TACGCTTCT TCCTGTTTGA GAACCTCTTC AATCTCTGCG TGCCAGGGA 1380
   CCGGAGGAGC CTGGAGGAGC GGCCTTGCGG CCACAGCAGC CATAGCCACG GGGGCCACAG 1440
   CCACGGTGTG TCCCTGCAGC TGGCACCAG CGAGCTCCGG CAGCCCAAGC CCCCCACG 1500
30  GGGCTCCCGC GCAGACTCTG TGGCGGAGGA GAGCCCGGAG CTGCTGAACC CTGAGCCAG 1560
   GAGACTGAGC CCAGAGTTGA GGCTACTGCC CTATATGATC ACTCTGGGCG ACGCGGTGCA 1620
   CAACTTCGCC GACGCGCTGG CCGTGGGCGC CGCCTTCGCG TCCTCTGGA AGACCGGGCT 1680
   GGCCACCTCG CTGGCCGTGT TCTGCCACGA GTTGCCACAC GAGCTGGGGG ACTTCGCCGC 1740
   CTGTCTGCAC GCGGGCTGT CCGTGCGCCA AGCACTGTCT GTGAACCTGG CCTCCGCGCT 1800
35  CACGGCTTTC GCTGCTCTCT ACGTGGCACT CGCGGTGGA GTGAGGAGG AGAGCGAGG 1860
   CTGGATCTCT GCACTGGCCA CCGGCTGTGT CCTCTACGTA GCACTCTGCG ACATGCTCCC 1920
   GCGCATGTTG AAGTACCGG ACCCGCGGCC CTGGCTCTCT TTCTGCTGCG ACACGTTGG 1980
   CCTGCTGGGC GGTGAGCCG TCCTGCTGCT GCTGTCCCTG TACGAGGATG ACATCACTT 2040
   CTGATACCTT GGCCTAGTCC CCACTCTTTC ACTTAAGATC CCACCTCA CAAACCTACA 2100
40  CCGCAAAAC CAGAAGCCCC TATAGAGGCC CCAGTCCCAA CTCCAGTAAA GACACTCTTG 2160
   TCCTTGGAAA AAAAAAAAAA AAAAAAAAAA AA 2192
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Seq ID NO: C175 DNA Sequence

Nucleic Acid Accession #: NM\_018971

Coding sequence: 1..1128

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   TGCTGCGCG ACGGGCTGCG CGCGCTCGCC TGCCCTCCCG CCGTCATGCT GCGCGCGCG 240
   GTGCGGCGCG CGCGCGCGCG GCGCGCGCG GCGCGCTGCG GCTGCAAGCT GCTCGCCTTC 300
   CTGGCGCGCG TCTTCTGCTT CCAACCGGCC TTCTGTGTC TGGCGGTGGG GCTCACCGCG 360
55  TACCTGGCCA TCGCGCACCA CCGCTTCTAT GCAGAGCGCC TGGCGGCTG GCGGTGCGCC 420
   GGCATGCTGG TGTGCGCCCG CTGGGCGCTG GCGCTGCGCG CGGCTTCCC GCCAGTCTG 480
   GACGGCGGTG GCGACGACGA GGCAGCGCGG TGCGCCCTG AGCAGCGGCG GAGCGCGCG 540
   CCGGCGCGCG TGGGCTTCTT GCTGCTGCTG GCGGTGCTG TGGGCGCCAC GCACCTGCTC 600
   TACCTCCGCC TGCTCTTCTT CATCCACGAC CGCGCAAGA TCGGCGCCCG GCGCTGCTG 660
60  CCGCGCTGCA GCCACGACTG GACCTTCCAC GCGCGGCGCG CCACCGGCGA GCGCGCGCG 720
   AACTGGAAGC CGGCTTCTG CCGCGGCGCG ACGCGCGCG CGCTTGTGG CATCGGCGCG 780
   GCAGGGCGCG GCGCGCGCG GCGCGCGCTC CTGCTGCTG AAGAATTCAA GACGGAGAAG 840
   AGGCTGTGCA AGATGTTCTA CCGCTGCTG CTGCTCTTCC TGCTCTCTG GGGGCCCTAC 900
   GTGCTGGCCA GCTACCTGCG GGTCTGCTG CCGCGCGCG CCGTCCCGCA GCGCTACCTG 960
65  ACGGCTTCCG TGTGGCTGAC CTTCGCGCAG GCGCGCATCA ACCCGTCTG GTGCTCTCT 1020
   TTCAACAGCG AGCTGAGGGA CTGCTCAGG GCCAGTTCC CTGCTGCCA GAGCCCCCG 1080
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Seq ID NO: C176 DNA Sequence

Nucleic Acid Accession #: NM\_005631

Coding sequence: 290..2653

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   GCGAGGGGCG CGGGCGCGCG GGAGCGTCCG GGGGGGCGCG GCGCGGATT CTCTGGGCGC 180
   ACAGGTGCGC TGAGCGCGCT CCGCGGCGCG CGAGGTGCTG CTGTGCGCG GGGGCTCCG 240
   AGGAGCAGGC GGGGCGCGCG GGGCTTTTGC TGAGTTGGCG GGGTTGGCCA TGGCCGCTGC 300
80  CCGCCAGCGC CGGGGCGCG AGCTCCCGCT CCTGGGGCTG CTGCTGCTGC TGCTGTGCG 360
   GGACCCGGGG CGGGGCGCG CCTCGAGCGG GAACGCGACC GGGCTTGGG CTGGAGCGC 420
   GGGCGGAGC GCGAGGAGGA GCGCGCGGT GACTGGCCCT CCGCGCGCG TGAGCCACTG 480
   CCGCGCGGCT GCGCCCTGCG AGCGCTGCG CTACCACTG TGCTTGGCT CCGTGTCTGC 540
   CTACGGGCGC ACCTCCACAC TGCTGGCGCG AGACTGGAC TCCAGGAGG AAGCGCACGG 600
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5	CAAGCTCGTG	CTCTGGTCGG	GCCTCCGGAA	TGCCCCCGCG	TGCTGGGCAG	TGATCCAGCC	660
	CCTGCTGTGT	GCCGTATACA	TGCCCAAGTG	TGAGAATGAC	CGGGTGGAGC	TGCCCAGCCG	720
	TACCCCTCTGC	CAGGCCACCC	GAGGCCCTTG	TGCCATOGTG	GAGAGGGAGC	GGGGCTGGCC	780
	TGACTTCTCT	CGCTGCACTC	CTGACCCGCTT	CCCTGAAGGC	TGCACGAATG	AGGTGCAGAA	840
	CATCAAGTTC	AACAGTTCAG	GCCAGTGCGA	AGTGCCCTTG	GTTCGGACAG	ACAACCCCAA	900
	GAGCTGGTAC	GAGGACGTGG	AGGGCTGCGG	CATCCAGTGC	CAGAACCCGC	TCCTTCACAGA	960
	GGCTGAGCAC	CAGGACATGC	ACAGCTACAT	CGCGGCCCTTC	GGGGCCGTCA	CGGGCCTCTG	1020
	CACGCTCTTC	ACCCTGGCCA	CATTCTGGGC	TGACTGGCGG	AATCTGAATC	GCTACCCCTGC	1080
	TGTTATTCTC	TTCTAGCTCA	ATGCGTGCTT	CTTTGTGGGC	AGCATTGGCT	GGCTGGCCCA	1140
10	GTTCATGAT	GGTGCCCGCC	GAGAGATCGT	CTGCCGTGCA	GATGGCACCA	TGAGGCTTGG	1200
	GGAGCCCAAC	TCCAATGAGA	CTCTGTCTTG	CGTCATCATC	TTTGTCTATG	TGTACTACGC	1260
	CCTGATGGCT	GGTGTGGTTT	GGTTGTGGT	CCTCACCCTAT	GCCTGGCACA	CTTCCTTCAA	1320
	AGCCCTGGGC	ACCACCTACC	AGCCTCTCTC	GGCAAGACC	TCCTACTTCC	ACCTGCTCAC	1380
	CTGGTCACTC	CCCTTTGTCC	TCAGTGTGGC	AATCCTTGCT	GTGGCCGAGG	TGGATGGGGA	1440
15	CTCTGTGAGT	GGCATTTGTT	TTGTGGGCTA	CAAGAACTAC	CGATACCGTG	CGGGCTTCGT	1500
	GCTGGCCCCA	ATCGGCCCTGG	TGCTCATCGT	GGGAGGCTAC	TTCTCTATCC	GAGGAGTCAT	1560
	GACTCTGTTC	TCCATCAAGA	GCAACCACCC	CGGGCTGCTG	AGTGAGAAGG	CTGCCAGCAA	1620
	GATCAACGAG	ACCATGCTGC	GCTTGGGCAT	TTTGTGGCTC	CTGGCCCTTG	GCTTTGTGCT	1680
	CATTACCTTC	AGCTGCCACT	TCTACGACTT	CTTCAACCAAG	GCTGAGTGGG	AGCGCAGCTT	1740
20	CGGGACTAT	TGCTATGTG	AGGCCAATGT	GACCATCGGG	CTGCCACCA	AGCAGCCCAT	1800
	CCCTGACTGT	GAGATCAAGA	ATCGCCCGAG	CCTTCTGGTG	GAGAAGATCA	ACCTGTTTGC	1860
	CATGTTTGA	ACTGGCATCG	CCATGAGCAC	CTGGGTCTGG	ACCAAGGCCA	CGCTGCTCAT	1920
	CTGGAGGGCT	ACCTGTGTCA	GGTTGACTGG	GCAGAGTGAC	GATGAGCCAA	AGCGGATCAA	1980
	GAAGAGCAAG	ATGATTGCCA	AGGCCCTTCT	TAAGCGGCAC	GAGCTCTCTG	AGAACCCAGG	2040
25	CCAGGAGCTG	CTCTTCAGCA	TGCACACTGT	GTCCCAAGAC	GGGCCCGTGG	CGGGCTTGGC	2100
	CTTTGACCTC	AATGAGCCCT	CAGCTGATGT	CTCCTCTGCC	TGGGCCCCAGC	ATGTACACCA	2160
	GATGGTGGCT	CGGAGAGGAG	CCATCTGCTC	CCAGGATATT	TCTGTACCC	CTGTGGCAAC	2220
	TCCAGTGCCC	CCAGAGGAAC	AAGCCAACCT	GTGGCTGGTT	GAGGCAGAGA	TCTCCCCAGA	2280
	GCTGCAGAA	CGCCTGGGCC	GGAAGAAGAA	GAGGAGGAAG	AGGAAGAAGG	AGGTGTGCCC	2340
30	GCTGGGCGCG	CGCCCTGAGC	TTCACCCGCC	TGCCCTGGCC	CCAGTACCA	TTCCTGACT	2400
	GCCTCAGCTG	CCCCCGCAGA	AATGCCCTGGT	GGCTGCAGGT	GCCTGGGGAG	CTGGGACTC	2460
	TTGCCGACAG	GGAGCGTGGA	CCCTGGTCTC	CAACCCATTC	TGCCCAGAGC	CCAGTCCCCC	2520
	TCAGGATCCA	TTTCTGCCCA	GTGCACCGGC	CCCGCTGGCA	TGGGCTCATG	GCCGCCGACA	2580
	GGGCCTGGGG	CCATTACACT	CCGCAACCAA	CCTGATGGAC	ACAGAACTCA	TGGATGCAGA	2640
35	CTCGGACTTC	TGAGCGTGCA	GAGCAGGACC	TGGGACAGGA	AAGAGAGGAA	CCAATACCTT	2700
	CAAGGCTCTT	CTTCTCTACC	GAGCATGCTT	CCCTAGGATC	CCGTCTTCCA	GAGAACCTGT	2760
	GGGCTGACTG	CCCTCCGAAG	AGAGTTCTGG	ATGTCTGGCT	CAAGCAGCA	GGAGCTGTGG	2820
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	GTCTCTGTTT	CTGCCCTGCC	AGCTGCAGCC	TGGTTGGCAG	CATCTGCTCC	ATCGGGGCAG	2940
40	GGGGATATGC	TGAGCTGTGG	TGGGGCAGGA	ACGGTGAGGG	CAGAGGTGAC	AGTTCCACGA	3000
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45	AACCCATCTT	TTGTTCTCCT	ATATCTCTCT	TCTCTGTTC	CATTTCAGTT	CAGTTTCAGC	3300
	GGTGCCAAAC	TCTTTTGGTT	TCCTTTTGT	TGATGAGGAC	CCAGAGTGC	TGCACACACT	3360
	CACCTCTAAC	CCCCCTCCCT	CGTGTCTGGG	CCCCATCTCC	ACAGGAGAGA	CTGGTTCGGC	3420
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50	CTGGGAAGCT	TGAGCTAGCTT	CAGCCAGGCA	AGAAAGCTTC	CTTCAACCTG	CATAGCCGGT	3600
	GGGTGAGGAG	ATTCCCACTT	TCCATAGCCT	CCAAACATGT	TCCCAAGGCC	CCACTTTCAA	3660
	GAATCAGACA	GCAGGAAGCC	ATAGATGCTG	GCTGGGTTC	AGGTTATGGG	GAGAAGAAAT	3720
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Seq ID NO: C177 DNA Sequence  
Nucleic Acid Accession #: AK094595  
Coding sequence: 1..2853

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65	AAGAACAGC	CTGTGGAGCT	CGCTGCGCG	GCCTTCCCG	CCACACAGAT	CTACTTCAAG	240
	TGCAACGCG	AGTGGGTGAG	CCAGAACGAC	CACGTACAC	AGGAAGGCCT	GGATGAGGCC	300
	ACCTTGGGG	CGCGGGGCGG	CCTGCGGGTG	CGCGAGGTGC	AGATCGAGGT	GTGCGGGCAG	360
	CAGGTGGAGG	AGCTCTTTGG	GCTGGAGGAT	TACTGCTGCC	AGTGCTGGC	CTGGAGCTCC	420
	GCGGGCACCA	CCAAGAGTGG	CCGAGCCTAC	GTCCGATCG	CCTACCTGCG	CAAGAACTTC	480
70	GATCAGGAGC	CTCTGGGCAA	GGAGGTGCC	CTGGACCATG	AGGTTCTCCT	GCAGTGGCGG	540
	CGCGCGGAGG	GGGTGCTGCT	GGCCGAGGTG	GAATGGCTCA	AGAAAGAGGA	TGTATCGAC	600
	CCACCCGAG	ACACCAACTT	CCTGCTCACC	ATGACACCA	ACCTCATCAT	CCGCCAGGCC	660
	CGCTGTGCG	ACACTGCCAA	CTATACCTGC	GTGGCCAAGA	ACATGCTGGC	CAACCGCCGG	720
	AGCACCACTG	CCACCGTCT	CGTCTACGTC	AATGGCGGCT	GGTCCAGCTG	GGCAGAGTGG	780
75	TCACCTGCT	CCACCGCTG	TGGCCGAGGC	TGGCAGAGC	GCACCGGAC	CTGCACCAAC	840
	CCCGCTCCAC	TCAACGGAGG	GGCTTCTGC	GAGGGCCAGG	CATTCCAGAA	GACCGCTGCG	900
	ACCACCACT	GGCCAGTGA	TGGGGGCTGG	ACGGAGTGA	GCAAGGTGTC	AGCCTGCAGC	960
	ACTGAGTGTG	CCCATGTGGC	TAGCCGCGAG	TGCATGGCGC	CCCCACCCCA	GAACGGAGGC	1020
	CGTGAAGTCA	CGGGGACGCT	GCTCGACTCT	AAGAACTGCA	CAGATGGGCT	GTGCATGCAA	1080
80	AATAAGAA	CTCTAGGCGA	CCCCAACAGC	CACCTGCTGG	AGGCCTCAGG	GGATGCGGGG	1140
	CTGTATGCGG	GGCTCGTGGT	GGCCATCTTC	GTGGTCTGTC	CAATCTCTAT	GGCGGTGGGG	1200
	GTGGTGGTGT	ACCGCCGCAA	CTGCCGTGAC	TTGACACAG	ACATCACTGA	CTCATCTGCT	1260
	GCCTTGACTG	GTGGTTTCCA	CCCCGTCAAC	TTTAAGACGG	CAAGGCCGAC	CAACCGGAG	1320
	CTCTACACCC	CCTCTGTGCC	TCCTGACTTG	ACAGCCAGCG	CCGGCATCTA	CCGCGGACCC	1380

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Seq ID NO: C178 DNA Sequence  
 Nucleic Acid Accession #: NM\_004625  
 Coding sequence: 310..1359

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75 Seq ID NO: C179 DNA Sequence OBR3  
 Nucleic Acid Accession #: NM\_003786  
 Coding sequence: 71..4654

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Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM\_004626  
Coding sequence: 124..1188

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Nucleic Acid Accession #: NM\_031866  
Coding sequence: 6..2090

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Nucleic Acid Accession #: NM\_006549.2

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	GAATTGTAGT	CAGGAAAACA	GAAAGGGCTT	GAAATTTAAT	AAGTGTCTGT	GGAAGGGGAT	3240
	TTTCCAAGCC	TGGAGGGGTA	TTGAGCAGCT	GTGGTGGGGA	AACATTTCTC	CTGAAAGACT	3300
15	GAACGTGTTT	CTTCATGACA	GCTGCTCAAA	GCAGGTTTCT	GAGATAGCTG	ACCGAGCTCT	3360
	GGTAAATCTC	TTGTTCAAAT	TACGAAAAC	TCAGGGTGAA	ATCCTATGCT	TTCATGTACA	3420
	TTACATGGCT	TAAAGATTAA	CAAAAACATT	TTTCAAGTCT	CTAAGTAGAG	TGAAGTCTAG	3480
	AGCACAGTAG	TTGACAAAAC	ATTTAGAGCT	TCCAGGATAT	ATTTACAGC	TTGAGGCATG	3540
	TGATCAGTTA	GAGCCGATGA	AACCTATGCC	CGCCTGTATA	TATATTAGCA	GCTTAGCTAG	3600
20	TTCATAACTC	GTATATTCTA	AAGACTGCTA	AGGTTTGTGT	TTTATTTTAA	ATCCTAGCTG	3660
	ATTGTTGTGG	TCAATGAAT	ACCCAGTTTC	TGAAGGGCCA	GGTGGGAAAT	GCTTTTACTG	3720
	GACCAACACA	CAATATGATCA	TCCAGAGGAT	CTGAGCTTCC	CTAGACTCCA	CACAATAACC	3780
	TTGGGGCACC	CTTTTAGAGA	AGACTGTTGA	AACCCACAGC	ACTCGTTGGG	GTATGAGGAA	3840
	ACCAGGGCTT	GACACAGGAA	GTTCCCTTTT	GTAGCTAAAA	GTCCAGAAAG	AAAGGGTTCA	3900
25	TCTTTTGTAC	TTCCAACATGA	TATTGGGAAG	TTTGGTTGAG	GTTCAGTGT	GACTCCTTCC	3960
	AGAGCCACAG	GTAGGGGAGT	GTGAAGTTGA	GGGGGAGGAA	AGCTGGAAGG	ACTCTGCCTT	4020
	GGGAGATTCC	CAGCTCTGCT	TTCCAGCGCT	TGGTGGAAAT	TGGCTGGGG	AAAGACGGCA	4080
	CCGGGAAACT	GTGCTTCCCC	ATTGTTTCCA	TCTGATCAGC	TGTGGTGTGA	GGACTTCTCA	4140
	GACAAAGGCA	ATGCTCTCGT	CCCTGCCCCA	GCCCATTCAT	GGAGCCCTGG	GCTTCTTGG	4200
30	CTTCCATAGA	TCTTAGCTC	TTGACTGTAG	TTTAGCCAGA	CTTGTTTTGC	TATCTTATAA	4260
	GCAGTTCAGA	ATTAGGGAAT	GCTGGTTTGT	AAGAGCAAAG	GACAGGTAGT	CTAGAGAGGG	4320
	TGCTCTGGCC	TGCTGTCTGG	GTCCTTGTAA	CCAGCAGCTT	CCTCTTGCCC	TCTTGGCTTT	4380
	ATGTTTATGG	GAGAGGACTC	AATAGCTCCA	CCCTTCTGG	CACAGATGG	GGCTTGGTTA	4440
	GTTTGCATAA	AGCACCTTGC	AGAGGTTAAA	GCCAGCGGGT	CCCTAGTCTT	AGGCCACGCC	4500
35	TGCTTGTGTG	GGCTCTGGCC	TGGCCTGGTG	GCTGGCCGAG	GGGGCAGCAG	TGCTTAGAGC	4560
	TTCTGACGGG	CTTCTCTTGT	TTACACAGCT	GCATCAGACA	ATGCCATTTT	TCCCCACCAAC	4620
	GGAACTTCTC	ATCTAAGATT	TCTTCCAGGG	AATGCCAGCA	ATCAGGCAGC	ACCCAGCTGT	4680
	GGGGGACGTG	GGGTGGGGGA	GACCCACATT	GATGACTTTT	TTTTTTTCTT	TTAATGAAGA	4740
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	TCGTGACAGG	AAGAGGTGCG	TGTTATGACA	GCTCTTCCAG	TGGGCAAGA	GGAGCCCAT	4920
	AATTTCTTCC	ATTGCTAGCT	CATCTGTGGG	ACCAATTTGG	TGTAAGCAAC	CTGTGGCCTG	4980
	CACTTGTGGC	CTCGAAGGAA	GCACAAACCC	TCCATCCACT	TCCCATTTCC	TCTGCCCTTT	5040
45	TCCACTCCCC	CTGCTCCATC	CACAGGCTGC	CAGTGGCTCC	CAGAAAGGCT	TATTGAGCCC	5100
	CTTGTGACGA	CTTGGGGCTG	CGGAGGCGCT	TCCCTACTGG	TCTGGCCTTT	CCTGAGAGGC	5160
	AGGTCTCCCG	TCTCTAGAGT	CTTCTGGGAA	CAGGAGAAAT	GCCTGTGCAG	GTGGACACAC	5220
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	GAACCATGAC	TCCACTTTCG	TTCCAAGGTG	CTAGGGAAGT	TTGAGGGTAC	GCTGGTTCCC	5340
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50	AATGCCCGAT	GCTTCTGTTT	CATTCCCGAC	CCTTCTACT	ATGCATTTTC	CTTTTATCAG	5460
	GTGTATAAAG	TAAATACATC	TGTTATTATC	ACTAAAAAGT	ACATGAACTT	AAGAGACAAC	5520
	TAAGCCTTTC	GTGTTTTTCC	ACAGGTGTTT	AAGCTTCTCT	GTACAGTTGA	AATAAACAGA	5580
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Seq ID NO: C193 DNA Sequence  
Nucleic Acid Accession #: NM\_018646  
Coding sequence: 217..2394

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	TCCCAAGGAA	CTCGTCAGGA	AGGCAGGAGA	CAGGAGACGG	GACCTCTACA	GGGAGACGGT	120
	GGGCGCGCCC	TTGGGGGGGG	TGATGTGGGC	CCAAGGCTGA	GTCCCGTCTG	GGTCTGGCCT	180
	CGGCCCTCAG	CCCCCAAGGA	GCCGGCCCTA	CACCCATAGG	GTTTGTCACT	GCCCAAGGAG	240
65	AAAGGGCTAA	TTCTCTGCCT	ATGGAGCAAG	TTCTGCAGAT	GGTTCAGAG	ACGGGAGTCC	300
	TGGGCCACGA	CCGAGATGTA	GCAGAACCTG	CTGCAGCAGA	AGAGGATCTG	GGAGTCTCCT	360
	CTCCTTCTAG	CTGCCAAAGA	TAAATGATGT	CAGGCCCTGA	ACAAGTTGCT	CAAGTATGAG	420
	GATTGCAAGG	TGCACACAGG	AGGAGCCATG	GGGGAACAG	CGCTACACAT	AGCAGCCCTC	480
	TATGACAACC	TGGAGGCGCG	CATGGTGTCT	ATGGAGGCTG	CCCGGAGCTG	GGTCTTTGAG	540
70	CCCATGACAT	CTGAGCTCTA	TGAGGGTCTG	ACTGCACTGC	ACATCGCTGT	TGTGAACCA	600
	AACATGAACC	TGGTGGGAGC	CCTGCTTGCC	CGCAGGGCCA	GTGTCTCTGC	CAGAGCCACA	660
	GGCACTGCGT	TCCGCGGTAG	TCCCTGCAAC	CTCATCTACT	TTGGGGAGCA	CCCTTTGTCC	720
	TTTGCTGCGT	GTTGGAACAG	TGAGGAGATC	GTGCGGCTGC	TCATTGAGCA	TGGAGCTGAC	780
	ATCCGGGCCC	AGGACTCCCT	GGGAAACACA	GTGTTACACA	TCTTCATCTT	CCAGCCCAAC	840
75	AAAACTTTTG	CCTGCCAGAT	GTACAACCTG	TTGCTGTCTT	ACGACAGACA	TGGGAGCCAC	900
	CTGCAGCCCC	TGGACCTCGT	GCCCAATCAC	CAGGGTCTCA	CCCTTTTCAA	GCTGGCTGGA	960
	GTGGAGGGTA	ACACTGTGAT	GTTTCAGCAC	CTGATGCAGA	AGCGGAAGCA	CACCCAGTGG	1020
	ACGTATGGAC	CACTGACCTC	GACTCTCTAT	GACCTCACAG	AGATCGACTC	CTCAGGGGAT	1080
	GAGCAGTCCC	TGCTGGAAC	TATCATCACC	ACCAAGAAGC	GGGAGGCTCG	CCAGATCCCTG	1140
80	GACCAAGCCG	CGGTGAAGGA	GCTGGTGAGC	CTCAAGTGGG	AGCGGTACGG	GCGGCGGTAC	1200
	TTCTGCAATG	CTGGTGCAT	ATATCTGCTG	TACATCATCT	GCTTCAACAT	GTGCTGCATC	1260
	TACCGCCCCC	TCAAGCCGAG	GACCAATAAC	CGCACGAGCC	CCCGGGACAA	CACCTCTTAA	1320
	CAGCAGAAGC	TACTTCAGGA	AGCCTACATG	ACCCCTAAGG	ACGATATCCG	GCTGGTCCGG	1380
	GAGCTGGTGA	CTGTCAATGG	GGCTATCATC	ATCCTGCTGG	TAGAGGTTC	AGACATCTTC	1440
	AGAATGGGGG	TCACTCGCTT	CTTTGGACAG	ACCATCCTTG	GGGGCCCAT	CCATGTCTCT	1500

5 ATCATCACTT ATGCTTCAT GGTGCTGGTG ACCATGGTGA TGGGCTCAT CAGTGCCAGC 1560  
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 GCCCGAGGAT TCCAGATGCT AGGCCCCCTT ACCATCATGA TTCAGAAGAT GATTTTGGC 1680  
 GACCTGATGC GATTCTGCTG GCTGATGGCT GTGGTCATCC TGGGCTTTGC TTCAGCCTTC 1740  
 10 TATATCATCT TCCAGACAGA GGACCCCGAG GAGCTAGGCC ACTTCTACGA CTACCCCATG 1800  
 GCGCTGTTCG GCACCTTCGA GCTGTTCTTT ACCATCATCG ATGCCCCAGC CAACTACAAC 1860  
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 CTCATGCTCA ACCTCCTCAT TGCCATGATG GCGACACTC ACTGGCGAGT GGCCCATGAG 1980  
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 15 CTTGCTGCTC TGTGCTGCTG CTCGGGATC TCGGAGCGGG AGTATGGCCT GGGAGACCGC 2100  
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 20 GGGATAATCA ACAGGGTCT GGAGGACGGG GAGAGCTGGG AATATCAGAT CTGACTGCGT 2400  
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 GGCAGAGAA GCCCAGCCA AGCAGGGGG TGGCAGGGG TGAGGAACCT TCCTGTGGCC 2640  
 25 TGCTCATGAC CCTTCGACA GGAGCACTGC ATGTGAGAGC ACTTTAAAAA CAGGACAGCC 2700  
 TGCTTGGGCG CTGCTCTCC ACCCCAGGGT CATAAGTGGG GAGAGAGCCC TTCCCAGGGC 2760  
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 TTTTCGGATC CCTGAAAAA AAAAAAATA AAAAAAATA 2918

Seq ID NO: C194 DNA Sequence  
 Nucleic Acid Accession #: NM\_021910.1  
 Coding sequence: 260..601

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 35 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACACA GGCCCGAGTT TCACCCAGTC 180  
 CCACTCCAC GGTGCAGCTG GGCCTTATCT CTCAGCCAG CGAGATGCCA GCCTTCTGT 240  
 CCCGGGCCAG CGCTCTGACA TGCAGAAGGT GACCTGGGC CTGCTTGTGT TCCTGGCAGG 300  
 CTTTCTGTGC CTGAGGCCCA ATGACCTAGA AGATAAAAC AGTCCTTCT ACTATGACTG 360  
 GCACAGCCTC CAGGTTGGCG GGCTCATCTG CGCTGGGGTT CTGTGGGCCA TGGGCATCAT 420  
 40 CATGCTATG AGTGAGTGA GGAGCTGGG GGAGCAGGCG GGCCGGGGCT GGGGCTCCCC 480  
 TCCCTGACC ACTCAGCTCT CCCCACAGG TGCAAAATGC AAATGCAAGT TTGGCCAGAA 540  
 GTCGGTCCAC CATCCAGGGG AGACTCCACC TCTCATCACC CCCGGCTCAG CCCAAGCTG 600  
 ATGAGGACAG ACCAGCTGAA ATTGGGTGGA GGACCGTTCT CTGTCCCGAG GTCTGTCTC 660  
 TGCACAGAA CTTGAATCCC AGGATGGAAT TCTTCTCTCT CTGCTGGGAC TCCTTTGCTC 720  
 45 GGCAGGGCCT CATCTCACTC CTCGCAAGAG GGTCTCTTTG TTCAATTTT TTTAATCTAA 780  
 AATGATTG TGCTCTGCCA AGCAGCCTGG AGACTTCCTA TGTGTGATT GGGGTGGGCG 840  
 TTGGGGCACC ATGAGAAGGT TGGCGTGCCC TGGAGGCTGA CACAGAGGCT GGCAGTGAGC 900  
 CTGCTGTGTT GGAAAAGCCC ACAGGCTGT TCCCTTGTGG CTGGGACAT GGCACAGGCC 960  
 CGCCCTCTGC CTCCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTAC TAGTAGCCAA 1020  
 50 AAGGAATGAA AGAGAGCTCT AACAGATGG AACATGGAA CATTCCAGTG GACCCCTGGAC 1080  
 CATTCCAGGA AAATCTGGAG ATAGGATCGT CCGCTATGA TGGAAAGTT CAGACAGTTT 1140  
 ATAATAGTAA GCCCTGTGA CCCTCTCACT TACCCGAGA CCTCACTTTA TTACAAGATC 1200  
 TTTCCAAATA CCCAAATATC CTGCAAGCC CGTTAAATA TTCCCTATGC TACCCTTAAT 1260  
 AACATACAT GACCAATAG TGTGAGAACT TCCAACAAGC CTCAAAGTCC CTGTGAGACTC 1320  
 55 CCCAATACCT AATAAGGCAT GCGAAATGTT CTCATGAAC ACCCCACAAC ACGCTTAAAA 1380  
 CTCAAAACAC CCAAAATAT CTCTCCAAT GTCTTGAGAC ATGAACCCAA AAAGAGACCC 1440  
 ACAATAAAT COTGACTTGT CCCCTC 1466

Seq ID NO: C195 DNA Sequence  
 Nucleic Acid Accession #: NM\_005971.2  
 Coding sequence: 176..439

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 65 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACACA GGCCCGAGTT CTGACATGCA 180  
 GAAGGTGACC CTGGGCTGCG TTGTGTTCTT GGCAGGCTTT CTGTCTCTGG ACCCAATGA 240  
 CCTAGAAGAT AAAACAGTC CTTTCTACTA TGACTGGCAC AGCCTCCAGG TTGGCGGGCT 300  
 70 CATCTGCGCT GGGGTTCTGT GCGCCATGGG CATCATCATC GTCATGAGTG CAAAATGCAA 360  
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 AGGCTCAGCC CAAAGCTGAT GAGGACAGAC CAGCTGAAAT TGGGTGGAGG ACGTCTCTCT 480  
 GTCCCGAGGT CCGTCTCTG CACAGAACT TGAACCTCAG GATGGAATTC TTCTCTCTCT 540  
 GCTGGGACTC CTTTGCATGG CAGGGCTCA TCTCACTCT CGCAAGAGGG TCTCTTGT 600  
 75 CAATTTTTT TAATCTAAAA TGATTGTGCC TCTGCCAAG CAGCCTGGAG ACTTCTATG 660  
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 CAGAGGCTGG CACTGAGCCT GCTGTGTGG AAAAGCCAC AGGCCTGTTT CCTTGTGGCT 780  
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 GGATTTACTA GTAGCCAAA GGAATGAAAG AGAGCTCTAA CCAGATGGAA CACTGGAACA 900  
 80 TTCCAGTGA CCCGAGACA TTCCAGGAAA ACTGGGACAT AGGATCGTCC CGCTATGATG 960  
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 TCACTTTAT ACAAATCTT TCCAAATACC CAAATATCCC TGCAAGCCCG TTAATAAAT 1080  
 CCCTATGCTA CCCTTAATAA CATACAATGA CCACATAGT TGAGAACTTC CAACAAGCCT 1140  
 CAAAGTCTCC TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTTCT CATGAACACT 1200  
 CCCACAACAC GCCTAAAAT CAAAACACCC AAAAAATATCT CCTCAATGT CCTGAGACAT 1260



GAACCCAAAA AGAGACCCAC AATAAACTCG TGACTTGTC CCTC

1304

Seq ID NO: C196 DNA Sequence  
 Nucleic Acid Accession #: NM\_004961.2  
 Coding sequence: 55..1575

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CCTCAGACTG	AATCAAGAA	TGAAGCCTCT	TCCCGTGATG	TTGTCTATGG	CCCCAGCCCC	180
CAGCCTCTGG	AAATCAGCT	CCTCTCTGAG	GAACAAAGT	CAACTGAGAC	TGAGACTGGG	240
AGCAGAGTTG	GCAAACTGCC	AGAAGCCTCT	CGCATCTCTG	ACACTATCCT	GAGTAATTAT	300
GACCACAAC	TGCGCCCTGG	CATTGGAGAG	AAGCCCACTG	TGGTCACTGT	TGAGATCGCC	360
GTCAACAGCT	TTGGTCTCT	CTCTATCCTA	GACATGGAAT	ACACCATGGA	CATCATCTTC	420
TCCAGACCT	GGTACGACGA	ACGCTCTGT	TACAACGACA	CCTTTGAGTC	TCTGTCTCTG	480
AATGGCAATG	TGGTGAGCCA	GCTATGGATC	CCGACACCT	TTTTTAGGAA	TTCTAAGAGG	540
ACCCACGAGC	ATGAGATCAC	CATGCCCAAC	CAGATGGTCC	GCATCTACAA	GGATGGCAAG	600
GTGTTGTACA	CAATTAGGAT	GACCAATTGAT	GCGGATGCT	CACCTCCAT	GCTCAGATTT	660
CCAATGGATT	CTCCTCTTG	CCCTCTATCT	TTCTCTAGCT	TTTCTATCC	TGAGAAATGAG	720
ATGATCTACA	AGTGGGAAAA	TTTCAAGCTT	GAAATCAATG	AGAAGAACTC	CTGGAAGCTC	780
TTCCAGTTTG	ATTTTACAGG	AGTGAGCAAC	AAAACCTGAA	TAATCACAA	CCCAGTTGGT	840
GACTTCATGG	TCATGACGAT	TTTCTTCAAT	GTGAGCAGCG	GGTTTGGCTA	TGTTGCCCTT	900
CAAAACTATG	TCCCTTCTTC	CGTGACCACG	ATGCTCTCCT	GGTTTCTCTT	TTGGATCAAG	960
ACAGAGCTG	CTCCAGCCCG	GACCTCTCTA	GGGATCACCT	CTGTTCTGAC	CATGACCAAG	1020
TTGGGACACT	TTTCTGCTAA	GAATTTCCCG	CGTGTCTCCT	ATATCACAGC	CTTGGATTTC	1080
TATATCGCCA	CTGCTCTCGT	CTTCTGCTTC	TGCGCTCTGT	TGGAGTTTGG	TGTGCTCAAC	1140
TTCTGTATCT	ACAACCCAGC	AAAAGCCCAT	GCTTCTCTTA	AACTCCGCCA	TCCTCGTATC	1200
AATAGCCGCT	CCCATGCCCG	TACCCGTGCA	CGTTCGCCAG	CCTGTGCCCG	CCAACATCAG	1260
GAAGCTTTTG	TGTGCGAGAT	TGTCAACCAT	GAGGGAAGTG	ATGGAGAGGA	CGCCCGCTCT	1320
TGCTCAGCCC	AGCAGCCCCC	TAGCCCAAGT	AGCCCTGAGG	GTCCCGCAG	CCTCTGCTCC	1380
AAGCTGGGCT	GCTGTGAGTG	GTCAAGCGT	TTTAAGAAGT	ACTTCTGCAT	GGTCCCGAT	1440
TGTGAGGGCA	GTACCTGGCA	GCAGGGCCGC	CTCTGCATCC	ATGTCTACCG	CCTGGATAAC	1500
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GGTCCAGGCC	CCTTGCCAA	GGAGTTGGGG	GAAAGCAGCA	GCAGCAGCAG	GAGCGACTAG	1680
AGTTTCTTCT	CCCCCATCTC	CCAAACAGAA	GCTTGACAG	GGTTTGTCTT	TGCTGCCCT	1740
CTCCCTTACC	TGGCCCATTC	ACTGAGTCTT	CTCAGCAGAC	CAITTCAAAT	TATTAATAAA	1800
TGGGCCACCT	CCCTCTTCTT	CAAGGAGCAT	CGTGATGCT	CAGTGTTCAA	AACCACAGCC	1860
ACTTAGTGAT	CAGCTCCCTA	AAACCATGCC	TAAGTACAGG	CGGATTAGCT	ATCTTCCAA	1920
AATGCTGACC	ACCAGACAAT	TACTGCAATT	TTCCAGAAGC	CCACTATTGC	CTTTGTAGTG	1980
CTTTGGGCTT	CCCTTGGGCC	TCAGCCTCAA	AGTGCACOGA	CTAGTTGCTT	GCCTATACCT	2040
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CAGTGGCAAT	ATCCCTTTAG	GAAGAGGGGG	GGGCAGCAAG	AGAGCCTATT	TGGGACAGCA	2220
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TACTCCCTGC	TTTATATGCC	ACCCCTCTTC	TTCTCTTTGA	CCCTGTGAC	TCTTCTCTGA	2400
ACTTTCCTAG	TGACTTCCCC	TAGCCCTGAC	CCAGGCACTA	GGCCTTGGTG	ACTTCTCTGG	2460
GCCAAGAAAC	TAAGGAAACT	CGGCTTTGCA	ACAGGCATTA	CTCGCCATTG	ATTGGTGCCC	2520
ACCCAGGGCA	CACGTGCGGA	GTTCTATCAC	TTGCTTGACC	CCTGGACCCA	TAAACCAAGT	2580
CACGTGTATA	CCCGGGGCAC	TCTAACCATC	ACAATCAATC	AATCAAAATC	CCTTAAATTT	2640
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GGCCTGAGGT	GCTCAGACTG	CCCCCAAGAT	CAAATCTCTC	CTGGCTGTAG	TAACCCAGTG	3000
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TGTTGGGGGG	TGGATAGGGT	GGGGTCTCCA	TCTACTTTT	GTCAACCTCA	TCTGAAATGG	3120
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Seq ID NO: C197 DNA Sequence  
 Nucleic Acid Accession #: NM\_021984.1  
 Coding sequence: 572..1753

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GTGTAAGAA	AGCCAAATCA	AGGACCGGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
CACCTGCCCT	CAGCAAGGCG	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGGACC	300
TCAGACTGAA	TCAAGAAATG	AAGCCTCTTC	CGTGATGTT	GTCTATGGCC	CCAGCCCCA	360
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CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAATTATGA	480
CCACAACCTG	CGCCCTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTGG	AGATCTCCGT	540
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TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
CCACAGGAT	GAGATCAACA	TGCCCAACCA	GATGGTCCGC	ATCTACAAGG	ATGGCAAGGT	780
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AATGATATCT	CACCTCTGCC	CTCTATCTTT	CTCTAGCTTT	TCCTATCCTG	AGAATGAGAT	900
GATCTACAAG	TGGGAAAAAT	TCAAGCTTGA	AATCAATGAG	AAGAATCCT	GGAGCTCTT	960

	CCAGTTGGAT	TTTACAGGAT	TGAGCAACAA	AACTGAAATA	ATCACAACCC	CAGTTGGTGA	1020
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	AAACTATGTC	CCTTCTTCGG	TGACCACGAT	GCTCTCTCGG	GTTTCCTTTT	GGATCAAGAC	1140
5	AGAGTCTGCT	CCAGCCCGGA	CCTCTCTAGG	GATCACTCTT	GTTCTGACCA	TGACCACGTT	1200
	GGGCACCTTT	TCTCGTAAGA	ATTTCCCGCG	TGTCTCCTAT	ATCAGAGCCT	TGGATTCTTA	1260
	TATGCCATC	TGCTTGTCT	TCTGCTTCTG	CGCTCTGTG	GAGTTTGTG	TGCTCAACTT	1320
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	CCCTTACCTG	GCCCATTCAC	TGAGTTTCTT	CAGCAGACCA	TTTCAAATTA	TTAATAAATG	1980
	GGCCACCTCC	CTCTTCTTCA	AGGAGCATCC	GTGATGCTCA	GTGTTCAAAA	CCACAGCCAC	2040
20	TAGTGTATCA	GCTCCCTAAA	ACCATGCCTA	AGTACAGGCG	GATTAGCTAT	CTTCCAAACAA	2100
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	TTCCGCCGAC	TTCTGGCCTC	AGCCTCAAAG	TGCACCGACT	AGTTGCTTGC	CTATACCTGG	2220
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25	CTGGCATTAT	CCCTTTAGGA	AGAGGGGGGG	GCAGCAAGAG	AGCCTATTG	GGACAGCATT	2400
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	CTGTTATACC	CGGGGCACTC	TAACCATCAC	AATCAATCAA	TCAAATTCCT	TTAAATTTGT	2820
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Seq ID NO: C198 DNA Sequence

Nucleic Acid Accession #: NM\_021987.1

Coding sequence: 572..1657

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	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
	CATGCTCTCC	CAGCAAGGCC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGAGCC	300
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55	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
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20 Seq ID NO: C199 DNA Sequence  
 Nucleic Acid Accession #: NM\_021990.1  
 Coding sequence: 1309..2490

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10 Seq ID NO: C200 DNA Sequence  
 Nucleic Acid Accession #: NM\_021819.1  
 Coding sequence: 39..1619

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50 Seq ID NO: C201 DNA Sequence  
 Nucleic Acid Accession #: XM\_117036.1  
 Coding sequence: 25..495

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70 Seq ID NO: C202 DNA Sequence  
 Nucleic Acid Accession #: XM\_167803.2  
 Coding sequence: 1162..1488

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CGTGA AAAAG T 1511

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Seq ID NO: C203 DNA Sequence  
Nucleic Acid Accession #: NM\_024780.1  
Coding sequence: 31..1023

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ACCTTCATTG GCCCAGGACAT CTACCGGCTC CTTCTGATGG ATTTTGTGTT CTCTTTAGTC 240
AATTCCTTCC TGGGGGAGIT TCTGAGGAGA ATCATTGGGA TGCAACTGAT CACAAGTCTT 300
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Seq ID NO: C204 Protein Sequence  
Protein Accession #: Eos sequence

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Seq ID NO: C205 DNA Sequence  
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 Coding sequence: 397..1680

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Seq ID NO: C206 DNA Sequence  
 Nucleic Acid Accession #: NM\_025257.1  
 Coding sequence: 1..2139

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Seq ID NO: C207 DNA Sequence  
 Nucleic Acid Accession #: NM\_016180.1  
 Coding sequence: 26..1618

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Seq ID NO: C208 DNA Sequence  
 Nucleic Acid Accession #: NM\_003273.1  
 Coding sequence: 255..2024

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Seq ID NO: C209 DNA Sequence  
Nucleic Acid Accession #: NM\_015720.1  
Coding sequence: 21..1838

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GCGGGGCCCT CAAAGCGCGG GGGAGCTGGG GGGCGCTCAT GGGGGGCAAG GGGGACCCCG 1800
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CCCGCGCTCA CCGGCGCGCC CCGCGCCTG GCGCTGGGG GGGCTCTCTT CCGCTTCC 1980
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AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2269

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Seq ID NO: C210 DNA Sequence  
Nucleic Acid Accession #: NM\_001197.3  
Coding sequence: 61..543

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5 CTCTGGAAC CCCGACCAT GGAGTTCTT GGCATGACTG ACTCTGAAGA GGACCTGGAC 180  
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 15 GAATAGATTC CGAGGAGCAG GAGTGCTCAA TAAATGTG GTTCCAGCA AAAAAAAAAA 960  
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Seq ID NO: C211 DNA Sequence  
 Nucleic Acid Accession #: AF272357  
 Coding sequence: 83..1060

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 CCGGATCTCG CCTGGGACCT AGCGGCTGGC ACAGAGCGCG GAGATGTACC ACTACCAGCA 840  
 CCAACGGCAA CAGATGCTGT GCCTGGAGCG GCATAAGAG CACCCCAAGG AGCTGGACAC 900  
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 GCCCTGCGC GCGCCAGCT CACCGCCTGC ACTGCCATGA CCTGGAGGCA GACAGACGCG 1080  
 CACCTGTCTC CCGACCTCGA GCGCCCGGGG GAGGGGCGAG GCCTGGAGCT TCCCACTAAA 1140  
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 TGCCAGGGAG ACCCCCGAAC CTTTGTGCCA GGACACCTCC TGGTCCCTCG CACTCTCCT 1260  
 45 GTTCGGTTTA GACCCCAAAA CTGGAGGGGG CATGGAGAAC CGTAGAGCGC AGGAACGGGT 1320  
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Seq ID NO: C212 DNA Sequence  
 Nucleic Acid Accession #: NM\_004445.1  
 Coding sequence: 799..3819

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 TGCCTGGAGG GCTTCTACCG GGCAGTTC GACCCACCA AGGCCCTCT CACTGTCTCT 1860  
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Seq ID NO: C213 DNA Sequence  
Nucleic Acid Accession #: XM\_043340.4  
Coding sequence: 195..1067

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Seq ID NO: C214 DNA Sequence  
Nucleic Acid Accession #: NM\_002151.1  
Coding sequence: 246..1499

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TGCCACGGCC TGGAGACTGA CCGAGCCCG GCACCTACCTC GAGGCTCCGC CCCACCTGCC 180
TGGACCCAGG GGTCCACACC TGGCCACAGA GGTGAGCCAG GGAATCATTA ACAAGAGGCA 240
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5 CAGCTCTCAC TGGCGGGACC CTGCTACTTC TGACAGCCAT CGGGGCGGCA TCCTGGGCCA 360  
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 25 CACCTCTCTG ACCCCATGTT AAATATTGTT CTGCTGTCTG GGACTCCTGT CTAGGTGCC 1740  
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Seq ID NO: C215 DNA Sequence  
 Nucleic Acid Accession #: AB037745.1  
 Coding sequence: 26..1744

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Coding sequence: 26-952

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Seq ID NO: C432 DNA Sequence

Nucleic Acid Accession #: NM\_052858.1

Coding sequence: 54..1259

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Seq ID NO: C434 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 261..2861

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VEKLQMQQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYYRIEN 120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
LAHAFQPGPG IGGDAHFDDE ERWTNNFREY NLHRVAHAEL GHSGLSLSHST DIGALMYP 240

```

TFSGDVQLAQ DDIDGIQAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
 PYMRTNFFYP EVELNFTISVF WQLPENGLEA AYEFAADRDEV RFFKGNKYWA VQGQNVLHGY 360  
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FVANKYWRY DEYKRSDMDP YPKMIAHDFP 420  
 GIGHKVDVAF MKDGFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence  
 Protein Accession #: NP\_055146.1

1 11 21 31 41 51  
 MVRKPVVSTI SKGGYQGNV NGRPLSLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA 60  
 GIFISPKGVL QNTGSVGMSL TIWTVCCVLS LFGALSYAEL GTTIKSGGH YTYILEVFGP 120  
 LPAPVVRVWE LLIIRPAATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180  
 SMSVSWASARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240  
 YGMYAYAGWF YLNFVTEVE NPEKTIPLAI CISMATTIGV YVLTNVAYFT TINAELLLS 300  
 NAVAVTFSEER LLGNFSLAVP IFVALSCFGE MNGGVFAVSR LFYVASREGH LPEILSMIHV 360  
 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSFARWLFI GLAVAGLIYL RYKCPDMHRP 420  
 FKVPLFIPAL FSFTCLFMVA LSLYSDFPST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480  
 SEKIITRLQI ILEVVPEDK L 501

Seq ID NO: C222 Protein Sequence  
 Protein Accession #: NP\_003237.1

1 11 21 31 41 51  
 MGLAWGLGVL FLMHVCGTNR IPESGGDNSV FDIFELTGAA RKSGRRLVK GPDPSSPAFR 60  
 IEDANLIPPV PDDKQDLVD AVRAEKGFLL LASLRQMKKT RTGLLALERK DHSQVQSVV 120  
 SNGKAGTLDL SLTVQGGQHV VSVEALLAT GQNKSTILFV QEDRAQLYID CEKMEAEID 180  
 VPIQSVFTRD LASIARLRIA KGGVNDNFQG VLQNVRFVFG TTPEDILRNK GCSSTSVLL 240  
 TLDNFWVNGS SPAIRTNVIG HKTDLQAIC GISCELSM VLELRGLRTI VTTLQDSIRK 300  
 VTEENKELAN ELRRPPLCYH NGVQYRNEE WTVDSCTECH QNSVTICK VSCPIMPEN 360  
 ATVPDGECCP RCWPSDSADD GWPSPSEWTS CSTSCGNGIQ QGRSCDSL NRCGSSVQT 420  
 RTCHIQCEDK RFKQDGGWSH WSPWSSCSVT CGDGVITRIR LCNSPSPQMN GKPCGEARE 480  
 TKACKQDACP INGGWGPWSP WDICSVTGGG GVQKRSRLCN NPAPQPGKD CVGDVTENQI 540  
 CNKQDCPIDG CLSNPCFAGV KCTSYPDGSW KCGACPPGYS NGIQCITDVD ECKEVPDACP 600  
 NHNGEHCEN TDGYNCLPC PPRFTGSQPF GQGVHATAN KQVCKPRNPC TDGTHDCNKN 660  
 AKCNYLGHYS DPMYRCECKP GYAGNGIICG EDTDLGWPN ENLVCVANAT YHCKKDCNCPN 720  
 LPNSGQEDYD KDGIGDACCDD DDDNDKIPDD RDNCPHYNP AQYDYDRDDV GDRCDNCPYN 780  
 HNPDAQDTDN NGEGDACAAD IDGDGILNER DMCQYVYVND QRTDMDGVG DQDCNCPLEH 840  
 NPDQLSDSD RIGDTCDNNQ DIEDGHQNN LDNCPYVYVNA NQADHDKDGK GDACDHDDDN 900  
 DGIPEDDKMC RLNVNPDQKD SDGDGRGDAC KDDFDHDSV DIDDICPENV DISEDFRRF 960  
 QMIPLDFKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDFSG TFFINTERDD 1020  
 DYAGFVFGY SSSRFVVMV KQVTQSYWDT NPTRAQYSG LSVKVVNSTT GPGEHLRNAL 1080  
 WHTGNTPGQV RTLWHDPRHI GWKDFTAYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD 1140  
 KTYAGGRGLL VFVSEQEMVFP SDLYEERCDP 1170

Seq ID NO: C223 Protein Sequence  
 Protein Accession #: NP\_002183.1

1 11 21 31 41 51  
 MPLLWLGRFL LASCWIIIVRS SPTPGSEHGS AAPDCPSCAL AALPKDVNS QPEMVEAVKK 60  
 HILNMLHLKK RPDVTQPVVK AALLNAIRKL HVKGVGENGY VEIEDDIGRR AEMNEMEQT 120  
 SEIITFAESG TARKTLHFEI SKEGSDLSV ERAEVLFLK VPKANRTRTK VTIRLFQKQK 180  
 HPQGLSDTGE EAEVGLKGE RSELLSEKV VDARKSTWHV FVSSSIQRL LDQGGKSSLDV 240  
 RIACEQCQES GASLVLLGKK KKEEKEGEGK KKGEGGEGAG ADEEKEQSHR PFLMLQARQS 300  
 EDHPPHRRRR GLECDGKVIN CCKKQFFVSF KDIGWMDWII APSGYHANYC EGECPSHIAG 360  
 TSGSSLSFHS TVINHYMRG HSPFANLKSC CVPTKLREMS MLYYDDGQNI IKKDIQNMIV 420  
 BECCGS 426

Seq ID NO: C224 Protein Sequence  
 Protein Accession #: NP\_000086.1

1 11 21 31 41 51  
 MVPDTACVLL LTLAALGASG QGQSPGLGSDL GPQMLRELQE TNAALQDVVD WLRQQVREIT 60  
 FLKNTVMEDC ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120  
 NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180  
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQRAQRFPC DGSFSECH 240  
 ADCVLERDGS RSCVCRVGA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSSQ 300  
 EDVDRDGDG ACDPDADGDG VFNEDKNCPL VRNPDQRNTD EDKWDGACDN CRSQKNDDQK 360  
 DTDQDGRGDA CDDIDIDGRI RNQADNCPRV FNSDQKDSG DGIGDADNOC POKSNPDQAD 420  
 VDHDVFGDAG DSDQDQDGDG HQDSRDNCPV VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480  
 RDNCRVLPNP GQEDADRQGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD PRAPQTVVLD 540  
 PEGDAQIDPN VVVLNQGRIE VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGPI 600  
 PGYQDSSFFY VVMWQMBQY YQWQNFRAV AEPGIQLKAV KSTGPGEQL RNALWHTGDT 660  
 ESQVRLWKD PRNVGKDKK SYRWFLQHRP QVGYIRVRFY BGPVLVADSN VVLDTTMRGG 720  
 RLGVFCFSQE NIWANLRYR CNDTIPEDYE THQLRQA 757

Seq ID NO: C225 Protein Sequence  
 Protein Accession #: NP\_612464

1 11 21 31 41 51

MRPQGPAAFP QRLRGLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSPG ANGIGPTPGI PGRDGFKEGK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120  
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIILYDQ 180  
 GSPENNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGADSTGW NSVSRIIEE 240  
 LPK 243

Seq ID NO: C226 Protein Sequence  
 Protein Accession #: NP\_003216.1

1 11 21 31 41 51  
 MATMENKVIC ALVLVSMAL GTLAEQTET CTVAPRERQN CGFPGVTPSQ CANKGCCFDD 60  
 TVRGVPWCFY PNTIDVPPEE ECEF 84

Seq ID NO: C227 Protein Sequence  
 Protein Accession #: NP\_056234.1

1 11 21 31 41 51  
 MPKRAHWGAL SVVLILLNGH PRVALACPHP CACYVPSEVH CTFRSLASVF AGIARHVERI 60  
 NLGFNSIQAL SETSFAGLTK LELLMIHGNE IPSIPDGALR DLSSLQVFKF SYNKLRVITG 120  
 QTLQGLSNLM RLHIDHNKIE FIHPQAFNGL TSLRLHLLEG NLLHLQHPST FSTFTFLDYP 180  
 RLSTIRHLYL AENMVRTLPA SMLRNMPLES NLYLQGNPWT CDCEMRWFLE WDAKSRGILK 240  
 CKDKKAYEGG QLCAMCFSPK KLYKHEIHLK KDMTCLKPSI ESPLRQNRSR SIEEBEQEE 300  
 DGGSQLILEK FOLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHLNQT DPPDIDINAT 360  
 VALDFECMPT RENYKELNKL IAYYSEVPVK LHRELMLSKD PRVSQYVRQD ADEEALYYTG 420  
 VRAQILAEPE WVMQPSIDIQ LNRROSTAKK VLLSYTQYS QTIISTKDTRO ARGRSWMVIE 480  
 PSGAVORDQT VLEGGPCQLS CNVKASESPS IFWVLPDGGI LKAPMDPPDS KFSILSSGWL 540  
 RIKSMEPSDS GLVQCIQVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN 600  
 ALAIPFAHLS WILPNRIIN DLANTSHVYM LFNGLTSLIPK VQVSDSGYYR CVAVNQGGAD 660  
 HFTVGTITVK KGSGLPSKRG RRGAKALSR VREDIVEDEG GSGMGDEENT SRLLHPKDQ 720  
 EVPLKTKDDA INGDKKAKKG RRLKLMWHS EKEPETNVAE GRRVFESRRR INMANKQINP 780  
 ERWADILAKV RGNLPGKTE VPPLIKTTSF PSLSLEVTTP FFAVSPSPAS PVQIVTSAAE 840  
 SSADVPLLGE EEHVLTGIS ASMGLEHNHN GVILVEPEVT STPLEEVVDD LSEKTEEITS 900  
 TEGDLKGTA APTLSEPEYEP SPTLHTLDTV YEKPTHEETA TEGWSAADVG SSPEPTSSEY 960  
 EPFLDAVSLA ESEPMQYFDP DLETKSQDE DKMKEDTFAH LTPTPTIWNV DSSTSOLFED 1020  
 STIGEPGVPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPHPS 1080  
 RSESEGESES KSITLDPDST GIMSSMSFPK KPAETTVGTL LDKDTTIVTT TPRQKVAPSS 1140  
 TMSTHPSRRR PNGRRRLRPN KFRHRHKQTP PTTFAPSETF STQPTQAPDI KISSQVSSL 1200  
 VPTAWDNTV NTPKQLEMEK NAEPTSKGTP RRGHGKRFNK HRYTPTSVSS RASGSKPSPS 1260  
 PENKRNIVT PSSETILLPR TVSLKTEGYP DSLDYMTTTR KIYSSYPKVQ ETLVPTYKPT 1320  
 SDGKEIKDDV ATNVDKHKS ILVTGESITN AIPTSRSLVS TMGEFKEESS FVGFGTPTW 1380  
 NPSRTAQPPR LQTDIPVTS GENLTDPLL KELEDVDFTS EFLSSLTVST PPHQEBAGSS 1440  
 TLLSSIKVEV ASSQAETTL DQDHLTTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500  
 MSLGQTTTK NLPAPSRISQ ASRDSKENVF LNYVGNPETE ATPVNNEGTQ HMSGPNELST 1560  
 PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620  
 LPFMSTQAS RYFVTSQSPR HWTNKPEITT YPSGALPENK QFTTPTLST TIPLPLHMSK 1680  
 PSIPSKFTDR RTDQFNYSK VFGNNNIFEA RNPVGKPPSP RIPHYSNGRL PFTTNTKLSF 1740  
 PQLGVTRRPQ IPTSPAPVMR ERKVIPGSYN RIHSHSTFHL DFGPPAPPLL HTPQTITGSPS 1800  
 TNLQNIQPMV STQSSISIF STSVQSSGSFH QSSSKFFAGG PPASKFWSLG EKPQILTKSP 1860  
 QTVSVTAETD TVFPCBATGK PKPFVWTKV STGALMTPTN RIQRFEVLKN GTLVIRKVOV 1920  
 QDRGQYMTA SNLHGLDRMV VLLSVTVQPP QILASHYQDV TVYLGDTIAM ECLARGTPAP 1980  
 QISWIFPDRR VMOQTVSPVES RITLHENRTL SIKEASFSDR GUYKCVASNA AGADSLAIRL 2040  
 HVAALPVIH QKLENIISLP PGLSIHICT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100  
 VFPNGTLYIR NLAPKDSGRY ECVAANLVGS ARRTVQLNVQ RAAANARITG TSPRRTDVRY 2160  
 GGTLKLDCA SGPDPWPRILW RLPSKRMIDA LPSFDSRIKV FANGTLVVKV VTDKADAGYL 2220  
 CVARNKVGD YVVLKVDVVM KPAKIEHKEE NDHKVYFGD LKVDCAVATGL PNPISWSLP 2280  
 DGLSVNSFMQ SDDSGGRTRK YVFPNGTLY FNEVGMRERG DYTCFAENQV GKDEMRVRVK 2340  
 VVTAPATRNR KTYLAVQVPY GDVVTACEA KGEPMKPVTV LSPTNKVIPT SSEKYQIYQD 2400  
 GTLLIQAQR SDSGNYTCLV RNSAGEDRKT VWIHVNVQPP KINGENPIT TVREIAAGGS 2460  
 RKLIDCKAEG IPTPRVLWAP PEGVVLPAFY YGNRITVRGN GSLDIRSLRK SDSVQLVOMA 2520  
 RNEGGEARLI VQLTVLEPME KPIPHDPISE KITAMAGHTI SLNCSAAGTP TPSLVVWLPN 2580  
 GTDLQSGQQL QRFYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVGILKPEAN 2640  
 KQYHNLVSII NGETLKLPCP PPGAGQGRFS WTLFNGMHLE GPQTLGRVSL LDNGTLTVRE 2700  
 ASVEDRGTYV CMETEYGPS VTSIPVIVIA YPPRITSEPT PVYITRPGNT VKLNCMAMGI 2760  
 PKADITWELP DKSHLKAQVQ ARLYGNRPLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820  
 KTTYIHVF 2828

Seq ID NO: C228 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MPGKTLRTG APADYRVILK TSQEDLDVPE DDISVRVMSS QSVLVSNDVP VLEKQKKVVA 60  
 SRQYTVRYRE KGLARWDYK QIANRRVLIE NLIPDVTYEF AVRISQGERD GKWSTSVQFR 120  
 TPESAPTTAP ENLNVWPNVG KPTVVAASWD ALPETEGKVK VCLLDLTGLFS VSSFQPSAKS 180  
 FQNTFFHTPR LSNHLEQSPS PILETLLLPW MWVCSLGNAI FSKSGPQTGE AWDLTTPKPSL 240  
 SLQQECSCCT QKDFSCLAYL IDIQTKQVKN DPQLEGSVFG PCFLFYFLTF MLDIGGFSPI 300  
 MCYEDPVSS LTGNSLKSVA ASKADVQNT EDNGKPEKPE PSSPSRAPA SSQHPSPVAS 360  
 PQGRNAKDLL LDLENKILAN GGAPRKPLR AKKAEELDLQ STEITGEEEL GSREDSPMSP 420  
 SDTQDQKRTL RPPSRHGSV VAPGRATAVA RMPALPRREG VDKPGFSLAT QPRPGAPPSA 480  
 SASPAHAST QGTSHRPSLF ASLNDNDLVD SDEDERAVGS LHPKGAPAP RPALSPSRQS 540  
 PSSVLDRSS VHPGAKPASP ARRTPHSGAA EEDSSASAPP SRLSPPHGGS SRLLETPQFHL 600  
 SSPLSKGGKD GEDAPATNSN APSRSTMSSS VSSHLSSRTQ VSEGAASDG ESHGDGDRED 660



5 GGRQAEATAQ TLRARPASGH FHLLRHKFFA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR 720  
AHPVPVSHSD SHPKLSSGIH GDEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPORG 780  
ASLHRKEPIP ENPKSTGADT HPQGYSSLA SKAQDVQOST DADTEGHSK AQSGSTDRHA 840  
SPARPPAARS QQHPSPVPRM TPGRAPQQP PPPVATSQHH PGQSRDAGR SPSPQRLSLT 900  
10 QAGRPRPTSQ GRSHSSSDPY TASSRGMFLP ALQNQDEDAQ GSYDDDDSTEV EAQDVRAPAH 960  
AARAKEAAS LPKHQQVESP TGAGAGGDHR SORGHASPA RPSRPGGPQS RARVPSRAAP 1020  
GKSEPPSKRP LSSKSQQSVS AEDEEEDAG FFKGGKEDLL SSSVPKWPS STPRGGKAD 1080  
GSLAKEEREP AIALAPRGGS LAPVKRPLPP PPGSSPRASH VPSRPPPSA ATVSFVAGTH 1140  
PWPRYTTRAP PGHFTTTPML SLRQRMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVL 1200  
15 GSNQKPNQOR IINGPQGTSL VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDLE 1260  
GTFVVSPDGL PLFGQGRHGT PLANADKPI LSLGGKPLVG LEVIKKTTHP FTTTMMQPTT 1320  
TTPLPTTTTPT RPTTATTMQP TTTTTPLTPT TPRETTATT TTTTTRPTT VRTTTRTTT 1380  
TTPKPTTPIP TCPPGTLEHR DDDGNLIMS NGIPECYAEE DEFSGLETDT AVPTTEAYVI 1440  
YDEDEYEFETS RPTTTEPST TATTTPRVIPE EGAISSEFEE EPDLAGRKRF VAPYVTVLNK 1500  
15 DPSAPCSLQD ALDHQVDLSL DEIIPNDLKK SDLPQHAHR NITVVAVEGC HSFVIVDWDK 1560  
ATFGDLVTGY LVYSASYEDF IRNKFSTQAS SVTHLPIENL KPNTYRYFKV QAQNPHGYGP 1620  
ISPSVSFVTE SDNPLLVVRP PGGELSGSHS LSNMIPATRT AMDGNM 1666

Seq ID NO: C229 Protein Sequence

Protein Accession #: NP\_003005.1

20  
25  
30  
1 11 21 31 41 51  
MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHST QENAILAIEQ 60  
YEBLVVNCNS AVLRFFFCAM YAPICTLEFL HDPIKPKCKSV CQRARDDCEP LMKMYNHSWP 120  
ESLACDELTV YDRGVCISPE AIVTDLPELV KNIDITEDMM VQERPLDVDC KRLSPDRCKC 180  
KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTOVPLITN 240  
SSQCPCPHLP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300  
KKKTAGRTSR SNPPKPKGKP PAKPASPKK NIKTRSAQKR TNPKRK 346

Seq ID NO: C230 Protein Sequence

Protein Accession #: NP\_005931.1

35  
40  
45  
1 11 21 31 41 51  
MAPAAWLRS AARALLPPML LLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA 60  
PAPATQEAEP PASSLRPPRC GVPDPDSGLS ARNRQKRFVL SGRWKEKTDL TYRILRFPWQ 120  
LVQEQVRQTM AEALKVMSDV TPLTTFTEVHE GRADIMIDFA RYWHGDDLPF DGPGGILAHA 180  
FFPKTHREGD VHFYDETWT IGDDQGTDLL QVAHEFEHGV LGLQHTTAAK ALMSAFYTFR 240  
YPLSLSDDDC RGVQHLVQGP WFTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300  
VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHQGLP SPVDAAFEDA QGHIWFQGA 360  
QYVYDGEKP VLGPAPLTEL GLVRFVHAHA LVWGPEKNKI YPFRGRDYWR FHPSTRRVD 420  
PVPERRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFD P VKKALEGEP RLVGPDFFGC 480  
AEPANTFL 488

Seq ID NO: C231 Protein Sequence

Protein Accession #: NP\_076927

50  
55  
60  
1 11 21 31 41 51  
MGENDPPAVE AFFSFRSLFG LDDLKISPVA PDADAVAAQI LSLPLKFPF IIVIGIALI 60  
LALAIGLGIH FDCSGKYRCR SSFKCIBLIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLVF 120  
TAASKWIMCS DDWKGHYANV ACAQLGFPYS VSSDNLRVSS LEGQFREFFV SIDHLLPDDK 180  
VIALHSHYVY REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQFW QASLQFGQYH 240  
LOGGSVITPL WIIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
LGNIDIALMKL AGPLITNEMI QPVCLNSEE NFPDGKVCNT SGWGATEDGG DASFVLNHA 360  
VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420  
GIGCAEVNKP GUYTRVTSFL DWIHEQMERD LKT 453

Seq ID NO: C232 Protein Sequence

Protein Accession #: NP\_003211

65  
70  
75  
1 11 21 31 41 51  
MLWKLTDNIK YEDCEDRHGD TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP 60  
PYQPIYPSQ DPYSHVNDPY SLNPLHAQPO POHPGWFGQR QSQESGLLHT HRGLPHQLSG 120  
LDPRRDYRRH EDLLHGPHAL SSGLDLSIH SLPHAIIEVP HVEDPGINIP DQTVIKGQPV 180  
SLSKSNSNAV SAIPINKDNL FGGVVNPNV FCSVPGRSL LSSTSKYKT VAEVQRLSP 240  
PECLNASLLG GVLRRAKSKN GGRSLREKLD KIGLNLPAGR RKAANVTLLT SILVEGEAVHL 300  
ARDFGVVCTE EPPAKAVAEF LNRQHSQDNE QVTRKNMLLA TKQICKBFTD LLAQDRSPLG 360  
NSRPNILEP GIQSCILTFN LISHGFGSPA VCAAVTALQ YLTELKAMD KMYLSNNPNS 420  
HTDNNAKSSD KEEKHRK 437

Seq ID NO: C233 Protein Sequence

Protein Accession #: NP\_002979.1

80  
1 11 21 31 41 51  
MKGLAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKPIVDYSET SPQCPKPGVI 60  
LLTRKRGRQIC ADPNKWKVQK YISDLKANA 89

Seq ID NO: C234 Protein Sequence

Protein Accession #: NP\_004054.1

1 11 21 31 41 51  
 5 MILQAHLSL CLMLYLATG YGQEGKFSGP LKPMFTSIYE GQEPSQIIFQ FKANPPAVTF 60  
 ELTGETDNIF VIEREGLLY NRALDRETRS THNLQVAALD ANGLIIVEGPV PITIEVKDIN 120  
 DNRPTFLQSK YEGSVQRNSR PGKPFLLVNA TDLDPPATPN GQLYYQIVIQ LPMINNVMYF 180  
 QINNKTGAIS LTREGSQELN PAKNPSYNLV ISVKDMGGQS ENSPSDITTS DIIVTENIWK 240  
 10 APKPVEMVEN STDHPHIKIT QVRWNPGBAQ YSLVDKEKLP RPPPSIDQEG DIYVTPQLDR 300  
 EEKDAYVFYA VAKDEYKPL SYPLEIHVKV KDINDNPPTC PSPVTVEFVQ ENERLGNISIG 360  
 TLTAHRDEE NTANSFLNRY IVEQTPKLFM DGLFLIQTYA GMLQALQSL KKQDTPQYNL 420  
 TIEVSDKDFK TLFQVQINVI DINDQIPIFE KSDYGNLTLA EDTNIGSTIL TIQATDADEP 480  
 FTGSSKILYH IIKGDSSEGLR GVDTPHTNT GYVVIKKPLD FETAAVSNIV FKAENPEPLV 540  
 FGKYNASSF AKFTLIVTDV NEAPQFSQHV FQAKVSEDAV IGTKVGNVTA KDPEGLDISY 600  
 15 SLRGDTRGWL KIDHVTGEIF SVAPLDREAG SPYRVQVAT EVGSSSLSSV SEFHLLIADV 660  
 NDNPPRLAKD YTGFLFFCHPL SAPGSLIFEA TDDQHLFRG PHFTFSLGSG SLQNDWEVSK 720  
 INGTHARLST RHTEFEEREY VVLIRINDGG RPFLEGIVSL PVTFCSCVEG SCFRPAGHQT 780  
 GIPTVGMVAV ILLTLLLVIG IILAVVFIRI KKDKGKDNVE SAQASEVKPL RS 832

20 Seq ID NO: C235 Protein Sequence  
 Protein Accession #: NP\_004434.1

1 11 21 31 41 51  
 25 MARARPPPPP SPFPGLLPLL PPLLLPLLL LPAGCRALEE TLMDTKWVTS ELAWTSHPES 60  
 GNEEVSGYDE AMNIRTYQV CNVRESSQNN WLRTGFIWRR DVQRYVELK FTVRDCNSIP 120  
 NIPGSCKETP NLFYYEADSD VASASSPFWM ENFYVKVDIT APDESFSRLD AGRVNTKVRS 180  
 FGPLSKAGFY LAFQDQGACM SLISVRAPYK KCASTTAGFA LPFETLTGAE PLSLVIAPGT 240  
 CIPNAVEVSF PLKLYCNGDG ENMVVPVACT CATGHEPAAK ESQCRPCPPG SYKAKQGEPP 300  
 30 CLPCPPNSRT TSPAASICTC HNNFYRADSD SADSACTTVP SPFRGVISNV NETSLILEWS 360  
 EPRDLGGRDD LLYNVICKKC HGAGGASACS RCDDNVEFVP RQLGLTERRV HISHLLAHTR 420  
 YTFEVQAVNG VSGSKPLPPR YAAVNITNQ AAPSEVPTLR LHSSSGSSLT LSWAPPERPN 480  
 GVILDYEMKY FEKSEGIASV VTSQMNVSQV DGLRPDARYV VQVRARTVAG YQYSRPAEF 540  
 ETTSESGSA QQLQQLPLI VGSATAGLVF VVAVVIAIV CLRQRHGS DSEYTKLQY 600  
 IAPGMKVYID PTYEDPNEA VREFAKEIDV SCVKIEEIVG AGEFGEVCRG RLKQPGRRREV 660  
 35 FVAIKTLKVG YTERQRDFL SEASIMQGF HPNIIRLEGV VTKSRPMIL TEFMENCALD 720  
 SPLRLNDGQF TVIQLVGLMR GIAAGMKYLS EMNVYHRDLA ARNIVNSNL VCKVSDFLGS 780  
 RLEDDPSDP TYTSLGKGI PIRWTAPEAI AYRKFTSASD VWSYGIVMME VMSYGERPYW 840  
 DMSNQDVINA VQDYRLPPP MDCPTALHQL MLDGWVRDRN LRPKFSQIVN TLDKLIRNA 900  
 40 SLKVIASQAS GMSQPLDRT VPDYTTFTTV GDWLDIAKMG RYKESFVSAG FASFDLVAQM 960  
 TAEDLLRIGV TLAGHQKIL SSIQDMRLQM NQTLFPVQV 998

Seq ID NO: C236 Protein Sequence  
 Protein Accession #: NP\_001795.1

45 1 11 21 31 41 51  
 MYGVYVLDKD SPVYGPAPR ASLGLGPANY GPPAPPPAPP QYPDFSSYSH VEPAPAPPTA 60  
 WGAPFPAPKD DWAAAYGPGP AAPAASPASL APGPPPDFSP VPAPPGPGPG LLAQPLGGPG 120  
 TPSSPGARQ TPYEWRRSV AAGGGGGSGK TRTKDKYRVV YTDQRLELE KEFHYSRIT 180  
 50 IRRKSELAAN LGLTERQVKI WQNRRAKER KVNKKKQQQQ QPPQPPMAHD ITATPAGPSL 240  
 GGLCPNNTSL LATSSPMPVK EEPLP 265

Seq ID NO: C237 Protein Sequence  
 Protein Accession #: NP\_068813.1

55 1 11 21 31 41 51  
 MGS DRARKGG GPKDFGAGL KYNRHEKVN GLEEGVEFLP VNNVKVKEH GPGRWVLLAA 60  
 VLIGLLLVLL GIGFLVWHIQ YRDVRVQKVF NGYMRITNEN FVDAYENSNS TEFVSLASKV 120  
 60 KDALKLLYSY VPLFLGPHYKE SAVTAFSEGS VIAYYWEFS IPQHLVEEAE RVMAEERVMV 180  
 LPPRARSLKS FVTVSVVAFV TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA 240  
 HARCQWALRG DADSVLSLTF RSPFLASCD E RGSOLVTVM TLSPMEPHAL VQLCGTYPPS 300  
 YNLTFHSSQN VLLITLITNT ERRHPGFAT FFQLPRMSSC GGRIRKAQGT FNSPYYPGHY 360  
 65 PFNIDCTWNI EVPNQHVQV RFKFFYLLEP GVPAGTCPKD YVEINGEKYC GERSQFVVT 420  
 NSNKITVRFH SDQSYTDTGF LAEYLSYDSS DPCPGQFTCR TGR CIRKELR CDGWADCTDH 480  
 SDELNCSCDA GHQPTCKNKF CKPLFWVCD S VNDGDNDSDE QGCSCAQTF RCSNGKCLSK 540  
 SQQCNKGDDC GDGSDASCP KVNVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSEK 600  
 DDCGLRSPT RQARVVGTD ADEGEWPQV SLHALGQGH I CGASLISPNV LVSAHACYID 660  
 70 DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH PPFNDFTFDY DIALLELEKP 720  
 AEYSSMVRPI CLPDASHVFP AGKAIWVTGW GHTQYGGTGA LILQKGEIRV INQTTCEML 780  
 PQQITPRMMC VQFLSGGVDS CQDSSGGPLS SVEADGRIFQ AGVWSWGDGC AQRNKPQVYT 840  
 RLPLFRDWIK ENTGV 855

75 Seq ID NO: C238 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 80 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMNCSAAV DIMFLLDGSN 60  
 SVKGSGFERS KFAITVCDG LDISPERVRV GAFQFSSTPH LEFLDSFST QQEVKARIK 120  
 MVFKGGTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180  
 FAVGVRRFRW BELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCW RGSRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPCPGD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDS SAGTTLDGFL 360

5 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVPLDVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480  
 EAVRAELEEI TGSPGHVMVY SDPQDLFNQI PELQGLCSR QRPQCRTQAL DLVFMMLDTSA 540  
 SVGPENFAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRNNGI 660  
 SVLVVGVGPV LSEGLRRLAG PRDSLHVA YADLRYHQDV LIEWLGEAK QPVNLCCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP 755

10 Seq ID NO: C239 Protein Sequence  
 Protein Accession #: Eos sequence

15 1 11 21 31 41 51  
 | | | | | |  
 MPPFLLLEAV CVPLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMPLLDGSN 60  
 SVGKGSFERS KHAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120  
 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIITDG KSQGDVALPS KQLKERGVTV 180  
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REPAGNAPCW RGSRRTLAVL AAHCFYSSWK RVFLTHPATC YRTTCPGPCD 300  
 20 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLPLDLS SAGTTLDGFL 360  
 RAKVPVVRV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVPLDVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480  
 EAVRAELEEI TGSPGHVMVY SDPQDLFNQI PELQGLCSR QRPQCRTQAL DLVFMMLDTSA 540  
 SVGPENFAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 25 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRNNGI 660  
 SVLVVGVGPV LSEGLRRLAG PRDSLHVA YADLRYHQDV LIEWLGEAK QPVNLCCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCVVCVS QGWILETPLR HMAFVQEGSS 780  
 RTPPSNYREG LGTEMYPTFW NVCAPGP 807

30 Seq ID NO: C240 Protein Sequence  
 Protein Accession #: XP\_097386.1

35 1 11 21 31 41 51  
 | | | | | |  
 MPKSEPLGCL SPASRAPGSA AATGAWLPAA SCGPGLGPP CTCPPRSLGR GRAGSRAGSS 60  
 PSGCVCVSGI LRVVSVGDPA SRRWVDLDSN SEDLSLLTLP MIVGTGGVGG GWARGWVPAQ 120  
 EKEVAEGSGH AGRNGRRRLQ RVYGARSWIL GRKPCILQRL PASGGPVQPQ PCPSPATACR 180  
 WGFKFGVAFW GAAQHPLPCR LGGGRAVPSA TRTLDGF 217

40 Seq ID NO: C241 Protein Sequence  
 Protein Accession #: CAC03433

45 1 11 21 31 41 51  
 | | | | | |  
 MLSSDTDFTA SWELVVRVDH PNEEQQKDV LRVSGDLHVG GVMLKLVEQI NISQDWSDF 60  
 LWWEQKHNL LKTHWTLDKY GVQADAKLLF TPQHKMLRLR LFNLMVRLR VSFSAVVFKA 120  
 VSDICKILNI RRSEELSLK PSGDYFKKK KKKNNKEPI IEDILNLESS PTASGSSVSP 180  
 GLYSKMTPI YDFINGTPAS STMTWFSDSP LTEQNCILS FSQPPQSPEA LADMYQPRSL 240  
 VDKAKLNAGW LDSSRSLMEQ GIOEDEQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300  
 50 LLEEIDCTEE EMLIPARLQY HISKLSLSAE TQDFAGESEV DEIEAALSNL EVTLEGGKAD 360  
 SLLEDITDIP KLDANLKLFR PKLLPKAFK QYWFIFKDT IAYFNKELE QGEPLKLNIL 420  
 RGCEVVPDYN VAGKFGIKL LIPVADGME MYLRCDHENQ YAQWMAACML ASKGTMTADS 480  
 SYQPEVLNLI SFLGMKNRNS ASQVASSLEN MDMNPECFVS PRCARHKHSK QLAARILEAH 540  
 QNVAQMPLVE AKLRFIQAWQ SLPEFGLTYY LVRFKSGKID DILGVSYNRL IKIDAATGIP 600  
 55 VITWRFTNIK QWNVNWETQ VVIEFDQNVF TAFTCLSADC KIVHEYIGGY IFLSTRSKDQ 660  
 NETLDEDLFH KLTGGQD 677

60 Seq ID NO: C242 DNA Sequence  
 Nucleic Acid Accession #: NM\_005170  
 Coding sequence: 337..918

65 1 11 21 31 41 51  
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 GGGCGTGAGA AAGCGGACGG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TTAATAACCA 60  
 GCCGCCTGCG CGCGCCTGCG GGAGACCTGG GAGAGTCCGG CGGCACGCGC GGGACACGAG 120  
 CGTCCACGCG TCCCTGGCGC GTACGCGCTG CCACCACTAG GCCTCCTATC CCGGGGCTCC 180  
 AGACGACCTA GGAGCGGTGC CCTGGGGAGT TGCTGGGCGG CGCGGTGCCA GAAGCCCTCT 240  
 TGGGGCGCCA CGCTTTTCCC CGTCGCTCC GGTCTCTCTG CTGCACTCTT CTGCGGCGC 300  
 70 GCCGGGACCT GAGGCGGGCG GGTGGATGCA GGCGCGATGG ACGGCGGCAC ACTGCCACAG 360  
 TCCGCGCCCC CTGCGCCCCC CGTCCCTGTC GGCTGCGCTG CCGGCGGAG ACCCGGCTCC 420  
 CCGGAACCTG TGCGCTGCAG CGGCGGGCGG CGACCGGCCA CGCAGAGAC CGGAGGCGGC 480  
 GCAGCGGCGG TAGCGGCGCG CAATGAGGCG GAGCGCAACC CGGTGAAGCT GGTGAACCTG 540  
 GGCTTCAGG CGCTCGGCGA GCACGTGCGG CACGCGGCGG CCAGCAAGAA GCTGAGCAAG 600  
 75 GTGAGACGCG TGCGCTCAGC CGTGGAGTAC ATCGCGCGCG TGACGCGCTT GCTGGCGGAG 660  
 CACGACGCGG TGCGCAACGC GCTGGCGGGA GGGCTGAGGC CGCAGGCGGT GCGGCGCTCT 720  
 GCGCCCGCGG GCGCGCCAGG GACCAACCGG GTGCGCGCT CGCCTCTCCG CGCTTCTCTG 780  
 TCCCGGGCGG GCGGGGGGAG CTCGGAGCCC GGCTCCCGCG GTTCCGCTTA CTCGTGGGAC 840  
 GACAGCGGCT GCGAAGGCGG GCTGAGTCTT GCGAGCGCG AGCTACTCGA CTCTCTCCAGC 900  
 80 TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence  
 Protein Accession #: NP\_060233.1

1 11 21 31 41 51

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MSGGHQLQLA	ALWFWLLMAT	LQAGFGRITGL	VLAADVESER	SAEQKAVIRV	IPLKMDPTGK	60
LNLTLEGVFA	GVAEITPAEG	KLMQSHPLYL	CNASDDDNLE	PGFISIVKLE	SPRRAPRPCL	120
SLASKARMAG	ERGASAVLFD	ITEDRAAAEQ	LQQPLGLTWP	VVLINGNDAB	KLMEFVYKNO	180
KAHVRIELKE	PPAWPDYDVW	ILMTVVGTIF	VIIASVLR	RCRPRHSRPD	PLQORTAWAI	240
SQLATRRYQA	SCROARGEW	DSGSSCSSAP	VCAICLEEPS	EGQELRVISC	LHEFHRCNVD	300
PWLHQHRTCP	LCVFNITEGD	SFSQSLGPSR	SYQEPGRRLH	LIRQHPGHAH	YHLPAAYLLG	360
PSRSARAVRP	RPGPFLPSQE	PGMGPRHHRF	FRAAHPRAPG	EQQLLAGAQH	PYAQGWGMSH	420
LQSTSQHPAA	CPVPLRRARP	PDSSGSGESY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
NCTDISLQGV	HGSSSTFCSS	LSSDFDPLVY	CSPKGDPRV	DMQPSVTSRP	RSLSVSVPTG	540
ETQVSSHVHY	HRHRHHYK	RFQWHGRKPG	PETGVQSPRP	PIPRTPQPE	PPSPDQQVTG	600
SNSAAPSRL	SNPQCPRALP	EPAPGPVDAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRRGGP	660
SEPTPGSRPQ	DATVHPACQI	PFHYTPSVAY	PWSPEAHPLI	CGPPGLDKRL	LPETPGPCYS	720
NSQPVMLCLT	PRQPLEPHPP	GEGPSEWSSD	TAEGRPCPYP	HCQVLSAQPG	SEEELEELCE	780
QAV						783

Seq ID NO: C244 DNA Sequence  
Nucleic Acid Accession #: NM\_004289  
Coding sequence: 493..1695

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1	11	21	31	41	51	
GCGGCGGCT	CGTCCACCGG	AGGAGCCGGC	GCCAGCGTGG	ACGGCGGCAG	CCAGGCTGTG	60
CAGGGGGGCG	GCGGGGACCC	CCGAGCGGCT	CGGAGTGGCC	CCTTGGACGC	CGGGGAAGAG	120
GAGAAGGCAC	CCGCGGAACC	GACGGCTCAG	GTGCGCGAGC	CTGGCGGATG	TGCGAGCGAG	180
GAGAATGGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTCCCA	GCATGAGGAA	240
AATGAAGAAA	GGGTGTGACG	CCAGAAGGAG	AACCTCACTT	AGCAGAATGA	TGATGATGAA	300
AACAAAATAG	CAGAGAAAAC	TGACTGGGAG	GCAGAAAAGA	CCACTGAATC	TAGAAATGAG	360
AGACATCTGA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAG	ACTTATTTCA	GTGTCTTTCA	420
TCACAGCGCT	AAAATTCAC	GGAGGGCATC	TCATTGGGAG	ATATTCTCT	TCCAGGCAGT	480
ATCAGTGATG	GCATGAATTC	TTCAGCACAT	TATCATGTAA	ACTTCAGCCA	GGCTATAAGT	540
CAGGATGTGA	ATCTTCATGA	GGCCATCTTG	CTTTGTCCCA	ACAATACATT	TAGAAGAGAT	600
CCAACAGCAA	GGACTTCACA	GTCACAAGAA	CCATTTCTGC	AGTTAAATTC	TCATACCACC	660
AATCCTGAGC	AAACCCCTCC	TGGAACCTAAT	TGACAGGAT	TTCTTTCACC	GGTTGACAA	720
CATATGAGGA	ATCTAACCAAG	CAAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGTAT	780
GAGATAAATC	TAAATGTCAT	GGCCACAGAA	GACAACTTTG	ATCCAATCGA	TGTTTCTCAG	840
CTTTTGTATG	AACCAAGATC	TGATTCTGGC	CTTTCTTTAG	ATTCAGTCA	CAATAATACC	900
TCGTGTATCA	AGTCTAATTC	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
ACTGACCATG	AATCTAGTTC	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCTG	ATTTCATGG	AGATCTTACA	1080
TTTCAACAG	TATTTATCAA	CCACACTTAC	CACCTACAGC	CAACTGCACC	AGAATCTACT	1140
TCGAACCTT	TCCGTCGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CCTTGAAGAC	1200
ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTTCT	1260
GTAGATGAAA	TGTGCGGCAT	GCCTGTGTAT	TCTTTCAATA	GCATGTTAAG	TAGATATTAT	1320
CTGACAGAAC	TACTAGTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
GCTGCGCAGA	ACTGTGTGTA	ACGCAAAATG	GACATAATTT	TGAATTTAGA	AGATGATGTA	1440
TGTAACCTGC	AAGCAAGAAA	GGAAACTCTT	AAGAGAGAGC	AAGCACAATG	TAAACAAAGT	1500
ATTAACATAA	TGAAACAGAA	ACTGCATGAC	CTTTATCATG	ATATTTTTAG	TAGATTAAGA	1560
GATGACCAAG	GTAGGCCAGT	CAATCCCAAC	CACATATGTC	TCCAGTGTAC	CCATGATGGA	1620
AGTATCTTGA	TAGTACCCAA	AGAACTGGTG	GCCTCAGGCC	ACAAAAGGAA	AAACCAAAAG	1680
GGAAAGAGAA	AGTGAGAGAA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTCTA	1740
GAAACTGATT	ATTTGGATCA	GAAACCATTG	AAACTGCTTC	AAGAATTGTA	TCTTTAAGTA	1800
CTGCTACTTG	AATAACTCAG	TAAACGCTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
CTTCAAGATC	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCAATGT	1920
ATACAAAAAT	ATCTTTATG	TCCAAAGAAT	AGGTTAACAT	GAAACCCGAG	TAAAGCTTTC	1980
CATCTTGGCA	GCCATCTCTT	TAAAGAGTAA	GTGTGTTACT	TCAAAAAGAG	CAAACTCTGG	2040
GGATCAAAAT	ATTTTAAAGG	GTATTTCACT	TTTAAATGCA	AAATAGCCTT	ATTTTCATTT	2100
AGTTTGTATG	CACTATAGTG	AGCTTTTCAA	ACACTATTTT	AATCTTTATA	TTTAACTTAT	2160
AAATTTGTCT	TTCT					2174

Seq ID NO: C245 Protein Sequence  
Protein Accession #: NP\_004433

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70  
75  
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1	11	21	31	41	51	
MALRLIGAAL	LLLPLLAAVE	ETLMDSTTAT	AELGWMVHFP	SGWEEVSGYD	ENMNTIRTYQ	60
VGNVFESSQN	NWLRTKFIRR	RGARRIHVEM	KFSVRDCSSI	PSVPGSCKET	FNLYYYEADF	120
DSATKTPPNW	MENPNVVKVDT	LADESFSQV	DLGGRVMKIN	TEVRSFGPVS	RSGEYLAQD	180
YGGCMSLIIV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	EEVDVPIKLY	240
CNGDGEWLVP	IGRCMKAGF	EAVENTVCR	GCPSTGFFKAN	QGDEACTHCP	INSRTTSEGA	300
TNCVCRNGY	RADLDPLMDP	CTTTPSAPQA	VISSVNETSL	MLEWTPPRDS	GGREDLVYNI	360
ICKSGSGRG	ACTRCGDNVQ	YAPROLGLTE	PRYISDLIA	HTQYTFEIQ	VNGVTDQSPF	420
SPQFASVNIT	TNQAPSALVS	IMHQVSRVTD	SITLSWSQPD	QFNGVILDYE	LQYYEKELSE	480
YNATAIKSPT	NTVTVQGLKA	GAIVYVQVRA	RTVAGYGRYS	GKMPQMTME	AEYQTSIQEK	540
LPLIIGSSAA	GLVFLIAVVV	IAIVCNRRRG	FERADSEYTD	KLQHYTSGHM	TPGMKIYIDP	600
FTYEDPNEAV	REFAKEIDIS	CVKIEQVIGA	GEFGEVCSGH	LKLPGKREIF	VAIKTLKSGY	660
TEKQRDRFLS	EASIMGQPDH	PNVHLEGV	TKSTPVMILT	EFMENGSLDS	FLRONDQOFT	720
VIQLVGLMRG	IAAGMKYALD	MNVVHRDLAA	RNVLVNSNLV	CKVSDFLSLR	FLEDDTSDPT	780
YTSALGGKIP	IRWTAPEAIQ	YRKFTASADV	WSYGIWMWEV	MSYGERPYND	MTNQDVINAI	840
EQDYRLPPPM	DCPSALHQLM	LDCWQKDRNH	RPKFGQIVNT	LDKMRNPNS	LKAMAPLSSG	900
INLPLLDRTI	PDYTSFNTVD	EWLEAIKMGQ	YKESFANAGF	TSFDVVSQNM	MEDILRVGLT	960
LAGHQKILN	SIQVMRAQNM	QIQSVEV				987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP\_114148.1

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1      11      21      31      41      51
5  MDARRVPQKD LRVIKQNLKKE RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
   RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNDSDEDES GMNFLEKRAL 120
   NIKQNKAMLA KLMSELEFPF GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180
   TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMWE DDLPRSSRRS SSVTLPHIIR 240
   PVEEITEGGV GERLQQPSKR RYITVHWALL VINAVRRLLI PKQTAETQTA GAFAESSVAP 300
10  AFETVMVKRS GMLCWIRTGI ARLVEESATA VSAGSEMDGV RLGSLCI 347

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Seq ID NO: C247 Protein Sequence  
Protein Accession #: NP\_036577.1

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1      11      21      31      41      51
15  MENPSPAAL GKALCALLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60
   PLPRPPAQWS SLLGAHSSD YSMWRKNQYV SNGLRDFAEER GEAWLMKEI EAAGEALQSV 120
   HAVFSAPAVP SGTGQTSAEL EVQRRHSLVS FVVRIVSPD WFGVVDLSDL CDGDRWRBEA 180
20  ALDLYPYDAG TDSGTFSSP NFATIPQDTV TEITSSSPSH PANSFYFRL KALPPIARVT 240
   LVRLRQSEPA FIPPAVLPS RNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTSK 300
   RTRYVRVQPA NNGSPCELE EEAECVPDNC V 331

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Seq ID NO: C248 Protein Sequence  
Protein Accession #: NP\_063947.1

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1      11      21      31      41      51
30  MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
   YFLCGQPLHF IPKQQLCDGE LDCPLGEDEE HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120
   GWNFSACFDN FTEALAEATAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
   GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWFWQV SIQYDKQHV GGSILDPHWV 240
   LTAACHCFRKH TDVFNWKVRA GSDKLGSPFS LAVAKIIIE FNPMPKOND IALMKLQFPL 300
   TFSGTVRIPC LPFFDEELTP ATPLWIIWIG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
35  AYQGEVTEKM MCAGIEGGV DTCQGDSSGP LMYQSDQWHV VGIWSWGYGC GGPSTPGVYT 420
   KVSAYLNWIY NVWKAE 437

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Seq ID NO: C249 Protein Sequence  
Protein Accession #: NP\_003036.1

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1      11      21      31      41      51
40  MGCKVLLNIG QOMLRKVVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60
   NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELMA FITGWNILIS 120
45  YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGV L AENPDIFAVI IILILTGLLT 180
   LGVKESAMYN KIFTICINLV LGFIMVSGFV KGSVKWQOLT EEDFGNTSGR LCLNNDTKEG 240
   KPGVGGFMFP GFSGVLSGAA TCFYAFVGFD CIATTGEEVK NPQKAIPIGI VASLLICFIA 300
   YFGVSAALTL MPMYFCLDNN SPLPDAFKHV GHEGAKYAVA VGSLCALSAS LLGSMFPMFR 360
50  VIYAMAEDGL LFKFLANVND RTKTPITATL ASGAVAAVMA FLFDLKDLDV LMSIGTLAY 420
   SLVAACVLVL RYQPEQNLV YQMASTDEL DPADQNELAS TNDSQLGLFP EAEMFSLKTI 480
   LSPKNMEPSK ISGLIVNIST SLIAVLIITE CIVTVLGRE A LTKGALWAVF LLGASALLCA 540
   VVTGVIWRQP ESKTKLSFKV PFLPVLPILS IFNVVYLAMQ LDQGTWVRFA VMMLIGFIY 600
   FGYGLWHSSE ASLDADQART PDGNLDQCK 629

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Seq ID NO: C250 Protein Sequence  
Protein Accession #: NP\_002767.1

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1      11      21      31      41      51
60  MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPMQ 60
   VSLFNGLSFH CAGVLVDQSW VLTAAHCGNK PLWARVGGDDH LLLLQGEQLR RTTRSVVHFK 120
   YHQSGGPILP RRTDEHDLML LKLARFVVFG PRVRALQLEPY RCAQPGDQCC VAGWGITAAR 180
   RVKYNKGLTC SSITILSPKE CEVFYPGVVT NNNICAGLDR GQDPCQSDSG GPLVCDETLQ 240
65  GLSWGVYPC GSAQHPAVYT QICKYMSWIN KVIKRN 276

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Seq ID NO: C251 Protein Sequence  
Protein Accession #: XP\_095088.3

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1      11      21      31      41      51
70  MTRAATAEPG RVSPASPARS TAGLPRAFLO SLRTLDDILD DWQRCVHLR EIQSLWVEAR 60
   ELPSGVLEGL SQRGPGQPGA AVRSRRGGAV PRGARAVPER CAGTETRGR RCSGLQLRG 120
   GFRGCPADPC ARGHRRTTI TSGVDCGLLK QMKELEQKE VLLQGLEMA QGRDWYQQQL 180
75  QQVQERQRL GQSRASADFG AVGSPPRLGR LLPKVQEVAR WLGLLEAEAC AGRALPTSSS 240
   GPSCALTST SSPGWQQQII LMLKEQNRLL TQEVTEKSR ITQLEQKSL IKQLFEARAL 300
   SQQDGGLSPA GPHEPLTRF RLPVLTWAGA LLSFSPQLL LPLSADSGGP LHELPDTWFP 360
   AVLLWVSPG KRTAARLHF HQRPAEGANQ LGCGAARPE TCGTLPHFES HKTCEPDSL 420
   GGPCPQEGDR SWSHLGAAPD VAPAVAKVTP NREDAAGSRH GDICPLCPKG LLTPFDIAIE 480
   FSLAEWQCLD HAQNLRYRDV MLENYRNLF S LGMTVSKPDL IACLEQNEF QNKRNEMAA 540
80  KHPVTCSEFN QDLQPEQSIK DSLQKVIPT YGKCGHENL LKCKCKRVD CEVHKGGYND 600
   LNQCLSNTQN KIFQTHKCVK VFSKFSNSNR HNARYTGKHH LKCKKYGKSF CMFSLNQHQ 660
   IHTKEKSYK CEECKSPNH SSGTTHKRI LTGEKPYRCE BCGKAFRWS NLTRHKRIHT 720
   GEKPYACEC GQAFRRSSTL TNHKRIHTGE RPYKCEBCK AFSVSSALI HKRIHTGEK 780
   YTCBEOGKAF NCSSTLTKTHK IHTGEKPYT CEECGRTFNC SSTVKAHKRI HTGEKPYKCE 840

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5 ECDKAFKWHK SLAKHKIIHT GEKPYKCSDS KALAKSSEVQ KVSXGDGNG IRVHKKKETQ 900  
 10 GWLVRNKNEN RTGLFQIRAA VRPNRDPSSG QQSGSLDPI QRKEEPLDN HYDHQNALED 960  
 QRTNGVGLL TFRDVVIEFS LEWQCLDHA QNLYRDVML ENYRNLVSLG IAVSKPDLIT 1020  
 CLEQNKPEWN IKRNMVTKH PDLPELGLIK DSLQKVIPIR YKSGHDNLQ VKTCKSMGEC 1080  
 EVQKGGCNEV NQCLSTTONK IFQTHKCVK FGKFSNSNRH KTRHTGKKHF KCKYKGSFC 1140  
 MVSQHLHQHI IHTRENSYQC EEOGKPFNCS STLKSHKRIH TGEKPYRCEE CGKAFWSSST 1200  
 LTKHRIHTG EKPYTCEECG QAFSRSSSTA NHRKRIHTGK PYTCEECGKA FSLSSSLTYH 1260  
 KRIHTGEKPY TCEECGKAFN CSSTLKKHKI IHTGEKPYKC KECGKAFAPS STLNTHKRIH 1320  
 TGEKPYKCEE CDKAFKWSST LANHKSMTG EKPYKCE 1357

Seq ID NO: C252 Protein Sequence  
 Protein Accession #: NP\_114433.1

15 1 11 21 31 41 51  
 MASRSMRLLL LLCLAKTGV LGDIIMRPSG APGWFFYHKS CVGYFRKLRL WSDAELECS 60  
 YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120  
 KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP 158

20 Seq ID NO: C253 Protein Sequence  
 Protein Accession #: XP\_051860.2

25 1 11 21 31 41 51  
 MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK FVRPKLTVTI DTNVNSTILN 60  
 LEDNVQSWKP GDTLVIASST YSMYQABEQ VLPSCRSCAPN QVKVAGKPMY LHIGEEIDGV 120  
 DMRAEVGLLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIFKALGFK AAHLEGTELK 180  
 HMGQQLVGOY PIHFLAGDV DERGGYDPPT YIRDLSEIHT FSRCVTVHGS NGLLIKDVVG 240  
 YNSLGHCFPT EDGPEERTFP DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300  
 30 DCNAVSTFWM ANPWNINLNC AAAGSEETGF WFIFHHVPTG PSVGMYSPTY SEHIPLGKPY 360  
 NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLISIARSY PHQDADPLKP REPAIRHFI 420  
 AYKNDQHGAW LRGGDVWLDS CRFADNGIGL TLASGGTFPY DDGSKQEIKN SLFVGESGNV 480  
 GTEMMDNRIW GPGGLDHSGR TLPICQNFPI RGIQLYDGPQ NIQNTCTFRK VALGGRHTSA 540  
 LAFLRLNNAW SCPHNNVTGI AFEDVPITSR VFFGEPGPWF NQLDMDGDKT SVFHDVDGVS 600  
 35 SEYPGSVLTK NDNWLVRHPD CINVDWRGA ICSGCYQMY IQAYKTSNLR MKIKNDFPS 660  
 HPLYLEGALT RSTHYQQYQP VVTLOKGYTI HWDQTAPEL AIWLINFNKG DWIRVGLCYP 720  
 RGTTFSLSD VHNRLKQTS KTGVPVRLTQ MDKVEQSYPG RSHYYWDEDS GLLFLKLKQ 780  
 NEREKFAFCS MKGCEKIKK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKRLFGSQLK 840  
 40 TKDHPLEVOM ESSKQHFHFL WNDFAFIEVD GKYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900  
 NSILQGIPIWQ LFNVTATIPD NSIVLMSKRG RYVSRGPWTR VLEKLQADRG LKLKEQMAFV 960  
 GPKGSFRPIW VTLDTEDHKA KIFQVPIPV VKKKKL 996

Seq ID NO: C254 Protein Sequence  
 Protein Accession #: NP\_055188.1

45 1 11 21 31 41 51  
 MTALSSENCN FOYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT QCNFMEYFCI 60  
 SLAFVDLLLL VNISILYFR DFVLLSIRPT KYHICLFTQI ISFTYGLHY PVFLTACIDI 120  
 50 CLNFSKTKL SFKQKLFYF FTVILWISV LAYVLGDPAL YQSLKAQNAV SRHCFFYVSI 180  
 QSYWLSFFMV MILFVAFITC WEEVTTLVQA IRITSYMET 1LYFPSSHS SYTVRSKKIP 240  
 LSKLVCFLS TWLPFVLQV IIVLLKQVPI AYIEMNIPWL YFVNSPLIAT VYVWNCHELN 300  
 LKIDGLPLDP FVNWKCCPIP LTIPLNEQIE KPTISIMIC 338

55 Seq ID NO: C255 Protein Sequence  
 Protein Accession #: Eos sequence

60 1 11 21 31 41 51  
 MALVLGSLLL LGLCGNSPSG QPSSSTDAPK AMNYELPATN YETQDSKAG PIGILFELVH 60  
 IFLYVQPRD FPEDTLRKL QLAKESKIDY DKIVVYEAGI ILCCVLGLF IILMPLVGYF 120  
 FCMCRCCNK GGMHQHQKE NGPFLRKCFA ISLVICIII SIGIFYGFVA NHQVTRIKR 180  
 SRKLADSNFK DLRTLLNETP EQIKYILAQY NTKDKAFTD LNSINSVLGG GILDRLRPN 240  
 65 IPVLDEIKSM ATAITEKEA LENMNSTLKS LEQSTQLSS SLTSVKTSLR SSINDPLCLV 300  
 HPSSETCNSI RLSSLQNSN PELRQLPFVD AELDNVNVVL RTDLGLVQV GYQSLNDIPD 360  
 RVQRQTITV AGIKRVLSI GSDIDNVTR LPIQDILSAF SVYVNTTESY IHRNLTLEE 420  
 YDSYWLGLL VICSLTLIV IFYLLGLLGG VCGYDREATP TTRGCVSNTG GVFLMVGVL 480  
 SFPLCWILMI IIVLTFVFGA NVEKLICEPY TSKELFVLD TPYLLNEDE YLGLGKLPK 540  
 SKMKLTFEQV YSDCKNRTG YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNINIFL 600  
 70 LGAAGRNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLIS PAYDLEAKAN SLFPGNLRNS 660  
 LKRDAQTIKT IHQQRVLPB QSLSTLVQSV KILQRTGNGL LERVTRILAS LDFQNFITN 720  
 NTSSVIEET KKYGRITIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYID 780  
 PLNLFWFGIG KATVFLPAL IFAVKLAKY RMDSSEVDYD DVETIPMKM ENGNNGYHKD 840  
 75 HVYGIHNPVM TSPSQH 856

Seq ID NO: C256 Protein Sequence  
 Protein Accession #: NP\_149038.1

80 1 11 21 31 41 51  
 MKAIHLTL ALLSVNTATN QNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60  
 PSFPTATSPA PPIIHTSSS TIPTAPPPII STHSSSTIPI PTAADSEST NVNSLATSDI 120  
 ITASSPNDGL ITMVPSSTQS NNEMSPPTED NQSSGPPTG ALLETSTLNS TGPSNCPQDD 180  
 PCADNSLCVK LNTSFCLCL EGYYSNSTC KKGKVPFGKI SVTVSETFDP EERHSMAYQD 240

5 LHSSEITSLFK DVFQTSVYQG TVILTVSTSL SPRSEMRADD KFNVTIVTI LAETTSNDEK 300  
 TVTEKINKAI RSSSSNFLNY DLTILRCOYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360  
 VASSLKCPDA CNAQHKQCLL KKSOGAPECA CVPGYQEDAN GNCQKCAFY SGLDCKDKFQ 420  
 LILITVGTIA GIVILSMIIA LITVARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480  
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY 512

Seq ID NO: C257 Protein Sequence  
 Protein Accession #: NP\_001423.1

10 1 11 21 31 41 51  
 | | | | | |  
 MTAGRRMEML CAGRVPALLL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60  
 AQVSITKCSS DMNGYCLHGG CIYLVDMSON YCRCEVGYTG VRCEHFFLTV HQPLSKEYVA 120  
 15 LTVILILFL ITVVGSTYYP CRWYRNRRKSK EPKKEYERVY SGDPELRQV 169

Seq ID NO: C258 Protein Sequence  
 Protein Accession #: AAC63902.1

20 1 11 21 31 41 51  
 | | | | | |  
 MDRSKENCIS GPVKATAPVG GPKRVLVTQQ IPCQNPLPVN SGQAQRVLCV SNSSQVRVLIQ 60  
 AQLVSSSHKP VQNKQKQKQLQ ATSVPHPVSR PLNNTQKSKQ PLPSAPENNP EEBELASKQKN 120  
 EESKQRQWAL EDFEIGRPLG KGFQGNVYLA REKQSKFILA LKVLFAKALE KAGVEHQLRR 180  
 25 EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL 240  
 ANALSYCHSK RVIHRRDIKPE NLLLSAGEL KIADFGWSVH APSSRRITLC GTLDYLPPEM 300  
 IEGRMHDEKV DLWSLGLVLCY EFLVGKPPFE ANTYQETYKR ISRVEFTFPD FVTEGARDLI 360  
 SRLKHNPSQ RPLRLREVLEH PWITANSSKP SNCQNKESAS KQS 403

30 Seq ID NO: C259 Protein Sequence  
 Protein Accession #: NP\_037504.1

1 11 21 31 41 51  
 | | | | | |  
 MSRTAYTVGA LLLLLGLTLLP AAEGKKKGSQ GAIPPPDKAQ HNDSEQTQSP QPQSRNRGR 60  
 35 GQGRGTAMPG EEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCY 120  
 QCNSEFYIPRH IRKEEGSFQS CSFCKPKKFT TMMVTLCNCP LQPPTKKRVR TRVKQCRCIS 180  
 IDLD 184

40 Seq ID NO: C260 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | | |  
 MKVGVWLWIS FFTFTDGHGG FLGKNDGIKT KKEILVNKKK HLGPFVEEYQL LLQVITYRDSK 60  
 45 EKRDRLNFKL LKPPPLWWSH GLIRIIRAKA TTDCNSLNGV LQCTCEDSYT WFPSPCLDPQ 120  
 NCYLHTAGAL PSCECHLNNL SQSVNFCERT KINGTFKINE RPTNDLLNSS SAIYSKYANG 180  
 IEIQLKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALEK 240  
 LPFLEDGSFR VFQKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300  
 50 LSLLEELNKN FSGMIVGNATE AAVSSFEVQNL SVIIRQNPST TVGNLASVVS ILSNISLSL 360  
 ASHFRVSNST MEDVISIADN ILNASAVTNW TVLLREKYA SSRLLLETLEN ISTLVPTTAL 420  
 PLNFSRKPID WKGIPVKNQK LKRGYSYQIK MCPQNTSIP I RGRVLIGSDQ FQSLPETII 480  
 SMASLTIGNI LPSVKNQNAQ VNGPVISTVI QNYSINEVFL PFSKIESNLS QPHCVFWDPS 540  
 HLQWMDAGCH LVNETQDITV CQCTHLTSFS ILMSPFVPST IFPVVWITY VGLGISIGSL 600  
 55 ILCLIEALF WQIIEKQTS HTRERICMVNI ALSLLIADWV FIVGATVDTT VNPSGVCTAA 660  
 VFTTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQLMMA VGFCLYGCP LIISVITIAV 720  
 TQPSNTYKRK DVCWLNWSNG SKFLAFVVP ALAIVAVNPF VVLLVLTKLM RPTVGERLSR 780  
 DDKATIIIRVG KSLLLITPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GPFILCFGIL 840  
 LDSKLRLQLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA FSHGDSDDN 900  
 60 IMLTQFVNSE 910

Seq ID NO: C261 Protein Sequence  
 Protein Accession #: NP\_000575.1

65 1 11 21 31 41 51  
 | | | | | |  
 MTSKLAVALL AAFILISAALC EGAVLPRSAK ELRCQCIKTY SKPFPKPKFIK ELRVIESGPH 60  
 CANTEIIVKL SDGRELCLDP KENWVQRVVE KPLKRAENS 99

70 Seq ID NO: C262 Protein Sequence  
 Protein Accession #: NP\_005594.1

1 11 21 31 41 51  
 | | | | | |  
 MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGSVA EPEQNRVRE AEENREPPFRK 60  
 75 ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAFTPIPM NLFEQFKRAA 120  
 NLYFLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTECV 180  
 IKDGRPFVAK WKEIQGVDVI RLKKNDFVPA DILLSSSEP NSLCYVETAE LDGETNLKPK 240  
 MSLEITDQYL QREDTATFD GFICEEPPNN RLDKFTGTIL WRNTPFPLDA DKILLRGCVI 300  
 80 RNTDFCHGLV IFAGADTKIM KNSGKTRPKR TKIDYLANFM VYTIFFVLIL LSAGLAIGHA 360  
 YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420  
 WDLQMYAEK DTPAKARTTT LNEQLGQIHY IPSDKTGTLT QNIMTFKCC INQIYGDHR 480  
 DASQHNHNKI EQVDFSWNTY ADGKLAPYDH YLIEQIQSGK EPEVRQFFFL LAVCHTMVD 540  
 RTDGLQNYQA ASFDEGALVN AARNFGPAFL ARTQNTITIS ELGTERTYNV LAILDPNSTR 600  
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIFANET LRTILCLCYKE 660

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IEEKEFTWVN KKFMAASVAS TNREALDKV YEEIEKDLIL LGATAIEDKL QDGVPEITISK 720
LAKADIKIWN LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
KFAPVQVESF FPPGGRNALI ITGSMWNEIL LEKKTTRNKI LKLFPRTEE ERMRTQSKR 840
RLEAKKEQRQ KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVMN 900
IKTAHIGVGI SQEGEMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNFA 960
FTLVHFWYSP FNGYSAQTAY EDWFTILYNV LYTSLPVLLM GLLDQDVSDK LSLRFPGLYI 1020
VGQRDLLENY KRFFVSLHLG VLTSMILFFI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL 1080
VITVNFQIGL DTSYWTFVNA FSIFGSIALY FGIMFDFHSA GIHVLFPSAF QFTGTASNAL 1140
RQFYIWLITII LTVAVCLLPV VAIRFLSMTI WPSSEDKIQK HRKRLKAEEQ WQRRQVFR 1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPDLAIVAD GTAEYRRTGD S 1251

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Seq ID NO: C263 Protein Sequence  
Protein Accession #: XM\_044533

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1 11 21 31 41 51
| | | | |
MLRTAMGLRS WLAAPWGALE PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPF 60
RFAEHISNY TALLLSRDRG TLVVGAREAL FALSSNLSPL PGGEYQELLW GADAEKKQCC 120
SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY IMENFTLAR DEKGNVLLED 180
GKGRCPDPDN PKSTALVVDG ELYTGTVSSF QGNDAISRS QSLRPTKTES SINWLQDPAF 240
VASAIPESL GSLQGDDEKI YFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
TSFLKAQLLC SRPDDGFPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
FTMKDVQRFV SGLYKEVNR TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
NFLKDHFLMD GQVSRMLLL QPQARYQVVA VHRVPGLIHT YDVLFLGTGD GRLLKAVSVG 480
PRVHIEELQ IFSSGQPQVN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
PYCAWSSGSC KHVSLYQPQL ATRFWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
FQNTVNTILA CPLLSNLATR WLENGAPVN ASASCHVLT GDLLLVGTQQ LGFEQCSWLE 660
EGFQQLVASY CPEVVEDGVA DQTEGGSSVP VIISTSRVSA PAGGKASWGA DRSYNKEFLV 720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
PLDHRGQSL SDSPGSRVFP TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV 837

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Seq ID NO: C264 Protein Sequence  
Protein Accession #: NP\_008950.1

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1 11 21 31 41 51
| | | | |
MASQNRDPA TSVAAARKGA EFGGGAARGP VGKRLQQLM TLMSGDKGI SAFPESDNLF 60
KWTGTHGAA GTTYEDLRYK LSLFPPSGYP YNAPTVMKLT PCYHENVDTQ GNICLDILKE 120
KWSALYDVRT ILLSIQSLLG EPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQEP 179

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Seq ID NO: C265 Protein Sequence  
Protein Accession #: NP\_055399.1

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1 11 21 31 41 51
| | | | |
MGRGWGFLFG LLGAVLLSS GHGEEQPPET AAQRFCQVVS GYLDDCTCDV ETIDRFNNYR 60
LFPRLQKLE SDYFRYYKVN LKRPCPFWND ISQCGRRDCA VKPCQSDEVP DGIKSASYKY 120
SEENANLIEE CEQAEERLAV DESLSEETQK AVLQWTKHDD SSDNFCEADD IQSPEAEVVD 180
LLLNPERYTG YKGPDAWKI NVIYEENCFK PQTIKRPLNP LASGQQTSEE NTPYSWLEGL 240
CVERAFYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEPQQRFDG ILTEGGPRR 300
LKNLYFLYLI ELRLSKVLP FFERPDQLF TGNKIQDEEN KMLLEILHE IKSPLHFDPE 360
NSFPAGDKKE AHKLKEDFRL HFRNISRIMD CVGCFKCLRW GKLTQQLGT ALKILFSEKL 420
IANMPESGPS YEFILTRQEI VSLFNAFGRI STSVKELENF RNLLQNIH 468

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Seq ID NO: C266 Protein Sequence  
Protein Accession #: NP\_002879.1

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1 11 21 31 41 51
| | | | |
MQPRRQLRPA FWSGPRGRPR TAPLLALLL LAFVAAPAGS GGPDDPGQPQ DAGVPRRLIQ 60
QKARAALHFF NFRSGSPSAL RVLAEVQEGR AWINPKEGCK VHVVFSTERY NPESLLQEGE 120
GRIGKCSARV FFKNQKPRPT INVTCTRLIE KKKRQQEDYL LYKQMKQLKN PLEIVSIPDN 180
HGHIDPSLRL IWDLAFGLSS YVMWEMTTQV SHYLLAQLTS VRQWVRKT 228

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Seq ID NO: C267 Protein Sequence
Protein Accession #: NP_005400.1
1 11 21 31 41 51
| | | | |
MSVKGMAIAL AVILCATVVQ GPMPFKRGRC LCIGPGVKAV KVADIEKASI MYPNNCDKI 60
EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

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75  
80

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Seq ID NO: C268 Protein Sequence
Protein Accession #: FGENSEH predicted
1 11 21 31 41 51
| | | | |
MLRQVLRRGL QSFCHRLGLC VSRHPVFFLT VPAVLITITG LSALNRFPQE GDLERLVAPS 60
HSLAKIERSL ASSLFPLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120
VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIISVLEDL RQAAVSNKTT ARVQVRYFNT 180
KLKVCSPCML LPKEAALHFF LP 202

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Seq ID NO: C269 Protein Sequence  
Protein Accession #: NP\_002429.1



	1	11	21	31	41	51	
5	MRLPLLLVFA	SVIPGAVLLL	DTRQFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	60
	VSESIQMSVA	FKLCGLVPSK	TDWVAITLYA	CDKSSEFQKW	ECKNDTLLGI	KGEDLFFNYG	120
	NRQEQINIMLY	KGSGLWSRWK	IYGTDDNLCS	RGYEAMYTL	GNANGATCAF	PFKFNKMYA	180
	DCTSAGRSDDG	WLNCGITTDY	DTDKLFGYCP	LKFEGSESLW	NKDPLTSVSY	QINSKSALTW	240
	HQARKSCQQQ	NAELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNSLSFNSGW	QMSDRSPFRY	300
10	LNLWPGSPSA	EPGKSCVSLN	PGKNKAWENL	ECVQKLGYYC	KKGNTTLNSF	VIPSESDVPT	360
	HCPSQWKPYA	GHCYKIHRRDE	KKIQRDALTT	CRKEGGDLTS	IHTIEELDFI	ISQLGYEPND	420
	ELWIGLNDIK	IQMYFWSDG	TPVTFTKWL	GEPSHENNRQ	EDCVVMKGKD	GYWADRGCW	480
	PLGYICKMKS	RSQCPETIVE	EKGCRKGWKK	HHFYCYMIGH	TLSTFAEANO	TNNENAYLT	540
	TIEDRYEQAF	LTSFVGLRPE	KYFWTGLSDI	QTKGTFFQWTI	EEEVRFTHWN	SDMPGRKPGC	600
	VAMRTGIAGG	LWDVLKCEK	AKFVCKHWA	GVTHPPKPTT	TPEPKCPEDW	GASSRTSLCF	660
15	KLYAKGKPYA	KTWFSRDFC	RALGGDLASI	NNKEEQQTW	RLITASGSYH	KLFWLGLTYG	720
	SPSEGGTDE	GSPVSYENWA	YGEFNNYQNV	EYCGELKQDP	TMSWMDINCE	HLNWMICQIQ	780
	KGQTPKPEPT	PAQDNPPFVT	EDGWVIYKDY	QYFYSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESEKPLMKY	VNRDQAQSA	FIGLLISLDK	KFAWMDGSKV	DYVSWATGEP	NFANEDENCV	900
20	TMYNSGPFVN	DINGCPNFA	ICQRHNSIN	ATTVMPTMPS	VPSGCKEGWN	FYSNCKPFIF	960
	GFMBEERQW	QBARAKACIG	GGNLVSIQNE	KEQAPLTYHM	KDSTFSAWTG	LNDVNSEHTF	1020
	LWTDGRGVHY	WTWCKGYPGG	RRSSLSEYDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPLKTNP	PAITQDTGCV	KYKSSYSLSM	RQKQWHEAE	TYCKLHNSLI	ASILDYFNSA	1140
	FAWLQMETSN	ERVHIALNSN	LTDNQYTWD	KWRVRYTNWA	ADEPKLSAC	VYLDLDGYWK	1200
25	TAHCNESFYQ	LCKRSDEIPA	TEPPQLPGR	PESDHTAWIP	FHGHCYIYES	SYTRNMGQAS	1260
	LECLRMGSSL	VSISAAESS	FLSYRVEPLK	SKTNFWIGLF	RNVEGTWLIW	NNSPVSVFNW	1320
	NTGDPGGERN	DCVALHASSG	FWSNIHCSSY	KGYICKRPKI	IDAKPTHELL	TTKADTRKMD	1380
	PSKPSNVAG	VVIIVILLIL	TGAGLAAYFF	YKRRVRLPQ	EGAPENTLYF	NSQSPGTS	1440
	MKDLVGNIEQ	NEHSVI					1456

Seq ID NO: C270 Protein Sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LLFPLSSRTQ	KLPTRDEELF	QMQIRDKAFF	HDSSVIPDGA	EISSYLFRDT	60
	PKRYFFVVEE	DNTPLSVTVT	PCDAPLEWKL	SLQELPEDRS	GGSGDLEPL	EQKQKQIINE	120
	BGTLELFSYK	NDVYEFISS	SPSGLYQLDL	LSTEKDTHFK	VYATTPESD	QYPPELPYDP	180
	RVDVTSLGRT	TUTLAWKPSP	TASLLKQPIQ	YCVVINKEHN	FKSLCAVEAK	LSADDAFMA	240
40	PKPGLDFSPF	DFAHFGFPSP	NSGKERSFQA	KPSPKLGRHV	YSRPKVDIQK	ICIGNKNIFT	300
	VSDLKPDQTY	YDFVFNININ	SNMSTAYVGT	FARTKEEAKQ	KTVELKDQGI	TDVFKRKGA	360
	KFLRFAPVSS	HQKVTFFIHS	CLDAVQIQVR	RDGKLLLSQN	VEISIQOQLR	GKPKAKYLVR	420
	LKGNKGASDM	LKILATTRPT	KQSPSLPED	TRIKAFDKLR	TCSSATVAML	GTQERNKFCI	480
	YKKEVDNIN	EDQKREQNO	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTE	TIKGLQPGKS	540
45	YLLDVYVIGH	GGHSVKYQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence  
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QMEKKLQEP	RSTRNKEKED	RESSEYWKKS	GKVGKLVNQ	YMSQNKGNV	60
	VKFSAGKVKL	KLLKQIQEP	VKPTVNYKMA	NSSECEKPKI	NGKVCQCEN	KAALLVCLCE	120
	GEDYCSGCPA	NVHQKQALKL	HRTTLLQARS	QILFNVLDA	HQFIKDVND	EPKEENNSTK	180
55	ETSKIQHKPK	SVLLQSSSE	VEITTMKRAQ	RTKPRKSLLC	EGSFDEEASA	QSPQEVLSQW	240
	RTGNHNDNKK	QNLHAAVKDS	LEECEVQTNL	KIWRREPLNIE	LKEDILSYMB	KLWLKXHRR	300
	PQEQLFKCYQ	IRSHHMKPL	VMHSVLKMK	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence  
Protein Accession #: NP\_078963.1

	1	11	21	31	41	51	
60	MEKLNKXKGR	RTPQEQLFQM	LSDTFFPHPE	TTGDAQCSQN	ENDEDSGDEE	TKVQHTALLL	60
	PVETLNIERP	EPSLKIVELD	DTYEEEFEEA	ENIVPYKVKL	ADADSQRSCA	PHDCQKNSFP	120
65	YENGIGHHV	FDKGRDPLN	LCLANSSTYY	KDNKGETSN	TDFDNIIVDP	VYSSDIEKIE	180
	ESTSPERNLK	EKNIGLESNQ	KSDSDCVSLE	SKDTLLGRDL	EKAPIEEKLS	QDIKESLELS	240
	NLYKRPSPFE	SKTTKSSLLL	QEIACRSKPI	TKQYQGLERF	FIFDTNERLN	LLPSHRLCEN	300
	NSSTRITLAE	DREWIPDHS	SEYADNAIVL	GVLQGAQSPS	SSRKQKQMGQ	KSQRPSTANF	360
70	PLNSVSKESS	SCLSSSHPRS	RSAAAQSSSR	AASEISEIEY	IDITDQNELS	LDDTTDQHTL	420
	DNLEKELQVL	RLADTSEKL	YSLTSEFPD	FSSQSLNISQ	ISTDFLKTSH	VRGPCGVVEEL	480
	SCSGRDTKIQ	SLSLSESST	DEEEDFLNK	QHVITLPSK	ST		522

Seq ID NO: C273 Protein Sequence  
Protein Accession #: NP\_005399.1

	1	11	21	31	41	51	
75	MKVSALLCLL	LLMTAAFNPO	GLAQPDALNV	PSTCCFTFSS	KKISLQRLKS	YVITTSRCPO	60
80	KAVIFRTKLK	KEICADPKEK	WVQNYMKHLG	RKAHTLKT			98

Seq ID NO: C274 Protein Sequence  
Protein Accession #: BAC05158.1

	1	11	21	31	41	51
--	---	----	----	----	----	----

1348

GSYEYPVAEK AELSCWEEGN GRIALQGTLL NTYVCSILIR TTMEVGFIIVG QYFIYGIFLT 180  
 TLHVCRNSPC PHVNVYVSR PTEKNVFIVF MLAVAALSLL LSLAELYHLG WKIKIRQRFVK 240  
 PRQHMAKQCL SGSPVGIVQS CTPPPDFNQC LENGPGGKFF NPFSNNMASQ QNTDNLVTEQ 300  
 VRGQEQTPEE GFIQVRYGQK FEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLVS 358

Seq ID NO: C281 Protein Sequence  
 Protein Accession #: NP\_055274.2

1 11 21 31 41 51  
 | | | | |  
 MYLSICCCFL LWAPALTKN LNYSVPBEEQ AGTVIGNIGR DARLQPLPFP AERGGGGRSK 60  
 SGSYRVLENS APHLLDWDAD SGLLYTKQRI DRESLCRHNA KCQLSLEVFA NDKEICMIKV 120  
 EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDPD AGENGLRITYL LTRDDHGLFG 180  
 LDVKSRRGDT KFPELVIQKA LDREQQNHHT LVLTAIDGGE PPRSATVQIN VKVIDSNDNS 240  
 PVFEAPSYLV ELPENAPLGT VVIDLNATDA DEGPNGEVLY SFSSYVPPDRV RELFSIDPKT 300  
 GLIRVKGNDL YEENGLMELID VQARDLGPNP IPAHCCKVTVK LIDRNDNAPS IGFVSVRQGA 360  
 LSEAPPGTV IALVRVTRDR SKNGQLQCR VLGGGCTGGG GGLGGPGGSV PFKLEENYDN 420  
 FTVTVTRDPL DRETQDEYNV TIVARDGGSP PLNSTKSFAP KILDENDNPP RFTKGLYVLQ 480  
 VHNNIPGEY LGSVLAQDPD LQNGTVSYVS ILPSHIGDVS IYTYVSVNPT NGAIYALRSP 540  
 NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTVLDVNDNA FVIVLPTLQN DTAELQVPRN 600  
 AGLGYLVSTV RALSDRFGES GRLTYEIVDG NDDHLFEIDP SSGEIRTLPF FWEDVTPVVE 660  
 LVVKVTDHGK PTLASAVAKLI IRSVSGSLPE GVPVRNGEQH HWDMSLPLIV TLSTISIILL 720  
 AAMITIAVKC KRENKEIRTY NCRIAESYSHP QLGGGKGKKK KINKNDIMLV QSEVEERNAM 780  
 NVMNVSSPS LATSPMYFDY QTRLPLSSPR SEVMYLPKAS NNLTVPQGHG GCHTSFTGQG 840  
 TNASETPATR MSIIQTDNFP AEPNYMGSRO QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence  
 Protein Accession #: NP\_005592.1

1 11 21 31 41 51  
 | | | | |  
 MELCRSLALL GSSGLMFCL IALSTDFWFE AVGPTHSAHS GLWPTGHGDI ISGYIHTQT 60  
 FSIMAVLWAL VSVSEFLVSC FPSLFPPGHG PLVSTTAFAA AAISMVVAMA VYTSEKWDQP 120  
 PHPQIQTFPS WSPYLGWVSA ILLCTGALS LGAHCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence  
 Protein Accession #: NP\_006424.2

1 11 21 31 41 51  
 | | | | |  
 MATWALLLLA AMLLGNPGLV FSRLSPEYYD LARAHLRDEE KSCPCLAQEG PQGDLLTKTQ 60  
 ELGRDYRTCL TIVQKLKXKV DKPTQRSVSN AATRVCTGR SRWRDVCNRF MRRYQSRVTQ 120  
 GLVAGETAQQ ICEDLRLCIP STGPL 145

Seq ID NO: C284 Protein Sequence  
 Protein Accession #: NP\_005594.1

1 11 21 31 41 51  
 | | | | |  
 MKVSAALAV ILIATLALCAP ASASPYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP 60  
 AVVFVTRKMR QVCANPEKKW VREYINSLEM S 91

Seq ID NO: C285 Protein Sequence  
 Protein Accession #: NP\_071437.1

1 11 21 31 41 51  
 | | | | |  
 MAPGRAVAGL LLLAAAGLGG VAECPGLAFS EDVLSVPGAN LSLSAAQLQH LLEQMGAASR 60  
 VGVPEPGQLH FNQCLTAEEI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPKHK 120  
 TRPSHSEVWG YGFLSVTIIN LASLLGLILT PLIKKSYFPK ILTFFVGLAI GTLFSNAIFQ 180  
 LIPEARGFDP KVDSYVEKAV AVFGGFYLLF FFERMLKMLL KTYGQNGHST PGNDNFGPQE 240  
 KTHQPKALPA INGVTCYANP AVTEANGHIH FDNVSVVSLQ DGKKEPSSCT CLKGPKLSEI 300  
 GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSIAT LCEEPFHELQ DVFILLNAGM 360  
 STRQALLFNF LSACSCYVGL AFGILVGNF APNIIIFALAG GMFLYISLAD MFPFEMNDMLR 420  
 EKVTRKRTDF TFFMIQNAGM LTGFTAILLI TLYAGEIELE 460

Seq ID NO: C286 Protein Sequence  
 Protein Accession #: NP\_004175.1

1 11 21 31 41 51  
 | | | | |  
 MPNSEPASLL ELFNSIATQG ELVRSKAGN ASKDEIDSAV KMLVSLKMSY KAAAGEDYKA 60  
 DCPFGNPAFT SNHGPDATEA EEDFVDPWTV QTSSAKGIDY DKLIVRFGSS KIDKELINRI 120  
 ERATGQRPFH FLRRGIFFSH RDMNQVLDAY ENKPPFYLYT GRGSPSEAMH VGHLPFFIFT 180  
 KWLQDVFNVE LVIQMTDEK YLWKDLTLDQ AYGDVAENAK DIIACGFDIN KTFIFSOLDY 240  
 MGMSSGPKYN VVKIQKHVTF NQVKGIFGFT DSDCIGKISF PAIQAAPSPS NSPPQIFRDR 300  
 TDIQCLIPCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF 360  
 LTDTAQIKT KVNKHAFSGG RDTIEHRQF GGCNDVDVSF MYLTFPLEDD DKLEQIRKDY 420  
 TSGAWLTGEL KKAIEVLQP LIAEHQARRK EVIDEIVKEF MTPRKLSDFF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP\_004929.1

	1	11	21	31	41	51	
5	MTVFRQENV	DYDTEGEE	LGSGQFAVVK	REKSTGLQYA	AKFIKKRRRTK	SSRRGVSRED	60
	IEREVSILKE	IQHPNVITLH	EVYENKTDVI	LILELVAGGE	LFDFLAEKES	LTEEEATEPL	120
	KQILNGVYYL	HSLQIAHFDL	KPENIMLLDR	NVPKPRIKII	DFGLAHKIDF	GNEFKNIFGT	180
	PEFVAPEIVN	YEPLGLEADM	WSIGVITYIL	LSGASPLFGD	TKQETLANVS	AVNYEFEDY	240
10	FSNTSALAKD	FIRRLVVKDP	KKRMTIQDSL	QHPWIKPKDT	QQALSRKASA	VNMEKFKKFA	300
	ARKKWKQSVR	LISLQQLRSR	SFLSRSNMSV	ARSDDTLDEE	DSFVMAIIH	AINDDNVPLG	360
	QHLGSLSNY	DVNQPNKHGT	PPLLIAAGCG	NIQILQLLIK	RGSRIDVDQK	GGSNNAVWAA	420
	RHGHVDTLKF	LSENKCPLDV	KDKSGEMALH	VAARYGHADV	AQVTCASQAQ	IPISRTKEEE	480
	TPLHCAAWHG	YYSVAKALCE	AGCNVNIKNR	EGETPLLTAS	ARGYHDIVCE	LAEHGADLNA	540
	CDKDGHIHAL	LAVRRQCMVE	TKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPVIVVACEA	600
15	NCNLDISKNY	GRTPHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSBQHEHVA	660
	GLLARLRKDT	HRGLFQQQLR	PTQNLQPRIK	LKLFQHGSGG	KTTLVESLKC	GLLSFFRRR	720
	RPRLSSTNSS	RFPSPPLASK	PTVSVSINN	YPCENVSVR	SRSMMFEPGL	TKGMLVFEVA	780
	PTHHPHCSAD	DQSTKAIDIQ	NAYLNGVGDF	SVWEFSGNPV	YFCYDYFAA	NDPTSIHVVV	840
	FSLEEPYEIQ	LNPFVFWLSE	LKSLVPVEEP	IAPGGKLNPN	LQVVLVATHA	DIMNVPRPAG	900
20	GEFGYDKDTS	LLKEIRNRFG	NDLHISNKL	VLDAGASGSK	DMKVLNRHLQ	EIRSQIVSVC	960
	PPMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQLHSTG	1020
	EINIMQSETV	QDVLLLDPRW	LCTNVLGKLL	SVETPRALHH	YRGYTVEDI	QRLVPSDSVE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPALIKT	DNLHRSWADE	EDEVVYGGV	RIVPVEHLTP	1140
	FPCGIFHKVQ	VNLRCWIIHQ	STEGDADIRL	WVNGCKLANR	GAEILVLVNV	HGQGIQVQVR	1200
25	GLETEKIKCC	LLLDSCVSTI	ENVMAITLPG	LLTVKHVYLS	QQLREHHEPV	MIYQPRDFPR	1260
	AQTLKETSIT	NTMGYKESF	SSIMCPGCHD	VYSQASLGMD	IHASDLNLLT	RRKLSRLLD	1320
	PDPLGKDWCL	LAMNLGLPDL	VAKYNTNNGA	PKDLPLSPLH	ALLREWTTPY	ESTVGTLMSE	1380
	LRELGRDDAA	DLILKASSVF	KINLDGNGQE	AYASSCNSGT	SYNSISSVVS	R	1431

Seq ID NO: C288 Protein Sequence  
Protein Accession #: NP\_002072.1

	1	11	21	31	41	51	
35	MELRARGWWL	LCAAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSQVP	QAEISGEHLR	60
	ICPGGYTCCT	SEMEENLANR	SHAELETALR	DSSRVQLAML	ATQLRSFDDH	FQHLNDSESR	120
	TLQATFPFAP	GELYTQNARA	FRDLYSELRL	YVRGANLHLE	ETLAEFWARL	LERLFKQLHP	180
	QLLLPDDYLD	CLGKQAEALR	PFGAEAPREL	LRATRAFVAA	RSFVQGLGVA	SDVVRKVAQV	240
40	PLGPECSRVA	MKLVCACHCL	GVPGARPCPD	YCRNVLGKCL	ANQADLDAEW	RNLLDSMVL	300
	TDKFWGTSGV	ESVIGSVHTW	LAEAINALQD	NRTDLTAKVI	QCGGNPKVNP	QGGPPEEKRR	360
	RGKLAPREPR	PSGTLEKLVS	EAKAQLRDVQ	DFWISLPGTL	CSEKMAISTA	SDDRCWNGMA	420
	RGRYLPEVMG	DGLANQINNP	EVEVDITKPD	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDFQD	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence  
Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILIYFLFL	LWEDTQGWGF	KDGIFHNSIW	LERAAAGVYHR	EARSQKYKLT	YAEAKAVCEP	60
	EGGHLATYKQ	LEAARKIGFH	VCAAGWMAKG	RVGYPIVPGK	PNCQGFQGTI	IDYGIRLNRS	120
	ERWDAYCYNP	HAKGCGVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELPPDDIIS	TGNVMTLKPL	SDASVTAGGF	240
55	QTKYVAMPDV	SKSSQCKNTS	TTSTGNKNFL	AGRFPSHL			277

Seq ID NO: C290 Protein Sequence  
Protein Accession #: NP\_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLFSLARGS	EVGNSQAVCP	GTLNGLSVTG	DAENQYQTLY	KLYERCEVVM	60
	GNLEIVLTGH	NADLSFLQWI	REVTGVVLVA	MNEFSTLPLP	NLRVVRGTQV	YDGKFAIFVM	120
	LNNTNNSSHA	LRQLRLTQLT	EILSGGVYIE	KNDKLCHMDT	IDWRDIVRDR	DAEIVVKDNG	180
	RSCPPCHEVC	KGRGCGPGSE	DCQTLTKTIC	APQCNHCFPG	PNPQCCCHDE	CAGGCSGPQD	240
65	TDCFACRHFN	DSGACVPRCP	QPLVYNKLT	QLEPNPHTKY	QYGGVCVASC	PHNFVVDQTS	300
	CVRACPPDKM	EVDKNGLKMC	EPCGGLCPKA	CEGTGSGSRE	QTVDSNNIDG	FVNCTKILGN	360
	LDPLITGLMG	DPWHKIPALD	PEKLNVERTV	REITGYLNIQ	SWPPHMHNSF	VFSNLTITIG	420
	RSLYNRGFSL	LIMKNLNVTS	LGFRSLKEIS	AGRIYISANR	QLCYHHSINW	TKVLRGPTEE	480
	RLDIKHNRPR	RDCVABGKVC	DPLCSSGGCW	GPQPGQCLSC	RNYSRGGVCV	THCNFLNGEP	540
70	REFPAHEAEC	SCHPECPMG	GTATCNGSGS	DTCAQCAHFR	DGPHCVSSCP	HGVLGAKGPI	600
	YKYPDVQNEC	RPCHENCTQG	CKGPELQDCL	GQTLVLIGKT	HLTMALTVIA	GLVVIFFMLG	660
	GTFLYWRGRR	IQNKRAMRRY	LERGESIEPL	DPSEKANKVL	ARIFKETELR	KLKVLGSGVF	720
	GTVHKGWVWP	EGESIKIPVC	IKVIEDKSGR	QSFQAVTDEM	LAIGSLDAH	IVRLGLGLCPG	780
	SSLQLVTQYL	PLGSLLDHVR	QHRGALGPQL	LLNMGVQIAK	GMYYLEEHGM	VHRNLAARNV	840
75	LLKSPSQVQV	ADFGVADLLP	PDDKQLLYSE	AKTPIKWMAL	ESIHFQKYTH	QSDVNSYGV	900
	VWELMTFGAE	PYAGLRLEAV	PDLLEKGERL	AQPICTIDV	YVMVVKCMI	DENIRPTFKE	960
	LANEFTRMAR	DPPRYLVIKR	ESGPGIAPGP	EPHGLTNKKL	EVELEPELD	LDLDLEAED	1020
	NLATTILGSA	LSLPVGTILN	PRGSQSLLSP	SSGYMPMNQ	NLGGSCQESA	VSGSSERCPR	1080
	PVSLHMPRPG	CLASESEGH	VTGSAELQ	KVSMCRSR	SRSPPRPGDS	AYHSQRHSL	1140
80	TPVTPLSPPG	LEEDVNGYV	MPDTHLKGTP	SSREGTLSSV	GLSSVLGTEE	EDEDEEYEM	1200
	NRRRRHSFPH	PPRPSLEEL	GVEYMDVGS	LSASLGSTQS	CPLHVPVIMP	TAGTTPDEDY	1260
	EYMNRRQDGG	GPGGDYAAAG	ACPAEQGYE	EMRAPQGGH	QAPHVHYARL	KTLSLEATD	1320
	SAFDNPDYWH	SRLFPKANAQ	RT				1342

Seq ID NO: C291 Protein Sequence  
Protein Accession #: NP\_001207.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MAPLCSPWL PLLIPAPAG LTVQLLSLL LLMPVHPQL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEGSLKL EDLPTVEAPG 120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPFW RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
ELLGQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
VEGHRFPAL EHVHLSTAF RVDALGRPG GLAVLAAPLE EGPEENSAYE QLLSRLEEIA 300
EEGSETQVPG LDISALLPSD PSRYFYEGS LTPPCAQGV INTVFNQTM LSAKQLHTLS 360
DTLWGPDSR LQLNFRATQ LNRGVIEAS PAGVDSSPRA AEFVQLNSCL AAGDILALVF 420
GLLFAVTSVA FLVQMRQRH RGTGGVSYR PAEVAETGA 459
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15 Seq ID NO: C292 Protein Sequence  
Protein Accession #: NP\_004198.1

```
20      1      11      21      31      41      51
      |      |      |      |      |      |
MGGAVVDEGP TGVKAPDGGW GMAVLEGCFF ITGFSYAFPK AVSVFFKELI QEFGIGYSDT 60
AWISSILLAM LYGTGPLCSV CVNRFGRCPV MLVGGPLASL GMVAASPCRS IIQVYLTIGV 120
ITGLGLALNP QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGRWGGF 180
LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFDRGRFVL YAVAASVMVL 240
GLFVPPPVFV SYAKDLGVDP TKAAPLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFPSF 300
SMFFNGLADL AGSTAGDYGG LVVFCIPFGI SYGMVGALQF EVLMAIVGTH KFSSAIGLVL 360
LMEAVAVLVG PPSGGLLDA THVVMYFVIL AGAEVLTSSL ILLGNFFCI RKKPKPEQPE 420
VAAEEEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSU 465
```

30 Seq ID NO: C293 Protein Sequence  
Protein Accession #: NP\_000349.1

```
35      1      11      21      31      41      51
      |      |      |      |      |      |
MALFVRLAL ALALALGPA TLAGPAKSPY QLVLQHSRLR GRQHGNVCA VQKVIGTNRK 60
YFTNCKQWY RKICCKSTVI SYECCPGYEK VPGEKGCFA LPLSNLYETL GVVGGTTTQL 120
YTDRTEKLRP EMEGPGSFTI FAPSNEAWAS LPAEVLDSL VSNVIELLNA LRYHVMGRRV 180
LTDELKHGMT LTSMYQNSNI QIHYPNGIV TVNCARLLKA DHATNGUVH LIDKIVSTIT 240
NNIQQIIEIE DTFETLRAAV AASGLNTMLE GNGQYTLAP TNEAFKIPS ETLNRLGDP 300
EALRDLNHN ILKSAMCAEA IVAGLSVETL EGTTLLEVCS GDMLTINGKA IISNKDILAT 360
NGVIHYDEL LIPDSAKTLF ELAASDVST AIDLFRQAGL GNHLSGSERL TLLAPLNSVF 420
KDGTPPIDAH TRNLRLNHI KDQLASKYLY HGQTLETGG KKLRFVYRN SLCIENS CIA 480
AHDKRGYGT LFTMDRVLT PMGTVMVLK GDNRFMSLVA AIQSAGLTET INREGVYTVF 540
APTNEAFRAL PPRERSRLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
LKQNVVSVNK EPVAEPDIMA TNGVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660
SRASQSVRL APVYQKLLER MKH 683
```

Seq ID NO: C294 Protein Sequence  
Protein Accession #: NP\_006527.1

```
50      1      11      21      31      41      51
      |      |      |      |      |      |
MTQRSIAGPI CNLKFVTLV ALSSLEPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLIEN 60
IKEMITEASF YLFNATKRRV PFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGHA 120
GDDPYTLQVR GCGKEGKYIH FTFNPLNDN LTAGYGSRRG VVFEHWAHLR WGVFDEYNND 180
KPFYINGQNG IKVTRCSSDI TGIFVCEKGP CPQENCIIISK LFKEGCTFIY NSTQNATASI 240
MFMQSLSSVV EFCNASTHNQ EAPNLQNM C SLRSAMDVIT DSADFHSFP MNGTELP PPP 300
TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAABPYLM QIVEIHTFVG IASFDKGEI 360
RAQLHQINSN DDKRLVSYL PTVSAKTDI SICSLKKGF EVVEKLANGKA YGSVMILVTS 420
GDDKLGNC L PTVLSSGSTI HSIALGSSAA PNLEELSLRT GGLKFPVFDI SNSNSMIDAF 480
SRISSTGDI PQHIQLEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540
FDPDGRKYIT NNFITNLTPR TASLWIPGTA KPGHWYTLN NTHSLQALK VTVTSRASNS 600
AVPPATVEAF VERDSLHFP PVMYIANVKQ GFYPILNATV TATVEPETGD FVTLRLDDG 660
AGADVIKNDG IYSRYFFSPA ANGRYSKLVH VNHSFSTIS AHSIPGSHAM YVPGYTANGN 720
IQMNA PRKSV GRNEERKMG PSRVSSGSGF SVLGVPAGPH PDVFPCKII DLEAVKVEE 780
LTLSTAPGE DFDQGGATSY EIRMSKSLQ IQDDFNAIL VNTSKRNFQ AGIREIFTFS 840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
LILKGVLTAM GLIGIICLII VVTHETLSRK KRADKENG T KLL 943
```

70 Seq ID NO: C295 Protein Sequence  
Protein Accession #: Eos sequence

```
75      1      11      21      31      41      51
      |      |      |      |      |      |
MKFLILLILQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFF REMPGGPVWR KHYITYRINN 120
YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAGD FHAFDGKGGI 180
LAHAFPGSG IGGDAHFDED EFWTHSGGT NLFLTAVHEI GHSGLGHSS DPKAVMFTTY 240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTVGNKIFP 300
FKDRFFNLK SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
EENYPKSIHS FGFPNFVKKI DAAVFNPFPY RTYFFVDNQY WRDERRQMM DPGYPKLITK 420
NQQIGPKID AVFYSKIKY YFPQGSNQFE YDFLLQRTK TLKSNSWFGC 470
```

Seq ID NO: C296 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 5 MKFLILLLQ ATASGALPLN SSTLEKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60  
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHVF REMPGGFVWR KHYITYRINN 120  
 YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAGHD FHFADGKGGI 180  
 LAHAFPGSG IGGDAHFEDD EFWTTHSGGT NLPLTAVHAI GHSILGLGHSS DPKAVMFPTY 240  
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300  
 10 FKDRFPWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360  
 EPNYPKSIHS FGPFNVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420  
 NFGIGPKID AVFYSKNKY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC 470

Seq ID NO: C297 Protein Sequence  
 Protein Accession #: NP\_008883.1

1 11 21 31 41 51  
 15 MAKDNSTVRC PQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60  
 IGIFVIGICLF CLSVLIGIVI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120  
 20 FLKQMLERYQ NNSPNNDDQ WKNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180  
 DADYPWPRQC CVMNNLKEPL NLEACKLGVF GFYHNNQCYE LISGPMNRHA WGVAVFGFAI 240  
 LCWTFWVLLG TMFYWSRIEY 260

Seq ID NO: C298 Protein Sequence  
 Protein Accession #: NP\_001784.2

1 11 21 31 41 51  
 25 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPQQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120  
 30 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180  
 YELFGHASE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 35 TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHVQRLT VTDLADPNP 360  
 AWRATYILMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGPEVC VYTAEDPDKE NQKISYRIIR 480  
 DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGILLTLTID 540  
 40 VNDEGFPVEP RQITICNQSP VRQVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KDQTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720  
 GLEAPPEVVL RNDVAPTIIP TMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMVGGGEDD 829

Seq ID NO: C299 Protein Sequence  
 Protein Accession #: NP\_005620.1

1 11 21 31 41 51  
 45 MAKKAENGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD 60  
 50 FIMSCVGFV IFSVGGMIGS LCYKNGGGVF LIPYVLIALV GGIPIFFLEI SLGQFMKAGS 120  
 INVWNICPLF KGLGYASPMI VFYCNITYIM VLAWGFYLV KSFTTLPLWA TCGHTWNTPD 180  
 CVEIFRHEDC ANASLANLTC DQLADRRSFV IEFWENKVL RSGGLEVPGA LNWEVTLCLL 240  
 ACWVLVYPCV WKGVKSTGKI VYFTATFPYV VLVVLLVRGV LLPGALDGII YYLKPDSKSL 300  
 55 GSPQWIDAG TQIFPSYAIG LGALTALGSY NFNNNNCKYD AIIALALINS TSFPAGFVVF 360  
 SILGFMAEQS GPGLAFIAYP RAVTIMPVAP LMAALFFPML LLLGLDSQFV 420  
 GVEGFTGLL DLLPASYFR FOREISVALC CALCFVIDLS MVTDDGMVYF QLFDDYSASG 480  
 TLLWQAWE CVVVAWVYGA DRFMDIACM IGYRCPWMK WCHSFTPLV CMGIFIFNVV 540  
 60 YYEPLVYMYT YVYPWNGEAM GWAPALSSML CVPLHLGLCL LRAKGTMAER WQHLTQPIWG 600  
 LHLLEYRAQD ADVRLTTLT PVSESSKVVV VESVM 635

Seq ID NO: C300 Protein Sequence  
 Protein Accession #: NP\_006507.1

1 11 21 31 41 51  
 65 MEPSSKKLTG RLMLAVGGAV LGSLLQFGYNT GVINAPQKVI EEFYNQTVWH RYGESILPFT 60  
 LTLNLSLVA IFSVGGMIGS FSVGLFVNRF GRNNSMLMMN LLAFLVSAVL GFSKLKGSPE 120  
 70 MLILGRFIIG VYQGLTTGFPV PMYVGEVSPT AFRGALGTLH QLSIVVGILI AQVFLGDSIM 180  
 GNKOLWPLLL SIIFIPALLQ CIVLPFCPEP PRLLINRNE ENRAKSVLKK LRGTADVTHD 240  
 LQEMKEESRQ MMREKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSIFEK 300  
 AGVQFPVYAT ICGSIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLE 360  
 75 LPWMSVLSIV AIFGVVAFVE VGPPIPWF1 VAEFLSQGPR PAALAVAGPS NWTSNFIVGM 420  
 CFQYVEQLCG PYVFIIFTVL LVLFIFTYF KVPETKGRTP DEIASGFRQ GASQSDKTPE 480  
 ELFHLGADS QV 492

Seq ID NO: C301 Protein Sequence  
 Protein Accession #: XP\_035292.2

1 11 21 31 41 51  
 80 MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60  
 GTIIGSGIFV TPTGLVKEAG SPGLALVWA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120  
 LEVYGSPLAF LKLWIELLII RPSSQYIVAL VPATYLLKPL PPTCPVEEA AKLVACLCLV 180  
 LLTAVNCYSV KAATRVQDAF AAACLALAL IILLGFVQIG KGDVSNLDPN FSEGTKLVDV 240

5 GNIVLALYSQ LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300  
 STEQMLSSSEA VAVDGNVYHL GVMWIIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360  
 SILSMIHQPL LTFPVSLVFT CVMTLLEYAFS KDIFSVINFF SFFNWLVCVAL AIGMIWLRH 420  
 RKPELERPIK VNLALPVFFI LACFLIAVS FWKTPVECGI GFTIILSGLP VYFPGVWKN 480  
 KFKWLLQGIF STTVLCQKLM QVVPQET 507

Seq ID NO: C302 Protein Sequence  
 Protein Accession #: NP\_005259.1

10 1 11 21 31 41 51  
 MNWSIFEGLL SGVKNYSTAF GRWLVLVFI FRVLVYLTA ERVNSDDHKD FDCNTRQPGC 60  
 SNVCFDEFFP VSHVRLMALQ LILVTCPSLL VVMHVAYREV QEKRRHREAHG ENSGRLYLNP 120  
 15 GKRRGGLMWT YVCSLVFKAS VDIAPLYVFH SFYPKYLPP VVKCHADPCF NIVDCPISKP 180  
 SEKNIFTLFM VATAICILL NLVELIYLV KRCHECLAAR KAAQAMCTGHH PHGTTSSCKQ 240  
 DLLSGDLIF LGSDSHPLL PDRPRDHVK TIL 273

Seq ID NO: C303 Protein Sequence  
 Protein Accession #: NP\_005121.1

20 1 11 21 31 41 51  
 MKICSLTLLS FLLAAQVLL VEGKKVKVNG LHSKVSEQK DTLGNTQIKQ KSRPGNKGKF 60  
 VTKDQANCRW AATQEEGIS LKVECTQLDH BFSCVFAGNP TSCLKLKDER VYWKQVARNL 120  
 25 RSQKIDICYS KTAVKTRVCR KDFPESLSKL VSSTLFGNTK PRKEKTEMSP REHKGKETT 180  
 PSSLAVTQM ATKAPECVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence  
 Protein Accession #: AAH22542

30 1 11 21 31 41 51  
 MCSEIILRQE VLKDGFRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPEYASLRE 60  
 RNITEAVMVS ENFDIEAPNY LSKESEVLIY ARRDSQCIDC FQAFLPVHCR YHRPHSEDEG 120  
 35 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180  
 WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence  
 Protein Accession #: NP\_004985.1

40 1 11 21 31 41 51  
 MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEYLY RYGYTRVAEM 60  
 RGEKSLGPA LLLQKQLSL PETGELDSAT LKAMRTPRCG VPDIGRFQTF EGDLEWHHNN 120  
 45 ITYWIQNYSE DLPRVIDDA PARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180  
 FDGKGLLAH AFPPGPIQG DAHFDDELW SLGKGVVPT RFGNADGAAC HFFPIFEGRS 240  
 YSACTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIPQGSYS 300  
 ACTTDGRSDG YRNCATTANY DRDKLFGFCP TRADSTVMOG NSAGELCVFP FTFIGKEYST 360  
 CTSEGRGDGR LWCATTNPD SDKKGWFCPD QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420  
 50 PMYRFTGEPF LHKDDVNGIR HLYGPRPEPE PRPPTTTTQ PTPAPTVCPT GPPTVHPSE 480  
 FTAGTGPSPS AGPTGPPTAG PSTATTVPLS FVDDACNVNI FDAIAEIGNQ LYLFDKDKYW 540  
 RFSEGRGSRP QGPFLIADKW PALPRKLDV FEEPLSKLF PFSGRQVWVY TGASVLGPRR 600  
 LDKLGLGADV AQVYGAIRSG RGMMLFPSCR RLWRFDVKAQ MVDPRSASEV DRMPFVPLD 660  
 55 THDVQYREK AYFQDRFYW RVSSRSBLNQ VDQVGYVTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence  
 Protein Accession #: NP\_000204

60 1 11 21 31 41 51  
 MAGPRPSPFA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVKDCAY CTDEMFRDRR 60  
 CNTQAEALLA GCQRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPEERHFEL 120  
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGONLARVL SOLTSDYITG FGKFDKVS 180  
 65 PQTDMRPEKL KEPFNSDPP FSFKNVISLT EDVDEPRNKL QGERISGNLD APEGGFDAIL 240  
 QTAVCTRDIG WRPDSTHLLV PSTESAFHYE ADGANVLGI MSRNDERCHL DTTGTYTQYR 300  
 TQDYPSVPTL VRLLAGHNI PIPAVTNYSY SYYEKLHTYF FVSSLGLVQE DSSNIVELLE 360  
 EAFNRIRSNL DIRALDSPRG LRTEVTSKMF OKTRTGSFHI RRGVEGVIQV QLRALHVDG 420  
 THVQQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480  
 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHVCYGEGR YEGQFCEYDN 540  
 70 FQCPRTSGFL CNDRGRCMVG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600  
 CHCHQQSLEY DTICEINYSI IHPGLCEDLR SCVQCQAWGT GEKKGRTECE CNPKVRMVD 660  
 LKRAEIVVVR CSFRDEDDC TYSYTMEDG APGFNSTVLV HKKDCPPGS FWWLIPLLLL 720  
 LFLPLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFEKD HYMLRENLMA SDHLDTPLMR 780  
 SGNLKGKRDV RWKVNTNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840  
 75 AQLRQEVVEN LNEVYRQISG VHKLQQTFR QQPNAGKQD HTIVDTVLMA PRSAKPALLK 900  
 LTEKQVEGRA FHDLVAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVFLI RPEDDDEKQL 960  
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQEFVS VSRGDQVARI FVIRRVLDGG 1020  
 KSQVSYRTQD GTAQGNRDYI FVEGELLQFP GEAWKELQVK LLELQEVDSL LRGRQVRRPH 1080  
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLAGP QNPNAKAAGS 1140  
 80 RKIHFNNLPP SGKPMGYRVK YWIKQDSESE AHLDSKVPVS VELTNLYPYC DYEMKVCAYG 1200  
 AQGEGPYSSL VSCRTHQVVP SEPGRLAFNV VSSTVTQLSW AEAETNGEI TAYEVCYGLV 1260  
 NDDNRPIGFM KKVLDVNDPN RMLLIENLRE SQPYRYTVKA RNGAGWGPFR EAINLATOP 1320  
 KRPMISIPPI DIPVDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSDDTG CGWKFEPLL 1380  
 EELDRLRRVTW RLPELIPRL SASSGRSSDA EAPTAPRTTA ARAGRAAAMP RSATPGPPGE 1440

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HLVNGRMDF	FPGSTNSLHR	MTTTSAAAYG	THLSPHVPHR	VLSTSSLTTR	DYNSLTRSEH	1500
SHSTTLPRDY	STLTSVSSHD	SRLTAGVPDT	PTRLVFSALG	PTSLRVSNQE	PRCERPLQGY	1560
SVEYQLLNGG	ELHRLNIPNP	AQTSVVVDEL	LPNHSYVFRV	RAQSQEGWGR	EREGVITIES	1620
QVHPQSPLCP	LFGSAFTLST	PSAPGPLVFT	ALSPDSLQLS	WERPRRNGD	IVGYLVTCEM	1680
AQGGGPATAF	RVDGDSPEER	LTVPGLSNV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	1740
FFPQLGSRAG	LFQHPQLQSEY	SSITTTHTSA	TEPFLVDGLT	LGAQHLEAGG	SLTRHVTQEF	1800
VSRTLTTSGT	LSTHMDQFF	QT				1822

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Seq ID NO: C307 Protein Sequence  
Protein Accession #: NP\_076404.1

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20

1	11	21	31	41	51	
MGFNLTLAKL	PNNELHGQES	HNSGNRSDGP	GKNTTLHNEF	DTIVLPVLYL	IIFVASILLN	60
GLAWWIFPHI	RNKTSFIFYL	KNIVVADLIM	TLTFFPRIVH	DAGFGPWYFK	FILCRYTSVL	120
FIYAMYSIV	FLGLISIDRY	LKVVKPFQDS	RMYSITFTKV	LSVCVWVIMA	VLSPNIIILT	180
NGQPTDENIH	DCSKLKSPLG	VKWHITAVTV	NSCLFVAVLV	ILIGCYIAIS	RYIHKSSRQF	240
ISQSSRRKRH	NQSIRVVAV	FFTCLPYHL	CRIPFTFSHL	DRLLDESAQK	ILYCKEITL	300
FLSACNVCLD	PIIYFMCRS	FSRRLPKKSN	IRTRSESIRS	LQSVRRSEVR	IYYDYTDV	358

25  
30  
35  
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Seq ID NO: C308 Protein Sequence  
Protein Accession #: NP\_065840.1

1	11	21	31	41	51	
MVWCLGLAVL	SLVISQGADG	RGKPEVSVV	GRAEESVVLG	CDLLPPAGRP	PLHVIEWLRF	60
GPLLPFIQF	GLYSPRIDPD	YVGRVRLQKG	ASLQIEGLRV	EDQGWYECRV	FFLDQHIPED	120
DFANGSVVHL	TVNSPPQFQE	TPPAVLEVQE	LEFVTLCRVA	RGSPLPHVTW	KLRGKDLQGG	180
QGVQVQNGT	LRIRRVGRGS	SGVYTQASS	TEGSATHATQ	LLVLGPPVIV	VPPKNSVTNA	240
SQDVSLACHA	EAYPANLTVS	WFQDNINVFH	ISRLQPRVQI	LVDGSLRLLA	TQFDDAGCYT	300
CVPSNGLLHP	PSASAYITVL	CMPGVIRCPV	RANPPLLFVS	WTKDGKALQL	DKFPWGSQGT	360
EGSLIIALGN	EDALGEYSCT	PYNLSGTAGP	SPVTRVLLKA	PPAFIERPKE	EYFQEVGREL	420
LIPCSAQGDP	PPVSVWTKVG	RGLQGOAQVD	SNSSLILRPL	TKEAHGHNEC	SASNAVARVA	480
TSTNVVYVLT	SEHVVTNVSV	VALPKGANVS	WEPGFDGGYL	QRFVSWYTP	AKRPDRMHHD	540
MVSLAVPVGA	AHLLVPLQLP	HTQYQFSVLA	QNKLGSGPFS	EIVLSAPEGL	PTTPAAPGLP	600
PTEIPPLSP	PRGLVAVRTP	RGVLLHWDPP	ELVPKRLDGY	VLEGRQGSQG	WEVLDPVAVG	660
TETELLVPGL	IDVLVYEFRL	VAFAGSFVSD	PSNTANVSTS	GLEVPFSRTQ	LPGLLPQPV	720
AGVVGVCFL	GVAVLVSILA	GCLLNRRAA	RRRKRLRQD	PPLIFSPTGK	SAAPSALGSG	780
SPDSVAKLK	QGSFVPSLRQ	SLWGDPAFT	PSPHDPDPSS	RGPLPLEPIC	RGPDRFVMO	840
PTVAAPQERS	GREQAEPRTP	AQRLARSFDC	SSSSPSGAPQ	PLCIEDISPV	APPPAAPSP	900
LPFGPGLLQY	LSLPFFREMN	VDGDWPPLEB	PSPAAPPDYM	DTRRCTSSSF	LRSPETPPVS	960
PRESLPGAVV	GAGATAEPY	TALADWTLRE	RLLPGLLPAA	PRGSLTSQSS	GRGSASFRLP	1020
PSTAPSAGGS	YLSAPAGDTS	SWASGPERWP	RREHVTVTSK	RRNTSVDENY	EMDSEFPQDM	1080
ELLETLHLGL	ASSRLRPEAE	TELGVKTPPE	GCLLNTAHTV	GPBARCAALR	EEFLAFRRRR	1140
DATRRLPAY	RQVPHPEQA	TLL				1163

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Seq ID NO: C309 Protein Sequence  
Protein Accession #:

1	11	21	31	41	51	
MLTKPLQGP	APPGTPTPPP	GGKDREAFAE	EYRLGPLLGK	GGFGTVFAGH	RLTDRLQVAI	60
KVIPRNVVLG	WSPLSDSVTC	PLEVALLWKV	GAGGGHPGVI	RLLDWFETQE	GFMLVLERPL	120
PAQDLFDYIT	EKGPLGEGPS	RCFFGQVVAA	IQCHSRGVV	HRDIKDENIL	IDLRRCARL	180
IDFGSGALLH	DEPYTFDFTG	RVYSPPPEWIS	RHQYHALPAT	VWSLGLILLY	MVCGDIPFER	240
DQEILEAELEH	FFAHVSPDCC	ALIRRLCLAPK	PSSRPSLEBI	LLDPWMTQPA	EDVTPQPLQR	300
RPCPFGLVLA	TLSLAWPLGA	PNGQKSHFMA	MSQG			334

65  
70  
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Seq ID NO: C310 Protein Sequence  
Protein Accession #: NP\_002501.1

1	11	21	31	41	51	
MECLYYFLGF	LLLAARLPLD	AAKRFHDVLG	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
VNKRGMRWK	NSWKGGRVQA	VLTSDSPALV	GSNITFAVNL	IFPRCQKEDA	NGNIVYERMC	120
RNEAGLSADP	YYYNWTAWSE	DSGEGNTGQ	SHHNVPDGGK	PPPHHPGWR	WNFIYVFTL	180
GQYFQKLGRC	SVRVSVNTAN	VTLGQPLMEV	TVYRRHGRAY	VPIAQVKDVY	VVTDQIPFV	240
TMFQKDRNS	SDETFLKDL	IMFDVLHDP	SHFLNYSTIN	YKWSFGDNTG	LFVSTNHTVN	300
HTYVLNGTFS	LNLTVKAAAP	GPCPPPPPPP	RPSKPTPSLG	PAGDNPLELS	RIPDENCQIN	360
RYGHFQATIT	IVEGILEVNI	IQMTDVLMPV	PWESSLIDF	VVTCQGSIPT	EVCTIISDPT	420
CEITQNTVCS	PVDVDEMCLL	TVKRTFNGSG	TYCVNLTLGD	DTSLALTSTL	ISVPDRDPAS	480
PLRMANSALI	SVGCLAIPTV	VISLLVYKKH	KEYNPNIENSP	GNVVRSGKLS	VFLNRKAVF	540
FPGNQEKDPL	LKNQEFKGV					560

80  
Seq ID NO: C311 Protein Sequence  
Protein Accession #: Eos seq

1	11	21	31	41	51	
MRILKRFLAC	IQLLCVCRID	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
QSPINIDEDL	TQVNVNKKL	KFGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
FKASKITFW	GKCNMSDGS	EHSLEGQKFP	LEMQIYCDA	DRFSSFEAAV	KGKGLKRLAS	180
ILPEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYIY	YNGSLTSPPC	240
TDTVDWIVFK	DTVSISESQ	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300



5	TGKEEIH EAV CSSEPENVQA DPENYTSLLV TWERPRVVD TMIEKFAVLV QQLDGEDQTK 360
	HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPEDLDLPE 420
	LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
	RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
	GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
	ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSSTDI 660
	TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
	TEVTPHAFPT SSRQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
10	LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
	IKHFPKHVAD LHASSGFTEE FEEVQSCFVD LGITADSSNH PDNKHKNRYI NIVAYDHSRV 900
	KLAQLAEKDG KLTDIYINANY VDGYNRPKAY IAAQGPLKST AEDFWRMINE HNVEVIVMIT 960
	NLVEKGRKRC DQYWPADGSE EYGNFLVTQK SVQVLAYYTV RNPTLRNTKI KKGSKQGRPS 1020
	GRVVTQYHYT QWPDGMVPEY SLFVLTFVRK AAYAKRHAVG PVVHCSAGV GRTGTYYIVLD 1080
15	SMLQQIQHEG TVNIFGFLKH IRSQRNYLVQ TEEQYVFIHD TLVEAILSKE TEVLDSHIHA 1140
	YVNALLIPGP AGKTKLEKQF QLLSQSNIQQ SDYSAALKQC NREKNRTSSI IPVERSRVGI 1200
	SSLSGEGTDY INASYIMGYI QSNFIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDQGNM 1260
	AEDEFVYWNF KDFPINCESF KVTLMAAEHK CLSNEEKLI QDFILEATQD DYVLEVRRHQ 1320
	CPKWNPDSPF ISKTFELISV IKEEAANRDG PMIVHDEHGG VTAGTFALIT TLMHOLEKEN 1380
20	SVQVYQVAKM INLMRPGVFA DIBQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI 1440
	AESLESVLV 1448

Seq ID NO: C312 Protein Sequence  
Protein Accession #: XP\_031379

25	1 11 21 31 41 51	MRILKRFLAC IQLLVCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
		QSPINIDEDL TQVNVNLLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
30		FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKGLRLALS 180
		ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYII YNGSLTSPPC 240
		TDTVDMIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSY 300
		TGKEEIH EAV CSSEPENVQA DPENYTSLLV TWERPRVVD TMIEKFAVLV QQLDGEDQTK 360
		HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPEDLDLPE 420
35		LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
		RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
		GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
		ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSSTDI 660
		TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
40		TEVTPHAFPT SSRQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
		LNTTPAASS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSE LFRHLHTVSO 840
		ILPQVTSATE SDKVPLHASL PVAGDGLLE PSLAQYSQVL STTHAASETL EFGSEGVLY 900
		KTLMEFSQVEP PSSDAMMHAR SSGPEPSYAL SDNBSQHIP TVSYSSAIPV HDSVGVTYQG 960
		SLFSGPSHF IPKSSLIPT ASLLQPTHAL SGDGEWSGAS SDSEFLPDT DGLTALNISS 1020
45		PVSVAEFTYT TSFVGDNDKA LSKSEIIYGN ETELQIPSFN EMVYPSSESTV MPNMVDNVNK 1080
		LNASLQETS SISSTKGMFP GSLAHTTKV FDHEISQVPE NNFVSQPTHT VSQASGDTSL 1140
		KPVLANSSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200
		AVPSDPIIVE TPKVDKISST MLHLIVNSA SSENMLHSTS VPVFDVSPTS HMHSASLQGL 1260
		TISYASEKYE PVLLKSESSH QVPSGLYND ELFQTANLEI NQAHPPKGRH VFATPVLSID 1320
50		EPLNTLINKL IHSDELITST KSSVTGKQVFA GIPTVASDTF VSTDHVPVIG NGHVAITAVS 1380
		PHRDGSVTST KLLFPKSKATS ELSHSAKSDA GLVGGGEDGD TDDGDGDDDD DRGSDGLSIH 1440
		KCMSCSSYRE SQEKVMNDSD THENSLMDQN NPISYSLSEN SEEDNRVTSV SSDSQTGMDR 1500
		SPGKSFSANG LSQKHMNDGKE ENDIQTGSAL LPLSPESKAW AVLTSDSESG SQGQTSDSL 1560
		ENETSTDPSF ADTNEKADG ILAAGDSEIT PGFPQSPTSS VTSENSEVFR VSEAEASNS 1620
55		HESRIGLAEG LESEKKAVIP LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR 1680
		VISTPPTPIF PISDDVGAIP IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCFVDLGI 1740
		TADSSNHPDN KHKRYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA 1800
		QGPKLSTAEF FWRMIWEHNV EVIVMITNLV EKGRRKCDQY WPDAGSEYNG NPLVTQKSVQ 1860
		VLAYTYVRNF TLRNKKIKKG SQKGRPSGRV VTQYHYTQWP DMGVPEYSLE VLTVPVRKAY 1920
60		AKRHAVGPVV VHCASAGVGT GTYIVLDSML QQIQHEGTVN IFGFLKHRS QRNYLVQTEE 1980
		QYVFIHDTLV EALLSKETEY LDSEIHAYVN ALLIPGPAGK TKLEKQFOLL SQSNIQSDY 2040
		SAALKQCNRE KNRSTSIIPV ERSRVGISSL SGEGTDYINA SYIMGYQSN EFTIITQHPLL 2100
		HTIKDFWRMI WDHNALQVVM IPDQGNMAED EFVYWNKDE PINCESPKVT LMAEHEKCLS 2160
		NEEKLIQDF ILEATQDDYV LEVRHFQCPK WFNPDSPISK TPELISVIKE EAANRDGPMI 2220
65		VHDEHGGVTA GTFCALITLM HQLEKENSVD VYQVAKMINL MRPGVFADIE QYQFLYKVIL 2280
		SLVSTRQEN PSTSLDNGA ALPDGNIAES LESLV 2315

Seq ID NO: C313 Protein Sequence  
Protein Accession #: NP\_002842

70	1 11 21 31 41 51	MRILKRFLAC IQLLVCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
		QSPINIDEDL TQVNVNLLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
75		FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKGLRLALS 180
		ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYII YNGSLTSPPC 240
		TDTVDMIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSY 300
		TGKEEIH EAV CSSEPENVQA DPENYTSLLV TWERPRVVD TMIEKFAVLV QQLDGEDQTK 360
		HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPEDLDLPE 420
80		LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
		RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
		GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
		ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSSTDI 660
		TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
		TEVTPHAFPT SSRQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVI 780

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PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
PIKHFPKHVA DLHASSGFTE EPETLKEFYQ EVQSCVDLGI ITADSSNHDP NKHKRYINI 900  
VAYDHSRVKLA QLAEDGKGL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
VEVIVMITNL VEKGRRKCDQ YWPDGSEY GNFLVTQKSV QVLAYTVRN FTLRNTKIKK 1020  
GSQGRPSGR VVTQHYHTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080  
TGTYIVLDSM LQIQHEGTV NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140  
VLDSHIAHAY NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260  
MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320  
VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALITL 1380  
MHQLEKENS SVDYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440  
AALPDGNIAE SLESIV 1456

Seq ID NO: C314 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
| | | | |  
20 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGA LNQKNWG KKYPTCNSPK 60  
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTPIHNTGK TVEINLTNDY RVSGGVSEMV 120  
MVFKASKITF HWGKCNMSSD GSEHSLEGQK FPLEMCIYCF DADRFSSEFE AVKGGKGLRA 180  
LSILFEVGTB ENLDFKAIID GVESVSRFGK QAALDPFILL NLLPNSTDKY YIYNGSLTSP 240  
PCTDWDIVF KDTVSISESQ LAVFCEVLTM QSGYVLMMD YLQNNFREQQ YKFSRQVFS 300  
25 YTGKEEIHAE VCSSEFENVQ ADPENYTSLL VTWERPRVY DTMIEKFAVL YQQLDGEDQT 360  
KHEFLTDGYQ DLGAILNLL NMSYVLQIV AICTNGLYK YSDQLIVDMT DNPELDLFP 420  
ELIGTEEIIK EEEEGKDIEE GAIVNPGRDS ATNQIRKKEP QISTTHYNR IGTYNEAKT 480  
NRSPTRGSEF SGKGDVPNTS LNSTSQPVTK LATEKDISLT SQTVELPPH TVEGTSASLN 540  
DGSKTVLRSP HMLSGTAES LNTVSIYEY EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600  
30 SENISQGIYF SSENPETITY DVLPESARN ASEDSTSSGS EESLKDPMS EGNVFPSTSD 660  
ITAQPDVSGS RESFLQNTYT EIRVDESEKT KSFSAAGPVM SQGPSVTDLE MPHYSTFAYF 720  
PTEVTPHAPT PSSRQDQLV TNNVVSQTT QPVYNEASNS SHESRIGLAE GLESEKKAIV 780  
PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
PIKHFPKHVA DLHASSGFTE EPETLKEFYQ EVQSCVDLGI ITADSSNHDP NKHKRYINI 900  
35 VAYDHSRVKLA QLAEDGKGL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
VEVIVMITNL VEKGRRKCDQ YWPDGSEY GNFLVTQKSV QVLAYTVRN FTLRNTKIKK 1020  
GSQGRPSGR VVTQHYHTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080  
TGTYIVLDSM LQIQHEGTV NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140  
VLDSHIAHAY NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
40 VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260  
MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320  
VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALITL 1380  
MHQLEKENS SVDYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440  
AALPDGNIAE SLESIV 1456

Seq ID NO: C315 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
| | | | |  
50 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGA LNQKNWG KKYPTCNSPK 60  
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTPIHNTGK TVEINLTNDY RVSGGVSEMV 120  
FKASKITPHW GKCNMSSDGS EHSLEGQKFP LEMCIYCFDA DRFSSFEAEV KGGKGLRALS 180  
ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240  
55 TDTVDWIVF KDTVSISESQ AVFCEVLTMO QSGYVLMMD YLQNNFREQQ KFSRQVFSY 300  
TGKEEIHAE VCSSEFENVQ DPENYTSLLV TWERPRVYD TMIEKFAVL YQQLDGEDQT 360  
HEFLTDGYQD LGAILNLL NMSYVLQIVA ICTNGLYK YSDQLIVDMT DNPELDLFP 420  
LIGTEEIIKE EEEEGKDIEE AIVNPGRDSA TNQIRKKEP QISTTHYNR IGTYNEAKT 480  
RSPTRGSEFS SGKGDVPNTS LNSTSQPVTK LATEKDISLT SQTVELPPH TVEGTSASLN 540  
60 GSKTVLRSPH HMLSGTAES LNTVSIYEY EESLLTSFKL DTGAEDSSGS PATSAIPFI 600  
ENISQGIYF SSENPETITY DVLPESARNA SEDSTSSGSE EESLKDPMS EGNVFPSTSD 660  
TAQPDVSGS RESFLQNTYT EIRVDESEKT KSFSAAGPVM SQGPSVTDLE MPHYSTFAYF 720  
TEVTPHAPT PSSRQDQLV TNNVVSQTT QPVYNEASNS SHESRIGLAE GLESEKKAIV 780  
LTVSALTFI CLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
65 IKHFPKHVA DLHASSGFTE EPETLKEFYQ EVQSCVDLGI ITADSSNHDP NKHKRYINI 900  
VAYDHSRVKLA QLAEDGKGL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
VEVIVMITNL VEKGRRKCDQ YWPDGSEY GNFLVTQKSV QVLAYTVRN FTLRNTKIKK 1020  
GSQGRPSGR VVTQHYHTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080  
TGTYIVLDSM LQIQHEGTV NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140  
70 VLDSHIAHAY NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
SRVAGTILLS QSNIIQSDYS AALKQCNREK NRTSSIIIPVE RSRVGISSLS GEGTDYINAS 1260  
YIMGYYSQNE FIITQHPLH LHTIKDFWRM IWDHNAQLVV MIPDQGNMAE DEFVYWPNDK 1320  
INCESFKVTL MAEEHKCLSN EEEKLIQDFI LEATQDDYVL EVRHFQCPK KWPNDPSPIS 1380  
FELISVKEE AANRDGPMIV HDEHGGVTAG TFCALITLH QLEKENSVDV YQVAKMINLM 1440  
75 RGPVFADIEQ YQFLYKVL LSGTRQENP STSLDSNGAA LPDGNIAESL ESLV 1494

Seq ID NO: C316 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
| | | | |  
80 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGA LNQKNWG KKYPTCNSPK 60  
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTPIHNTGK TVEINLTNDY RVSGGVSEMV 120  
FKASKITPHW GKCNMSSDGS EHSLEGQKFP LEMCIYCFDA DRFSSFEAEV KGGKGLRALS 180  
ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240

5	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPEASNSH	420
	ESRIGLAESL	ESEKKAIVPL	VIVSALTFIC	LVVLVGILY	WRCKQTAFH	YLEDSTSPRV	480
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGFTEEP	ETLKEFYQEV	QSCTVDLGIT	540
	ADSSMHDNKH	HKRNYINIVA	YDHSRVKLAQ	LAEKDGKLT	YINANYVDG	NRPKAYIAAQ	600
	GPLKSTAEAF	WRMIWEHNV	VIVMITNLVE	KGRRCQDQY	PADGSEEGY	FLVTQKSVQV	660
	LAYYTVRNF	LRNTKIKKGS	QKGRPSGRV	TQYHYTQWPD	MGVPEYSLP	LTFVRKAAYA	720
10	KRHAVGPVVV	HCSAGVGRG	TYIVLDSMLQ	QIQHEGTVNI	FGFLKHRSQ	RNYLVQTEEQ	780
	YVFIHDTLVE	AILSKETEVL	DSHIHAYVNA	LLIPGPAGKT	KLEKQFQLS	QSNIQQSDYS	840
	AALKQCNREK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	YIMGYQSN	FIITQHPLH	900
	TIKDFWRMIW	DHNAQLVVM	PDGQNMAEDE	FVYWPNKDEP	INCESFKVT	MAEEHKCLSN	960
	EELKLIQDFI	LEATQDDYVL	EVRFHQCPKW	PNPDSPISKT	FELISVIKEE	AANRDGPMIV	1020
15	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	RPGVFADIEQ	YQFLYKVILS	1080
	LVSTRQENP	STSLDSNGAA	LPDGNIAESL	ESL			1113

Seq ID NO: C317 Protein Sequence  
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQVNVNLKLL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
25	FKASKITFWH	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEAAV	KGKGLRALS	180
	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPE	420
30	LIGTEEIIKE	EEEGKDIEEG	AINVPGRDSA	TNQIRKKEPQ	ISTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAEAL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETIITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
35	TEVTPHAFIP	SSRQQLVST	VNVVYSQTTQ	PVYNEASNS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCTVDLGI	TADSSNHDPN	HKRNYINIV	900
	AHDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAEF	FWRMIWEHNV	960
	EVIVMITNLV	EKGRRKCDQY	WPADGSEEGY	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
40	SQKGRPSGRV	VTOYHYTQWP	DMGVPEYSLP	VLTFRKAAY	AKRHAVGPVV	VHCSAGVGRG	1080
	GTIVLDSML	QIQHEGTVN	IFGFLKHRS	QRNYLVQTEE	QYVFIHDTLV	BAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQL	TLSPLRECRG	TISAHCNLPL	PGLTDPPTSA	1200
	SRVARTILLS	QSNIQQSDYS	AALKQCNREK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYQSN	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMAEDE	FVYWPNKDEP	1320
45	INCESFKVT	MAEEHKCLSN	EELKLIQDFI	LEATQDDYVL	EVRFHQCPKW	PNPDSPISKT	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	1440
	RPGVFADIEQ	YQFLYKVILS	LVSTRQENP	STSLDSNGAA	LPDGNIAESL	ESL	1493

Seq ID NO: C318 Protein Sequence  
Protein Accession #: Eos sequence

50	1	11	21	31	41	51	
	MRILKRFAC	QQLLCVCRLD	WANGYYRQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKLL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
55	FKASKITFWH	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEAAV	KGKGLRALS	180
	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPE	420
60	LIGTEEIIKE	EEEGKDIEEG	AINVPGRDSA	TNQIRKKEPQ	ISTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAEAL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETIITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
65	TEVTPHAFIP	SSRQQLVST	VNVVYSQTTQ	PVYNEASNS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCTVDLGI	TADSSNHDPN	HKRNYINIV	900
	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAEF	FWRMIWEHNV	960
	EVIVMITNLV	EKGRRKCDQY	WPADGSEEGY	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
70	SQKGRPSGRV	VTOYHYTQWP	DMGVPEYSLP	VLTFRKAAY	AKRHAVGPVV	VHCSAGVGRG	1080
	GTIVLDSML	QIQHEGTVN	IFGFLKHRS	QRNYLVQTEE	QYVFIHDTLV	BAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQL	QSNIQQSDYS	SAALKQCNRE	NRTSSIIPE	1200
	ERSRVGISS	SGEGTDYINA	SYIMGYQSN	FIITQHPLH	HTIKDFWRMI	WDHNAQLVVM	1260
75	IPDGQNMAED	EFVYWPNKDE	PINCESFKVT	LMMAECHKLS	NEEKLIQDF	ILEATQAWRS	1320
	DGRNFLCSDN	PVAPTRKRKF	RGCLPGSQDD	QSDEARSLC			1359

Seq ID NO: C319 Protein Sequence  
Protein Accession #: XP\_002914.4

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	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKPRR	TRPLECQDAL	ETAARAEGLS	60
	LDASMHSLR	ILDEEHKPKG	YHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSSLAR	120
	VHKKKGELSM	EDVWSLSKHE	SSDVNCRRL	RLWQEEELNEV	GPDAASLRV	VWIFCRTL	180

Seq ID NO: C320 Protein Sequence  
Protein Accession #: NP\_005679.1

Seq ID NO: C321 Protein Sequence  
Protein Accession #: NP\_005553.1

80 Seq ID NO: C322 Protein Sequence  
Protein Accession #: NP\_066924.1

1 11 21 31 41 51  
| | | | |  
MANAGLQLLG FILAFLGWIG AIVSTALPOW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60

QIQCKVFDLS LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120  
 IGGAIFLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGA 180  
 LLCCSCPRKT TSYPTPRYP KPAPSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence  
 Protein Accession #: AAM77876

1 11 21 31 41 51  
 10 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLTIIVD SGLKFVAHKA FLKNSNLQHI 120  
 NFRTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLP SAN LAAPNLVTEE GKISITLSCSV AGDPVPMYMW DVGNLVSKHM 240  
 15 NETSHTQGS L RITNISDDSD GKQISCVAEN LVGEDQDSVN LTVHFAPIT FLESPTSDDH 300  
 WCIPFTVKGN PKPALQWFFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHPMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence  
 Protein Accession #: NP\_006171.1

1 11 21 31 41 51  
 25 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLTIIVD SGLKFVAHKA FLKNSNLQHI 120  
 NFRTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLP SAN LAAPNLVTEE GKISITLSCSV AGDPVPMYMW DVGNLVSKHM 240  
 NETSHTQGS L RITNISDDSD GKQISCVAEN LVGEDQDSVN LTVHFAPIT FLESPTSDDH 300  
 30 WCIPFTVKGN PKPALQWFFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHPMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGPASV ISNDDDSASP 480  
 LHHISNGSNT PSSSEGGGDA VIIGMTKIPV IENPQYFGIT NSQLKPDTEV QHKKRHNIVL 540  
 KRELGEAGFG KVFLEACYNL CPEQDKILVA VKTLKADSDN ARKDFHREAE LLTNLQHEHI 600  
 35 VKFYGVCEVG DPLIMVF EYM KHGDLNKLFLR AHGPDALVMA EGNPPTTELQ SQMLHIAQQI 660  
 AAGMVYLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG GHTMLPIRM 720  
 PPESIMYRK F TTESDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ 780  
 EYELMLGCW QREPHMRNI KGIHTLLQL AKASPVYLDI LG 822

40 Seq ID NO: C325 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 45 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLTIIVD SGLKFVAHKA FLKNSNLQHI 120  
 NFRTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLP SAN LAAPNLVTEE GKISITLSCSV AGDPVPMYMW DVGNLVSKHM 240  
 NETSHTQGS L RITNISDDSD GKQISCVAEN LVGEDQDSVN LTVHFAPIT FLESPTSDDH 300  
 50 WCIPFTVKGN PKPALQWFFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHPMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence  
 Protein Accession #: NP\_570843.1

1 11 21 31 41 51  
 60 MPLKHLYLLL VGCQAWGAGL AYHGCPS ECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60  
 LNTHTIELNE SPFINISALI ALRIEKNELS RITPGAFNRL GSLRYLSLAN NKQLVLPGL 120  
 FQGLDSLES L LSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFD HLVLGTRKLN 180  
 GKNSLTHISP RVFOHLNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240  
 PHNHNHLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL 300  
 YDNHISLPD NVFSNLRQL VLILSRNQIS FISPGAPNGL TELRELSLHT NALQDLGDNV 360  
 65 FRMLANLQNI SLQNNRLRL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCERL 420  
 YDNPWRCDS ILPLRNWLL NQPRLGTDIV PVCFS PANVR GQSLIIINVN VAVPSVHVP 480  
 VPSYPETFWY PDTPSYPTDT SVSSTITELTS PVEDYIDLTT IQVTDDRSVW GMTQAQSGLA 540  
 IAAIVIGIVA LACSLAACVG CCCCCKRSQA VLMQMKAFNE C 581

70 Seq ID NO: C327 Protein Sequence  
 Protein Accession #: NP\_002649.1

1 11 21 31 41 51  
 75 MRALLARLLL CVLVVSDSKG SNEHQVPSN CDCINGGTCV SNKYFSNIHW CNCPKKPGGQ 60  
 HCEIDKSKTC YEGNGH FYRG KASTDTMGRP CLPWN SATVL QQTYHAHRSD ALQLGLGHKN 120  
 YCRNPDRRR PWCYVQGLK PLVQECMVHD CADGKKPSSP PEELKFQCCG KTLRPRFKII 180  
 GGEFTTIENQ PWFAYIRRH RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240  
 RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNDAIALK IRSKEGRCAQ PSRTIQTICL 300  
 80 PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVVKLI SHRECCQPHY YGSEVITTKL 360  
 CAADPQWKTD SCQGGSGGPL VCSLQGRMTL TGVSVNGRC ALKDKPGVYT RVSHFLPWIR 420  
 SHTKENGLA L 431

Seq ID NO: C328 Protein Sequence  
 Protein Accession #: XP\_087254.1

	1	11	21	31	41	51	
5	MQFRECSING	MKYQEINGRL	VPEGPTPDSS	EGNLSYLSL	SHLNNLSHLT	TSSSFRTSPE	60
	NETELIKEHD	LFFKAIVSLCH	TVQISNVQTD	CTGDGPWQSN	LAPSQLEYA	SSPDEKALVE	120
	AAARIGIVFI	GNSEETMEVK	TLGKLERVKL	LHILEFSDSR	RRMSVIVQAP	SGEKLFLFAG	180
	AESSILPKCI	GGEIEKTRIH	VDEPALKGLR	TLCIAVRKFT	SKEYEEIDKR	IFEARTALQQ	240
	REEKLAAPVQ	PIEKDLILLG	ATAVEDRLQD	KVRETIEALR	MAGIKVWVLT	GDKHETAVSV	300
10	SLSCGFHFHT	MNILELINQK	SDSECAEQLR	QLARRITEDH	VIQHGLVVDG	TSLSLALREH	360
	EKLMEVFCRN	CSAVLCCRMA	PLQKAKVIRL	IKISPEKPIT	LAVGDGANDV	SMIQEAHVGI	420
	GIMGKEGRQA	ARNSDYAIAR	FKFLSKLLFV	HGHFYIIRIA	TLVQYFFYKN	VCFITPQFLY	480
	QPYCLFSQQT	LYDSVYLTLV	NICFTSLPIL	IYSLLEQHVH	PHVLQNKPTL	YRDISKNRLL	540
	SIKTFLLWTI	LGFSHAFIFF	FGSYLLIGKD	TSLLGNGQMF	GNWTFGLTVF	TVMVITVTVK	600
15	MALETHFWTW	INHLVTWGS	IFYFVFLSFY	GGILWPFPLG	QNMYPVFYQL	LSSGSAWFAI	660
	ILMVVTLCLF	DIKKVFDORH	LHPTSTAKAQ	LTETNAGIKC	LDSMCCFPFG	EAACASVGRM	720
	LERVIGRCSP	THISRSWSAS	DPFYTNDRSI	LTLSTMDSST	C		761

Seq ID NO: C329 Protein Sequence  
Protein Accession #: XP\_087461.1

20	1	11	21	31	41	51	
	MLPLLAALLA	AACPPLPPVRG	GAADAPGLLG	VPSNASVNAS	SAASPSPRGC	WPRRPPGPPS	60
	ARARRRRRRR	RRLCNISVQR	QMLSSLLVRW	GRPRGFCQDL	LLFSTNAHGR	APFAAAAFHRV	120
25	GPPLLIHHLG	LAAGGAQDDL	RLCVGCGWVR	GRRTGRLRPA	AAPSAAAAATA	GAPTALPAYP	180
	AAEPGPPLWL	QGEPLHPCCL	DPSLEELQGE	PGNRLNRKPI	ESTLVACFMT	LVIVVWSVAA	240
	LWVPVPIIAG	FLPNMGMEQR	TTASTTAATP	AAVPAGITAA	AAAAAAAAAA	AVTSGVATK	299

Seq ID NO: C330 Protein Sequence  
Protein Accession #: XP\_051522.2

30	1	11	21	31	41	51	
	MDLHLFDYSE	PGNFSDISWP	CNSSDCIIVD	TVMCPNMPNK	SVLLYTLSEI	YIFIFVIGMI	60
35	ANSVVVVWNI	QAKTTGYDTH	CYILNLAIAD	LWVVLITPVV	VVSLVQHNQW	PMGELTCKVT	120
	HLIFSINLFG	SIFFLTCSMV	DRYLSITYFT	NTPSSRKMMV	RRVVCILVWL	LAFCVSLPDT	180
	YYLKTVTSAS	NNETYCRSFY	PEHSIKEWLI	GMELVSVVLG	FAVPFSSIAV	FYFLARAIAS	240
	ASSDQKHSS	RKIIIFSYYVV	FLVCWLPYHV	AVLLDIFISL	HYIPFTCRLE	HALFTALHVT	300
40	QCLSLVHCCV	NPVLYSFINR	NYRYELMKAF	IFKYSARTGL	TKLIDASRV	ETEYSALEQS	360
	TK						362

Seq ID NO: C331 Protein Sequence  
Protein Accession #: NP\_000341.1

45	1	11	21	31	41	51	
	MGFVRQIQLL	LMKNWTLRKR	QKIRFVVVEL	WPLSLPLVLI	WLRNANPLYS	HHECHFPNKA	60
	MPSAGMLPWL	QGIFCNVNNP	CFQSPPTGES	PGIVSNYNN	ILARVYRDFQ	ELLMNAPESQ	120
50	HLGRIWTEHL	ILSQFMDTLR	THPERIAGR	IRIRDILKDE	ETLTLFLIKN	IGLSDSVVYL	180
	LINSQVRPEQ	FAHGVDPDLA	KDIACEALL	ERFIIFSQR	GAKTVRYALC	SLSQGTQLWI	240
	EDTLIANVDF	FKLPRVLPPL	LDSRSQGINL	RSWGGILSDM	SPRIQEIFHR	PSMQDLLWVT	300
	RPLMQNGGPE	TFTKLMGILS	DLLCGYPEGG	GSRLVSFNWY	EDNRYKAPLG	IDSTRKDPIY	360
	SYDRRTTSFC	NALIQSLESN	PLTKIAWRAA	KPLLMGRILY	TPDSPAARRI	LKNANSTFEE	420
55	LEHVRKLKVA	WEEVGPIQWY	FFDNSTQNMN	IRDTLGNPTV	KDFLNRQLGE	EGITAEAILN	480
	FLYKPRESEP	ADDMANFDWR	DIFNITDRTL	RLVNQYLECL	VLDKFESYND	ETQLTORALS	540
	LLEENMFVAG	VVPDMYFPT	SSLPPHVKYK	IRMDIDVVEK	TNKIKDRYWD	SGPRADPVED	600
	FRYIWGGPAY	LQDMVEQGIT	RSQVQAEAPV	GIYLQMPYP	CFVDDSPHII	LNRCPPIFMV	660
	LAWIYSVMT	VKSIVLEKEL	RLKETLKNQG	VSNVAVICTW	FLDPSFISMS	SIFLITIFIM	720
60	HGRILHYSDP	FILFLFLLAF	STATIMLCFL	LSTFFSKASL	AAACSGVIYP	TLYLPHILCF	780
	AWQDMYAEI	KKAVSLLSPV	AFGFGTEYLV	RFEEQGLGLQ	WSNIGNSPTE	GDEFSELLSM	840
	QMMLLDAACY	GLLAWYLDQV	FPGDVGTPLP	WYELLQESYV	LSGEGCSTRE	ERALEKTEPL	900
	TEETEDPEHP	EGIHDSFFER	EHPGVWPGVC	VKNLVKIFEP	CGRPAVDRLN	ITFYENQITA	960
	FLGHNGAGKT	TTLSILTGLL	PPTSGTVLVG	GRDIETSLDA	VRQSLGMCPO	HNILPHHLTV	1020
65	AEHMLFYAQL	KGKSQEEAQL	EMESAMLEDTG	LHHKRNEBAQ	DLSGGMQRKL	SVIAFVGDGA	1080
	KUVILDEPTS	GVDPSYRRSI	WDLKLYRSG	RTIIMPTHM	DEADHGQDRI	AIIAQGRLYC	1140
	SGTFLPLKNC	FTGILYLTIV	RKMKNIQSOR	KGSEGTCSGS	SKGFSTTCFA	HVDDLTPQV	1200
	LDGDNVELMD	VVLHHVPEAK	LVECIQELI	FLLPNKNFKH	RAYASLFREL	EETLADLGLS	1260
	SPGISDTPLE	EIFLKVTEDS	DSGPLFAGGA	QOKRENVNPR	HPCLGPREKA	GQTPQDSNVC	1320
70	SPGAPAAHPE	GQPPPEPECP	GPQLNTGTQL	VLQHVQALLV	KRFQHTIRSH	KDFLAQIVLP	1380
	ATFVFLALML	SIVILFPGFY	PALTLPWMIY	GQYTFFSMD	EPGSEQFTVL	ADVLLNKPGF	1440
	GNRCLKEGWL	PEYPCGNSTP	WKTSPSVNPI	TQLEFQKQWT	QVNEPSPCRC	STREKLTMLP	1500
	ECPEGAGGLP	PPQRTQRSTE	ILQDLTDRI	SDFLVKTYPA	LIRSSLKSKF	WVNEQRYGGI	1560
	SIGGKLPVVP	ITGEALVGLF	SDLGRIMNVS	GGPITREASK	EIPDFLKHLE	TEDNIKWVFN	1620
75	NKGHALYSF	LANVANNAILR	ASLPKDRSPE	EYGITVISQP	LNLTKQLSE	ITVLTTSVDA	1680
	VVAICVFISM	SVGPASFLVY	LIQERVNKS	HLQFISGVSP	TTYVNTFLW	DIMNYSVSAG	1740
	LUVGIPIGFQ	KKAYTSPENL	PALVALLLLY	GWAVIEMMPY	ASFLEDVPS	AYVALSCANL	1800
	FIGINSSAIT	FILELFDNNR	TLRFPNAVLR	KLLIVFPFHC	LGRGLIDLAL	SOAVTDVYAR	1860
	FGEEHSANPF	HWDLIGKNLF	AMVVEGVVYF	LLTLVLQRHF	FLSQWIAEPT	KEPIVDEDDD	1920
80	VABERGRIT	GGMKTDLRL	HELTKIYLG	SSPAVDRLCV	GVRPGECFGL	LGVNAGAKTT	1980
	TFQMLTGDTT	VTSGDAFTVAG	KSILTNISEV	QNMGYCQPF	DAIDELLTGR	EHLVLYARLR	2040
	GVPABIEKV	ANNSIKSLGL	TVYADCLAGT	YSGGNKRKLS	TAIALIGCPP	LVLLDEPTTG	2100
	MDPQARRMLW	NVIVSIIRKG	RAVVLTSISM	EECEALCTRL	AIMVKGAFCR	MGTIQLHLSK	2160
	FGDGYIVTMK	IKSPKDDLLP	DLNPFVEQFFQ	GNFPGSVQRE	RHYNMLQFQV	SSSSLARIFQ	2220
	LLLSHKDSLL	IEEYSVTQTT	LDQVFVNFAK	QQTESHDLPL	HPRAAGASRQ	AQD	2273

Seq ID NO: C332 Protein Sequence  
Protein Accession #: NP\_006662.2

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5      1      11      21      31      41      51
|      |      |      |      |      |
MVPHAILARG RDVCRRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQEISYF QPFGELLMRM 60
LKMMILPLVV SSLMSGSLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIIHPGSAA 120
QKETTEQSGK PIMSSADALL DLIRNMFPAN LVEATFKQYR TKTTTPVVKSP KVAPEEAPPR 180
10    RILYGVQEE NGSHVQNFAI DLTPPEVVY KSEPGTSDGM NVLGIVFFSA TMGIMLGRMG 240
DSGAPLVSPC QCLNESVMKI VAVAVWYFPF GIVFLIAGKI LEMDDPRAVG KKLGPYSVTV 300
VCGLVHLGLF ILPLLYFFIT KKNPIVFIRG ILQALLIALA TSSSSATLPI TFKCLLENMH 360
IDRIARFVL PVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA 420
15    GIPQAGLVMT VIVLTSVGLP TDDITLIIAV DWALDRFRMT INVGLDALAA GIMAHICRDK 480
PARDTGTGK LFCETKPVSL QEIVAAQONG CVKSVAEASE LTLGPTCPHH VPVQVERDEE 540
LPAASLAHCT IQISELETNV

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Seq ID NO: C333 Protein Sequence  
Protein Accession #: NP\_005680.1

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20    1      11      21      31      41      51
|      |      |      |      |      |
MVTGNYCEA EGPVGPAMWQ DGLSPCFFFT LVPSTRMALG TLALVLALPC RRRERPAGAD 60
SLSWGAGPRI SPYVLQLLLA TLQAALPLAG LAGRVGTARG APLPSYLLLA SVLESAGAC 120
25    GLWLLVVERS QARQLAMGI WIKPRHSPGL LLLWTVAFAA ENLALVSWNS PQWWARADL 180
GQQVQFSLWV LRYVVSGLLF VLGLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQQTNR 240
DFGRKLRLLS GYLWPRGSPA LQLVVLICLG LMGLERALNV LVPIFYRNIV NLLTEKAPWN 300
SLAWTVTSYV FLKFLQGGGT GSTGPFVSNLR TFLWIRVQQF TSRRVELLIF SHLHELRLW 360
30    HLGRRTGEVL RIADRGTSV TGLLSYLVEN VIPTLADIII GIIFYSMFFN AWFGLIVFLC 420
MSLYTLTIV VTEWRTKFRF AMNTQENATR ARAVDSLNNF ETVKYNAES YEVEYREAI 480
IKYQGLEWKS SASLVLLNQT QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYYIQL 540
YMPLNWFGTY YRMIQTNFID MENMFLLKE ETEVKDLPGA GPLRFQKRI EFENVHFSYA 600
DGRETLQDVS FTVMPQQTIA LVGPSGAGKS TILRLFRFY DISSGCIRID QDISQVTOA 660
35    SLRSHIGVVP QDVLFNFTI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM APFEGYRTQV 720
GERGKLKSGG EKORVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV 780
VAHRLSTVNV ADQILVIKDG CIVERGRHEA LLSRGVGYAD MWQLQQQEE TSEDTKPQTM 840
ER

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Seq ID NO: C334 Protein Sequence  
Protein Accession #: NP\_000667.1

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40    1      11      21      31      41      51
|      |      |      |      |      |
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVGLFA 60
45    IFAITISLG FCTDFYGLCF LACFVLVLTO SSIFSLLAVA VDRYLAICVP LRYKSLVTGT 120
RARGVIAVLW VLAFGIGLTP FLGWNKDSA TNNCTEPWDG TTNECCCLVK CLFENVVPM 180
YMYVFNFFGC VLPLLLIMLV IYIKIFLVAC RQLQTELM D HSRTTLQREI HAAKSLAMIV 240
GIFALCWLFP HAVNCVTLFQ PAQGNKPKK AMNMAILLSE ANSVVNPIV AYRNDRDFRYT 300
50    FHKIISRYLL CQADVKSNG QAGVQPALGV GL

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Seq ID NO: C335 Protein Sequence  
Protein Accession #: NP\_443164

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55    1      11      21      31      41      51
|      |      |      |      |      |
MGLGARGAWA ALLLGTQLVL ALLGAHESA AMAETLQHPV SDHTNETSNS TVKPPTSVAS 60
DSSNTVTITM KPTAASNTT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMTVTHNS 120
SVTSAASSVT ITTTHSEAK KGSKFDTSF VGGIVTLGV LSILYIGCM YYRRRGIRYR 180
60    TIDEHDAII

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Seq ID NO: C336 Protein Sequence  
Protein Accession #: NP\_004186.1

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65    1      11      21      31      41      51
|      |      |      |      |      |
MAQHGMAGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60
YPGECCSEW DCMCVQPEFH CGDPCCTTCR HHPCPGQGV QSQGKPSFGF QCIDCASGTF 120
SGGHEGCKP WTDCTQFGFL TVFPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL 180
70    TSAQLGLHIW QLRSCMMPR ETQLLLEVPP STEDARSCQF PEEERGERSA EEKRLGDLW 240
V

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Seq ID NO: C337 Protein Sequence  
Protein Accession #: BAC03767.1

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75    1      11      21      31      41      51
|      |      |      |      |      |
MGCDGRVSG LRRNLQPTLT YWSVFFSFLG CIAFLGPTLL DLRCQTHSSL PQISWVFSQ 60
QLCLLLGSAL GGVFKRTLAQ SLNALFTSSL AISLVFAVIP FCRDVKVLAS VMALAGLAMG 120
CIDIYANMQL VRMYQKDSAV FLQVLHFFVG FGALLSPLIA DPPLSEANCL PANSTANTTS 180
80    RGLFHVSRV LGQHVDVAKP WSNQTFEGLT PKDGAGTRVS YAFWIMALID LPVPMVIML 240
LSKERILLTC PQRRLLLSA DELALETQPP EKEDASSLPP KFQSHLGHEE LFSCCQRKNL 300
RGAPYSFFAI HITGALVLEF TDGLTGAYSA FVYSYAVEKP LSVGHKVAGY LPSLFWGFIT 360
LGRLLSIPIS SRMKPATMVF INVVGVVVTF LVLLIFSYNV VFLFVGTASL GLFLSSTPFS 420
MLAYTEDSLQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QSSYSFLVCG VIFGCLAPTF 480

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YILLFFHRM HGPLSPVPTQ DRSIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence  
Protein Accession #: NP\_002194.1

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1	11	21	31	41	51	
MGPERTGAAP	LPLLLVLALS	QGILNCCLAY	NVGLPEAKIF	SGPSSEQFGY	AVQQFINPKG	60
NWLLVGSFWS	GFENRMGDV	YKCPVDLSTA	TCEKLNQTS	TSIPNVTEMK	TNMSLGLILT	120
RNMGTGGFLT	CGPLWAQCG	NQYTTGVCS	DISPDFQLSA	SFSPATQPCP	SLIDVVVVD	180
ESNSIYPMDA	VKNFLEKFFQ	GLDIGPTKTQ	VGLIQYANNP	RVVFNLTNYK	TKEEMIVATS	240
QTSQYCGDLT	NTFGAIQYAR	KYAYSASGG	RRSATKVMV	VTDGESHDGS	MLKAVIDQCN	300
HDNILRFGIA	VLGYLNRNAL	DTKNLIKEIK	AIASIPTERY	FFNVSDAAL	LEKAGTLGEO	360
IPSIETVQO	GDNFQMEMSQ	VGFSADYSSQ	NDILMLGAVG	AFGWSGTIVQ	KTSHGHLIFP	420
KQAFDQILQD	RNHSSVFLGS	VAAISTGEST	HFVAGAPRAN	YTGQIVLYSV	NENGNITVIQ	480
AHRGDQIGSY	FGSVLCSDVD	DKDTITDVL	VGAPMYMSDL	KKEEGRVYLF	TIKKGILGQH	540
QFLEGEPEGIE	NTRFGSAIAA	LSDINMDGFN	DVIVGSPLN	QNSGAVYIYN	GHQGTIRTKY	600
SQKILGSDGA	FRSHLQYFGR	SLDGYGDLNG	DSITDVSIGA	FGQVVQLWSQ	SIADVAIEAS	660
FTPEKITLVN	KNAQIILKLC	FSAKFRPTKQ	NNQVAIVYNI	TLDADGFSSR	VTSRGLFKEN	720
NERCLQKNMV	VNQASCPHE	IYIQEPSDV	VNSLDLRVDI	SLNENPGTSPA	LEAYSETAKV	780
ESIPFHKDCG	EDGLCISDLV	LDVRQIPAAQ	EQPFIVSNQN	KRLTFSVTLK	NKRESAYNTG	840
IUVDFSENLF	FASPSLVDVG	TEVTCQVAAS	QKSVACDVGY	PALKREQVQT	FTINFDNLQ	900
NLQNASLSF	QALSESQEN	KADNLVNLKI	PLLYDAEHL	TRSTNINFYE	ISSDGNVPSI	960
VHSEFVGVK	FIFSLKVTTC	SVPVSMATVI	IHIPQYTKK	NPLMYLTGVQ	TDKAGDISCN	1020
ADINPLKIQD	TSSSVFSKSE	NFRHTKELNC	RTASCNVTC	WLKDVHMKEG	YFVNVTIRW	1080
NGTFASSTFQ	TVQLTAAAEI	NTYNPEIYVI	EDNTVTIPLM	IMKPDEKAEV	PTGVIIGSII	1140
AGILLALLLV	AILNKLGF	KRYENMTKNP	DEIDETTELS	S		1181

Seq ID NO: C339 Protein Sequence  
Protein Accession #: NP\_113648.1

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1	11	21	31	41	51	
MYRPRARAAP	EGRVRCGAVP	STVLLLLLAYL	AYLALGTGVF	WTEGRAAQD	SSRSFQDKW	60
ELLQNTCLD	RPALDSLIRD	VQAYKNGAS	LLSNTTSMGR	WELVGSFFFS	VSTITTIGYG	120
NLSPTMAAR	LFCIEFFALVG	IPLNLVVLNR	LGHLMQGGVN	HWASRLGGTW	QDPDKARWLA	180
GSGALLSGLL	LPPLLPLLF	SHMEGWSYTE	GFYFAFITS	TVGFGDYVIG	MNPSQRYPLW	240
YQNMVSLWIL	FGMAWLALII	KLILSQLETP	GRVCSCHHS	SKEDFKSQSW	RQGEDREPES	300
HSPQGGCYE	GPMGIQHLE	PSAHAAGCGK	DS			332

Seq ID NO: C340 Protein Sequence  
Protein Accession #: NP\_004145.1

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1	11	21	31	41	51	
MEWDNGTQGA	LGLPPTTCVY	RENFKQLLLP	PVYSAVLAAG	LPLNICVITQ	ICTSRRALTR	60
TAVYTLNLAL	ADLLYACSLP	LLIYNVAQGD	HWPFQDFACR	LVRFLFYANL	HGSILFLTCI	120
SFQRYLGICH	PLAPWHKRG	RAAAILVCVA	VWLAVTTQCL	PTAIFATGII	QRNRTVCYDL	180
SPPALATHYM	PYGMALTVIG	FLLPFAALLA	CYCLLACRLC	RQDGPAPVPA	QERRGKAARM	240
AVVVAAPAFI	SLPLPHITKT	AYLAVERSTPG	VPCTVLEAFA	AAYKGTTPFA	SANSVLDPIL	300
FYFTQKKFRR	RPHELLQLKT	AKWQRQGR				328

Seq ID NO: C341 Protein Sequence  
Protein Accession #: NP\_009128.1

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1	11	21	31	41	51	
MQRPGFRLWL	VLQVMGSCAA	ISSMDMERPG	DGKCQPIEIP	MCKDIGVNTM	RMPNLMGHEH	60
QREAAIQLEH	FAPLVEYGCH	GHLRFFLCSL	YAPMCTEQVS	TPIPACRVMC	EQARLKCSPI	120
MEQNFNFKWD	SLDCRKLPNK	NDPNYLCMEA	FNNGSDEPTR	GSGLFPPPLFR	PQRPHSAQEH	180
PLKDGGEGRG	GCDNPGKPHH	VEKSASCAPL	CTPGVDVYWS	REDKRFVAVW	LAIWAVLCFF	240
SSAFTVLTFL	IDPARFRYPE	RPIIFLSMCY	CVYSVGYLIR	LPAGAESIAC	DRDSGQLYVI	300
QEGLESTGCT	LVFLVLVYPG	MASSLWVVVL	TLTWFLAAGK	KWGHEAIEAN	SSYFHLAANA	360
IPAVKTILIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGFVLI	PLACYLVIGT	SFILSGFVAL	420
PHIRRVMTKG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLNMD	YWKILAAQHK	480
CKMNQTKTL	DCLMAASIPA	VEIPMVKIFM	LLVVGITSGM	WIWTSKTLQS	WQVCSRRLLK	540
KKSRRKPASV	ITSGGIYKKA	QBPQKTHHGK	YEIPAQSPTC	V		581

Seq ID NO: C342 Protein Sequence  
Protein Accession #: NP\_005752.1

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1	11	21	31	41	51	
MEVSRRKAPP	RPPRPAAPLP	LLAYLLALAA	PGRGADEFVW	RSEQAIGAIA	ASQEDGVFVA	60
SGSCLDQDLY	SLEHSLSRLY	RDQAGNCTEP	VSLAPPARPR	PGSSFSKLIL	PYREGAAGLG	120
GLLLTGTWTF	RGACEVRPLG	NLSRNSLRNG	TEVVSCHPQG	STAGVVYRAG	RNNRWYLAVA	180
ATYVLPETPE	ASRCNPAASD	HDTAIALKDT	EGRSLATQEL	GRLLKCEGAG	SLHFVDAFLW	240
NGSIYFPYYP	YNYTSGAATG	WPSMARIAQS	TEVLFGQOAS	LDCGHGHPDG	RRLLSSSLV	300
EALDVWAGVF	SAAAGEGQER	RSPTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
ERVQFIASST	LHSDLTSVY	GTVMNRTVL	PLGTGQGQLL	KVILGENLTS	NCPEVIYEIK	420
BETPVFKLV	PDVKNYIYI	LTAGKEVRII	RVANCNKHK	CSECLTATDP	HCGWCHSLQR	480
CTFQGDVCHS	ENLEWLDIS	SGAKKCPKIQ	IIRSSKEKTT	VTMVGSFSFR	HSKCMVKNVD	540
SSRELQCNKS	QPNRTCTCSI	PTRATYKDV	VNVVMFSGS	WNLSDRFNFT	NCSLKECPA	600
CVETGCACWK	SARRCIHPPT	ACDPSDYERN	QEQCPVAVEK	TSGGGRPEKN	KGNRTNQALQ	660
VFYIKSIEPQ	KVSTLGKSNV	IVTGANFTRA	SNITMILKGT	STCDKDVIVQ	SHVLNDTHMK	720



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FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMMGRNFD 780  
VIDNLIISHE LKGNINVSSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLOY 840  
REDPRPTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LPHGNGQLN CSFENITRNO 900  
DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF 960  
AAVGVTTRHS KELSRKQSQQ LELLESELRK EIRDGFALQ MDKLDVVDSE GTVPFLDYKH 1020  
FALRTFFPES GGFTHIPTED MNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS 1080  
VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLLRTE SVVEKLLTNW 1140  
MSVCLSGFLR ETVGEPFYLL VTLNQKINK GPVDVITCKA LYTLNEDWLL WQVPEFSTVA 1200  
LNVVPEKIPE NESADVCRNI SVNVLCDDTI GQAKEKIFQA FLSKNGSPYQ LQLNEIGLEL 1260  
QMGTRQKELL DIDSSSVILE DGITKLNTIG HYEISNGSTI KVPFKIANFT SDVEYSDDHC 1320  
HLILPDSEAF QDVQGRHRG KHKEFKVEMY LTKLLSTKVA IHSVLEKLF SIWSLPNSRA 1380  
PFAIKYFFDF LDAQAENKKI TDPDVVHIWK TNSLPLRFVW NILKNPQFVF DIKKTPHIDG 1440  
CLSVIAQAFM DAFSLTEQQL GKEAPTNNLL YAKDIPTYKE EVKSYKPAIR DLPLSLSSSEM 1500  
EEFLTQESKK HENEFNEEVA LTEIYKIVK YFDEILNKLE RERGLEEAQK QLLHVVKVLPD 1560  
EKKCKKWM 1568

Seq ID NO: C343 Protein Sequence  
Protein Accession #: NP\_002176.1

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1 11 21 31 41 51  
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MTILGTTFGM VFSLLQVVSQ ESGYAQNGDL EDALDDYSF SCYSQLEVNG SOHSLTCAFE 60  
DPPVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK 120  
IDLTTIVKPE APFDLSVIYR EGANDFVVF NTSHLQKKYV KVLMDHVAYR QEKDENKWTN 180  
VNLSSTKLTL LQRKLQPAAM YEIKVRSIPD HYFKGFSEW SPSYFFRTPE INNSSGEMDP 240  
ILLTISILSF FSVALLVILA CVLKKRIKP IVWPSLPDHK KTLHLCKGK RNKLVNVSFNP 300  
ESFLDQIHR VDDIARDEV EGFLQDTFPQ QLEESEKQRL GGDVQSPNCP SEDVVVTPE 360  
FGRDSSLTCL AGNVACDAP ILSSSRSLDC RESGKNGPHV YQDLLLSLGT TNSTLPPPPS 420  
LQSGILTLPN VAQQPILTS LGSNQEEAYV TMSSFYQNG 459

Seq ID NO: C344 Protein Sequence  
Protein Accession #: NP\_002713.1

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1 11 21 31 41 51  
| | | | |  
MAAARCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60  
TRPRYGRKHK EDTLAPSEWG SPHAAVPREL SPLDL 95

Seq ID NO: C345 Protein Sequence  
Protein Accession #: NP\_115934.1

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1 11 21 31 41 51  
| | | | |  
MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP INWTSSEHFE 60  
VTGSAEGWGP EEPLFYSRAF GEGASARPRC CRNGGTCVLG SPCVCPAHT GRYCEHDQRR 120  
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHANGP SAGGAPSLLL 180  
LLPCALLHRL LRPDAPAHPR SLVPSVLORE RRPCGRPGLG HRL 223

Seq ID NO: C346 Protein Sequence  
Protein Accession #: NP\_006524.1

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1 11 21 31 41 51  
| | | | |  
MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LDYMAPDCR 60  
FLTIHRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPKQVD 120  
VKTDKNDFYC Q 131

Seq ID NO: C347 Protein Sequence  
Protein Accession #: Eos sequence

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1 11 21 31 41 51  
| | | | |  
MTQVTEKSTE HPEKTTSTTE KTTRTPKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60  
TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSFTLI 120  
TSRTKLSSIT SEATGNESH YLNKDGSKG IHAGQMGEND SPPAWAIVIV VLVAVILLV 180  
FLGLIFLVSY MMRTRRTLQ NTQYNDAEDE GGFNSYPVYL MEQQLGMGQ IPSR 235

Seq ID NO: C348 Protein Sequence  
Protein Accession #: NP\_543146.1

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1 11 21 31 41 51  
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MTQVTEKSTE HPEKTTSTTE KTTRTPKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60  
TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSFTLI 120  
TSRTKLSSIT SEATGNESH YLNKDGSKG IHAGQMGEND SPPAWAIVIV VLVAVILLV 180  
FLGLIFLVSY MMRTRRTLQ NTQYNDAEDE GGFNSYPVYL MEQQLGMGQ IPSR 235

Seq ID NO: C349 Protein Sequence  
Protein Accession #: FGENSEH predicted

1 11 21 31 41 51  
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5	MMPLAFCCW GLALVSGWAT FQOMSPSRNF SFRLFPETAP GAPGSIPAPP APGDEAAGSR 60
	VERLQAFRR RVRLRLRESE RLELVFLVDD SSSVGEVNFRL SELMFVRKLL SDFPVVPTAT 120
	RVAVITFSSK NYVVRVDYI STRRARQHKC ALLLQEIPIA SYRGGGYTK GAFQQAQIL 180
	LHARENSTKV VFLITDGYSN GGDPRPIAAS LRDSGVEIFT FGIWQGNIRE LNDMASTPKE 240
	EHCYLLHSFE EFELALARRAL HEDLPSSGFI QDDMVHCSYL CDEGKDCDR MGSCCKGTH 300
	GHFECICEKG YYGKGLQYEC TACPSGTYPK EGSPGGISSC IPCFDENHTS PPGSTSPEDC 360
	VCREGYRAS QTCELVHCPA LKPPENGYFI QNTCNNHFNA ACQVRCHPGF DLVGSIIILC 420
	LPNGLWSGSE SYCRVRTCPH LRQPKHGHS CSTREMLYKT TCLVACDEGY RLEGSCLKTC 480
10	QGNQWDGPE PRCVERHCST FQMPKDVIS PHNCGKQPAK FGITCYVSCR QGFILSGVKE 540
	MLRCTTSGKW NVGVQAAYCK DVEAPQINCP KDIEAKTLEQ QDSANVTWQI PTAKDNSGEK 600
	VSVHVPAPT PPYLFPIDGV AIVYTATDLS GNQASCFIHI KVDAEPPVI DWCRSPPPVQ 660
	VSEKHAAAS DEPOFSDNSG AELVITRSH T QGDLFPOGET IVQYATDPS GNNRTCDIHI 720
	VIKGSPCEIP FTPVNGDFIC TPDNTGVNCT LTCLEGYDFT EGSTDKKYCA YEDGVWKFTY 780
15	TTWPDCAK RFANHGKSF EMFYKAARCD DTDLMKKFSE AFETTLGKMV PSFCSAEDI 840
	DCRLEENLTK NGVQAVYDY ENGFAIGPGG WGAANRLDYS YDDFLDTVQE TATSIGNAKS 900
	SRKRSAPLS DYKIKLIFNI TASVPLPDER NDTLEWENQ RLLQTLTIT NKLKRTLNKD 960
	PMYSQLASL IIAIDNSLE TKKASPFRCR GSULRGRCV NCPLGTYYNL EHTCESCRI 1020
	GSYQDEBQL ECKLCPSGMY TEYIHSRNI DCKAQCKQGT YSYGLETCE SCPLGTYYPK 1080
20	FGSRSCLECP ENTSTVKRGA VNISACGVPC PEGKFSRSLG MPCHPCRDY YQPNAGKAF 1140
	LACPYGTTP FAGSRITEC STSVLNTIF GGFGHLELLN CPSEVHECF FNPCHNSGTC 1200
	QQLGRGYVCL CPLGYTGLKC ETDIDECSPL PCLNNGVCKD LVGEFICECP SGYTQRCCE 1260
	NINECSSPC LKNGICVDG AGYRCTCVKG FVGLHCETE NECQSNPCLN NAVCEDQVGG 1320
	FLCKCPRGFL GTRCGKNVDE CLSQPCNGA TCKDGANFR CLCAAGTGS HCELNINECQ 1380
25	SNPCRNQATC VDELANYSCK QPFGSGKRC ETEQSTGFNL DFEVSGIYGY VMLDGMPLSL 1440
	HALTCTFMK SSDDMNYGTF ISYAVDNGSD NTLLLTDYNG WVLVYNGREK ITNCPVNDG 1500
	RWHIAITWT SANGIKWYI DGKLSGGAG LSVGLPIPGG GALVLGQEQD KKGEGSPAE 1560
	SFVSGISQLN LWDYVLSPQ VKSLATSCPE ELKGNVLAW PDFLSGIVGK VKIDSKSIFC 1620
	SDCPRLGGSV PHLTASEDL KPGSKVNLFC DPGFQLVGNP VQYCLNQGW TOPLPHCERI 1680
30	SCGVPPPLEN GFHSADDFYA GSTVTYQCNN GYLLGDSRM FCTDNGSWG VSPSCLDVDE 1740
	CAVGSDESEH ASCLNVDSGY ICSCVPPYTQ DGKNCAPPIK CKAPGNPENG HSSGEIYTVG 1800
	AGVTSCQEG YQMGVTKIT CLESGEWNHL IPYKAVSCG KPAIPENGCI EELAFTEGSK 1860
	VTRYCNKGYT LAGDKSSCL ANSSWSHSP VCEPVKCSSP ENINNGKYL SGLTYLSTAS 1920
	YSCDTGYSLO GPSIIIECTAS GIWDRAPPAC HLVFCGEPPA IKDAVITGN FTRNTVTYT 1980
35	CKEGYTLAFL DTEICLADGK WSRSDQCLA VSCDEPIVD HASPETAHL FGDIIFYCS 2040
	DGYSLADNSQ LLCNAQKQW PPEGQDMPRC IAHFCEKPPS VSYSILESVS KAKFAAGSVV 2100
	SFKCMGGFVL NTSAKIECMR GGQWNPSPMS IQCIPVRCE PPSIMNGYAS GSNYSFGAMV 2160
	AYSCNKGFIY KGEKKSTCEA TGQWSSPIPT CHFVSCGEP KVENGFLEHT TGRIFESEVR 2220
	YQCNPGYKSV GSPVFCQAN RHWHSSEPLM CVPLDCGKPP PIQNGFMKE NFEVGSKVQF 2280
40	PCNEGVELVG DSSWTCQKSG KWNKSNPKC MPAKCEPEPL LENQLVLKEL TTEVGVVTF 2340
	CKBHVLPQF ASCLNLFQSG WDSFPVCKI VLCTPPPLIS FGVPIPSAL HFGSTVKYSC 2400
	VGGFFLRGMS TTLCPQDGTW SSPLBECVPV ECPQPEEIPN GIIDVQGLAY LSTALYTCKP 2460
	GFELVGNLTT LCGENGHWLG GKPTCKAIEC LKPKELNGK PSYTDLHYGQ TVTYSNCRGF 2520
	RLEGPSALTC LETGDWVDVA PSCNAIHCD SPOPIENGFE GADYSYGAI IYSCFPFGV 2580
45	AGHAMQCEE SGWSSSIPTC MPIDCGLPPH IDFGDCTKLK DDQGYFEQED DMMEVPTVT 2640
	HPPYHLGAVA KTWENTKESP ATHSSNLYG TMVSYTCNPG YELGNPVL I CQEDGTWNGS 2700
	APSCISIEDC LPTAPENGPL RFTETSMGSA VQYSCKGHI LAGSDLRCL ENRKWSGASP 2760
	RCEAISCKP NPVNGSIKG SNYTYLSTLY YECDPGYVLN GTERRTCQDD KNWDEDEPIC 2820
	IPVDCSSPPV SANGQVRGDE YTFQKELEYT CNEGFLLEGA RSRVCLANGS WSGATPDCVP 2880
50	VRCATPPQLA NGVTGLDYG FMKEVTFCH EGYILHAPK LTCQSDGNWD AEIPLCKPVN 2940
	CGPPEDLAHG PFNGFSPFHG GHIQYQCFPG YKLHGNSSRR CLSNGSWSGS SPSCLPCRS 3000
	TPVIEYGTN GTDDPCGKAA RIQCFKGFKL LGLSEITCEA DGQWSSGFFH CEHTSCGSLP 3060
	MIPNAFSET SSWKENVITY SCRSYVIOG SSDLICTEK VWSQPYVCE PLSCGSPPSV 3120
	ANAVATGEAH TYESEVKLRC LEGYTMDDT DTFTQCKDGR WPPERISCP KKCPLPENIT 3180
55	HILVHGDDPS VNRQVSVSCA EGYTFEGVNI SVCQLDGTWE PPFSDSCSP VSCGKPESPE 3240
	HGFVVGSKYT FESTIYQCE PGYLEGNRE RVCQENRQWS GGVAICKETR CETPLEFLNG 3300
	KADIENRTTG PNVVYSCNRG YSLEGPSEAH CTENGWTSHP VPLCKENPCP VPFPVPENAL 3360
	LSEKEFVVDQ NVSIKREGF LLQHGHIITC NPDETWTQTS AKCEKISCOP PAHVENAIAL 3420
	GVHYQYDMI TYSCYSYML EGFLRSVCL E NGTWTSPPIC RAVCRPPCQNG GGIQCRPNAC 3480
60	SCPEGWMLR CEEPICILPC LINGRCVAPY QCDCPPGWTG SRCHTAVCQS PCLNGGKCVR 3540
	PNRCHCLSSW TGHNCSE 3557

Seq ID NO: C350 Protein Sequence  
Protein Accession #: FGENESH predicted

65	1 11 21 31 41 51
	MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLQCPAPR CGDKIYNPLE 60
	QCCYNDIAVS LSETRQCGPP CTFWPCFELC CLDSPLGLTND FVVLLKVQGV NSQCHSSPIS 120
70	SKCERGRIC 129

Seq ID NO: C351 Protein Sequence  
Protein Accession #: AAH35671.1

75	1 11 21 31 41 51
	MVPGARGGGA LARAAGRGLL ALLLAVSAPL RLQASELGDG CGHLVTVQDS GMTSKNYPG 60
	TYPNHTVCEK TITVPKGRLL ILRLGDLDE SQTCAADYLL FTSSSDQYGP YCGSMTVPKE 120
	LLNLTSEVTV RFESGSHISG RGFLITYASS DHPDLITCLE RASHYLKTEY SKFCPAGCRD 180
80	VAGDISGMNV DGYRDTSLC KAAIHAGIIA DELGQISVL QRKGLISRYEG ILANGVLSRD 240
	GSLSDRFLP TSNGCSRLS FEPDGQIRAS SSWQSVNESG DQVHWSGQA RLQDQGPSWA 300
	SGDSSNNHKP REWLEIDLGE KKKITGIRT GSTQSNFNFY VKSFVMNFKN NNSKWKTYKG 360
	IVNNEEKVFQ GNSNFRDPVQ NNFIPPIVAR YVRVVPQTH QRIALKVELI GCQITQGNDS 420
	LWVRKTSQST SVSTKKEDET ITRPIPSEET STGINITTVA IPLVLLVVLV FAGMGIFAAP 480
	RKKKKKGSPY GSABEQKTDK WKQIKYPPAR HQSAEFTISY DNEKEMTKQL DLITSDMAG 539

Seq ID NO: C352 Protein Sequence  
Protein Accession #: Eos sequence

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MGFGAGQRLR	FVPAPRSSAE	EAARPGQLRL	GIRRGAEALA	KLAPSGVMVP	GARGGGALAR	60
AAGRGLLALL	LAVSAPLRLO	AEELGDGCGH	LVTYQDSGTM	TSKNYPGTYP	NHTVCEKIT	120
VPGKRLILR	LGDDIESQT	CASDYLLFTS	SSDQYGPYCG	SMTVPKELLL	NTSEVTVRFE	180
SGSHISGRGF	LLTYASSDHP	DLITCLERAS	HYLKTEYSKF	CPAGCRDVAG	DISGNMVDGY	240
RDTSLLCKAA	IHAGIIADEL	GGQISVLQRK	GISRYEGILA	NGVLSRDGSL	SDKRFLFTSN	300
GCSRSLSFEP	DGQIRASSSW	QSNFESGDQV	HWSPGQARLQ	DQGPSWASGD	SSNNHKPREW	360
LEIDLGEKKK	ITGIRTTGST	QSNFNFYVKS	FVMNFKNNNS	KWKTYKGIVN	NEEKVFQGNS	420
NFRDPVQNNF	IPPIVARYVR	VVPQTWHQRI	ALKVELIGCQ	ITQGNDSLWV	RKTSQSTSVS	480
TKKEDBTITR	PIPSEETSTG	INITTVAIPL	VLLVVLVFAG	MGIFAAPRKK	KKKGSPYGSA	540
EAQKTDCKWQ	IKYPFARHQS	AEFTISYDNE	KEMTQKLDLI	TSDMAG		586

Seq ID NO: C353 Protein Sequence  
Protein Accession #: FGENESH predicted

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MFQRQERFLD	LSSAEVAAM	ILHQHPDIIN	KGDGCGHLVT	YQDSGTMSTK	NYPGTYPNHT	60
VCEKTIITVPK	GKRLILRLGD	LDIESQTCAS	DYLLFTSSSD	QYGMQKEEET	EVLCLSVAGA	120
QRVDIPVQLL	PSFLEGWKSH	ADARGPYCGS	MTVPKELLIN	TSEVTVRFES	GSISHGRGFL	180
LTYASSDHPD	LITCLERASH	YLKTEYSKFC	PAGCRDVAGD	ISGNMVDGYR	DTSLCKAAI	240
HAGIIADELG	GQISVFLQRK	ISRYEGILAN	GVLSRDGSL	DKRFLFTSNG	CSRSLSFEPD	300
GQIRASSSWQ	SVNESGDQVH	WSPGQARLQD	QGPSWASGDS	SSNNHKPREWL	EIDLGEKKKI	360
TGIRTTGSTQ	SNFNFYVKSF	VNMFKNNNSK	WKTYKGIVNN	EEKVFQGNIN	FRDPVQNNFI	420
PPIVARYVRV	VVPQTWHQRI	LKVELIGCQI	TQGNDSLWVR	KTSQSTSVST	KKEDETITRP	480
IPSEETSTDA	MPVQIVGDHT	QMISQRENLG	PDEGKIPFKG	TAESMVRVVF	AVVVNDLGM	540
PLAHTPEEDI	DHYCNKQIKY	PFARHQSAPF	TIISYDNEKEM	TQKLDLITSD	MADYQQPLMI	600
GTGTVTRKGS	TFRPMDTDAE	EAGVSTDAAG	HYDCPQQRGR	HEYALPLAPP	EPEYATPIVE	660
RHVLAHTFS	AQSGYRVPGP	QPGHKHSLSS	GGFSPVAVGV	AQDGDYQRP	SAQPADRGYD	720
RPKAVSALAT	ESGHPSQKPF	PTHPGTSDSY	SAPRDLCTPL	NQTAMTALL		769

Seq ID NO: C354 Protein Sequence  
Protein Accession #: NP\_004607.1

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1	11	21	31	41	51	
MAGVSACIKY	SMFTNFLEFW	LCGILILALA	IWVRVNSDSQ	AIFGSEDVGS	SSYVAVDILI	60
AVGAILIMLG	FLGCCGAIKE	SRMILLFFI	GLLLILLLQV	ATGILGAVFK	SKSDRIVNET	120
LYENTKLLSA	TGESEKQFKE	AIIVFQEEFK	CCGLVNGAAD	WGNFQHYYPE	LCACLDKQRP	180
CQSYNGKQVY	KETCISFIKD	FLANLIIVI	GISPLGAVIE	ILGLVFSMVL	YCQIGNK	237

Seq ID NO: C355 Protein Sequence  
Protein Accession #: NP\_004608.1

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MCTGGCARCL	GGTLIPLAFF	GFLANILLFF	PGGKVIDDND	HLSEQIWFEG	GILGSGVIMI	60
FPALVFLGLK	NNDCCGCCGN	EGCGKRFAMP	TSTIFAVVGF	LGAGYSFIIS	AISINKGPKC	120
LMANSTWGYF	FEHGDYLNDE	ALWNKCREPL	NVVPWNLTIF	SILLVVGIGI	MVLCAIQVNN	180
GLLGLTLCGDC	QCCGCCGSDG	PV				202

Seq ID NO: C356 Protein Sequence  
Protein Accession #: NP\_002372.1

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MPRPAPARRL	PGLLLLLLWPL	LLPSAAPDP	VARPGFRRL	TRGPGGSPGR	RPSAAPDGA	60
PASGTSEPGR	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRII	DTLDIGPADT	120
RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVEAGA	180
REPSSNIPKV	AIIVTDGRQP	DQVNEVAARA	QASGIELYAV	GVDRAIMASL	KMMASEPLEE	240
HVFYVETYG	IEKLSSRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHCE	CSQGYTLNAD	300
KKTCALDRIC	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCQAQD	KCALGTHGCO	360
HICVNDRTGS	HNCECYEGYT	LNADKKTCV	RDKCALGSHG	CQHICVSDGA	ASYHCDCYPG	420
YTLNEDKKTC	SATEEARRLV	STEDACGCEA	TLAQDKVSS	YLQRLNTKLD	DILEKLKINE	480
YQQIHR						486

Seq ID NO: C357 Protein Sequence  
Protein Accession #: NP\_057723.1

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MARGSLRRL	RLVLGLWLA	LLRSVAGEQA	PGTAPCSRGS	SWSADLDKCM	DCASCRRAPH	60
SDFCLGCAAA	PPAPFRLLWP	ILGGALSLTF	VLGLLSGLFLV	WRRCRRRREK	TTPIETTGGE	120
GCPAVALIQ						129

Seq ID NO: C358 Protein Sequence  
Protein Accession #: NP\_001810.1

1 11 21 31 41 51  
 5 MQPTLLLSLL GAVGLAAVNS MPVDNRNHNH GMVTRCIIEV LSNALSKSSA PPITPECRQV 60  
 LKTSRKDVVD KETTENTNK FEVRLLADPA DASEAHESSE RGEAGAPGEE DIQGPTKADT 120  
 EKWAEGGCHS RERADEPQWS LYPDSQVSE EVKTRHSEKS QREDEEEEEE ENYQKGERGE 180  
 DSSEKHLLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG 240  
 EEAGSQENHP QESKQQPRSQ ESEEGEEDA TSEVDKRRTR PRHHHGRSRP DRSSQGGSLP 300  
 10 SEEKGHPQEE SEESNVSMAS LGEKRDHST HYRASEEPE YGEEIKGYPG VQAPEDLEWE 360  
 RYRGRGSEFY RAPRPOSEES WDEEDKRNYP SLELDKMAHG YGESEEEERG LEPGKGRHHR 420  
 GRGGEPRAYF MSDTREEKRF LGEGHHRVQE NQMDKARRHP QGAWKELDRN YLNYGEEGAP 480  
 GKWQQQDLQ DTKENREEAR FQDKQYSSHH TAEKRKRLGE LFNPHYDPLQ WKSSHFERRD 540  
 NMNDNLEGE EENELTLNEK NFFPEYNYDW WEKKPPSEDV NWGYEKRNL A RVPLDLKRO 600  
 YDRVAQLDLQ LHYRKSAEF PDFYDSREP STHQEAENEK DRADQTVLTE DEKKELENLA 660  
 15 AMDLELQKIA EKPSQRG 677

Seq ID NO: C359 Protein Sequence  
 Protein Accession #: XP\_093082.1

1 11 21 31 41 51  
 20 MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QMLTELEFSE TKLEASALKL 60  
 LYGGKLDPNK KLQKLNQPS LSVTAALKPV GMVGNCSGFS GSLVQSHFGY CQDSSPKCDL 120  
 CKLLWPSTRV AAADKCGSPK SFLSEGLNWA GRLEAVEEVL GLGVLVQPGD PASQGGHCE 180  
 25 NYGSRDLVD LEVKAEPRLR KGGMDLQRP LQVLLCKIF SLKFLFIAL PNSPGQSVV 240  
 QVTIPDGFVN VTVGSNVTLI CIYTTVASR EQLSIQWSFF HKKEMEPISS PWEEGKWDV 300  
 EAVKGTLDGQ QAEQIYFSP GQOAVAIQF KDRITGSNDP GNASITISHM QPADSGIYIC 360  
 DVNNPPDFLG QNQGILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLSLALG TPSFVYVWHK 420  
 LEGRDIVPVK ENFNPTTGIL VIGNLTNFEQ GYYQCTAINR LGNSSCEIDL TSSHPVVGII 480  
 30 VGALIGSLVG AAIISVVCF ARNKAKAKAK ERNSKTIAEL EPMTKINPRG ESEAMPREDA 540  
 TQLEVTLPSS IHETGPDITQ EPDYEPKPTQ EPAPEPAPGS EPMVAVDLDI ELELEPETQS 600  
 ELEPEPEPEP ESEPGVVVER LSEDEKGVVK A 631

Seq ID NO: C360 Protein Sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 35 MVPAFWKVFLL ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICITYTTTVA SREQLSIQWS 60  
 FPHKMEMEPI SSFWEKGKWP DVEAVKGTLD GQQAELQIYF SQGQOAVAIQ QPKDRITGSN 120  
 40 DPGNASITIS HMOPADSGIY ICDVNNPPDF LQONQGILNV SVLVKPSKPL CSVQGRPETG 180  
 HTISLSCLSLA LGTSPFVYVY HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYQCTAI 240  
 NRLGNSSCEI DLTSSHPVEG IIVGALIGSL VAAIIISVV CFARNKAKAK AKERNKTYA 300  
 ELEPMTKINP RGESEAMPRE DATQLEVTLF SSIHETGPDITQ EPDYEPKPTQ EPAPEPAP 360  
 45 GSEPMVAVDL DIELELEPET QSELEPEPEP EPESEPGVVV EPLSEDEKGV VKA 413

Seq ID NO: C361 Protein Sequence  
 Protein Accession #: NP\_003011.1

1 11 21 31 41 51  
 50 MVSRMVSTML SGLLFWLASG WTPAPAYSPP TFDVSEADI QRLLEGVMEQ LGIARPRVEY 60  
 PAHQAMNLVG PQSIEGGAHE GLQHLGPPGN IPNIVAELETG DNIPKDPSED QGYDPDPNPK 120  
 PVGKTDGCL ENTPTDAEFS REFQLHQHLE DPEHDYPLGL KWNKLLYEK MKGGERRKRR 180  
 55 SVNPLYQGR LDNVVAKKSV PHFSDEKDP E 211

Seq ID NO: C362 Protein Sequence  
 Protein Accession #: NP\_076926.2

1 11 21 31 41 51  
 60 MTTMQCMEQA MPGAGPGVPO LGNMAVIHSH LWKGLQEKFL KGEPKVLGVV QILTALMSLS 60  
 MGITMCMAS NTYGSNPISV YIGYTINGSV MFIISGSLSI AAGIRTTKGL VRGSLGNIT 120  
 SSVLAASGIL INTFSLAFYS FHHPYCNYG NSNNCHGTMS ILMGLDGMVL LLSVLEPCIA 180  
 65 VLSAFACKV LCCTPGGVVL ILPSHSHMAE TASPTPLNEV 220

Seq ID NO: C363 Protein Sequence  
 Protein Accession #: NP\_002082.1

1 11 21 31 41 51  
 70 MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTMYPR GNHWAUGHLM GKSTGESSS 60  
 VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPO PKALGNQOPS WDSSESSNFK 120  
 DVGSKGKVR LSAPGSQREG RNPQLNQ 148

Seq ID NO: C364 Protein Sequence  
 Protein Accession #: NP\_036393.1

1 11 21 31 41 51  
 80 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60  
 EPAAFKIVFY DVWASNYVDL ITEQADIALT RGAEVKGRG HSQSELQVFW VDRAYALKML 120  
 FVKESHNSK GPEATWRLSK VQPVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180  
 ECQAQQTISL ASSDPQKTVT MILSAVHIQ FDIISDFVS EEHKCPVDER EQLESTLPLI 240  
 LGLILGLVIM VTLAIYHVH KMTANQVQIP RDRSQYKHM 280

Seq ID NO: C365 Protein Sequence  
Protein Accession #: NP\_003217.1

5 1 11 21 31 41 51  
MLGLVLALLS SSSAEEYVGL SANQCAVPAK DRVDCGYPHV TPKECNNRGC CFDSRIPGVP 60  
WCFKPLTRKT ECTF 74

10 Seq ID NO: C366 Protein Sequence  
Protein Accession #: NP\_002984.1

15 1 11 21 31 41 51  
MSLPSSRAAR VPGPSGSLCA LLALLLLLT PGLASAGPV SAVLTELRCT CLRVTLRVNP 60  
KTIGKLQVFP AGPQCSKVEV VASLKNGKQV CLDPEAPFLK KVIQKILDSG NKKGN 114

20 Seq ID NO: C367 Protein Sequence  
Protein Accession #: NP\_005233.2

25 1 11 21 31 41 51  
MRSPSAAWLL GAAILLAAAL SCSGTIQGTN RSSKGRSLIG KVDGTSHTVG KGVTVETVFS 60  
VDEFSASVLT GKLTTVFLPI VYTIIVFVGL PSNGMALWVF LFRTKKKHPA VIYMANLALA 120  
DLSVIVFPL KIAYHIHANN WIYGEALCNV LIGFFYGNMY CSILFMTCLS VQRYWVIVNP 180  
MGHSRKKANI AIGISLAIAL LILLVTIPLY VVKQTIFIPA LMITTCHDVL PEQLLVGDMF 240  
NYFLSLAIGV FLFPALFAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLICF 300  
TPSNLLLVVH YFLIKSQQS HVYALYIVAL CLSTLNSCID PFVYFVSHD FRDHAKNALL 360  
CRSVRTVKQM QVSLTSKHS RKSSSYSSSS TTVKTSY 397

30 Seq ID NO: C368 Protein Sequence  
Protein Accession #: NP\_003460.1

35 1 11 21 31 41 51  
MAEAKTHWLG AALSLIPLIF LISGAEEASF QRNQLLQKEP DLRLNVQKF PSPEMIRALE 60  
YIENLRQAH KEESFPDYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRILLEALRQ 120  
AENEPQSAPK ENKPYALNSE KNFFPMDSDD YETQONPERK LKHMQFFPMY EENSNDNPFK 180  
RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDE DDIYKANNIA 240  
YEDVVGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSGQLGI QEEDLRKESK 300  
DQLSDVSKV IAYLKRLLVA AGSGLRQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLIQ 360  
PPEDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYKPTPG 420  
RAGTEALPDG LSVEDIILNL GMESAANQKT SYFENPYNQE KVLPRLPYGA GRSRSNQLPK 480  
AAWIPHVNR QMAYENLNDK DQELGEYLAR MLVKYPEIN SNQVKRPVPG GSSEDDLQEE 540  
EQIEQAIKEH LNQSSQETD KLAPEVSKRFP VGPPKNDTDP NRQYWEDELL MKVLEYLNQE 600  
KAEGREHIA KRAMENM 617

50 Seq ID NO: C369 Protein Sequence  
Protein Accession #: NP\_112217.1

55 1 11 21 31 41 51  
MPCAQRSLWA NLSVVAQLLN FGALCYGRQP QPGPVRFPDR ROEHFIKGLP EYHVVGPEVRV 60  
DASGHFLSYG LHYPIITSSRR KRDLDGSEDW VYIRISHEEK DLFFNLITVQ GPLSNSYIME 120  
KRYGNLSHVK MMASAPLCH LSGTVLQQGT RVGTAALSAC HGTLGFFQLP HGDFPIEPVK 180  
KHLPLVGGVH PHIVYRRQKV PETKEPTCGL KDSVNISQKQ ELWREKWERH NLPSSRLSRR 240  
SISKERWVET LVVADTKMIE YHGSENVESY ILTIMNMVTG LFHNPISIGNA IHIVVRLIL 300  
LEEEBQGLKI VHHAETLSS FCKWQKSINP KSDLPVPHHD VAVLLTRKDI CAGFNRPCE 360  
LGLSHLSGMC QPHRSCNINE DSGPLAFTI AHELGHSGFI QHDGKENDCE FVGRHPYIMS 420  
RQLQYDPTPL TWSKCSSEYI TRFLDRGWGF CLDDIPKKKG LKSKVIAPGV IYDVHHCQL 480  
QYGENATFCQ EVENVCOTLW CSVKGFCRSK LDAAADGTQC GEKKWCMAGK CTVGKPKPES 540  
IPGGWGRWSP WSHCSRTCGA GVQSAERLCN NPEPKFGGKY CTGERKRYRL CNVHPCRSEA 600  
PTFRQMCQSE FDTVPYKNEL YHWFPFNPFA HPCELYCRPI DQGFSEKMLD AVIDGTPCFE 660  
GGNSRNVGIN GICKMVGCDY EIDSNATEDR CGVCLGDGSS CQTVRKMFKQ KEGSGYVDIG 720  
LIPKGARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGPIIQ WNGNYKLAGT VFQYDRKGDL 780  
EKLMAATGPTN ESWIQLLFQ VTNPGIKYEV TIQKDGDLND VEQMYFWQYG HWTECSVTCG 840  
TGIRRTAHAC IKKGRGMVKA TFCDPETQFN GRQKKCHEKA CPFRWAGWEW EACSATCGPH 900  
GEKKRTVLICI QTMVSDQAL PPTDCQHLLK PKTLLSCNRD ILCPSDWTVG NWSECSVSCG 960  
GGVRIISVTC AKNHDEPCDV TRKPNRSLC GLQQCPSSRR VLKPNKGTIS NGKNPPTLKP 1020  
VFPPTSRRPM LTTPTGPESM STSTPAISSP SPTTASKEGD LGGKQWQDSS TQPELSSRYL 1080  
ISTGTSQPI LTSQSLSIQ SEENVSSSDT GPTSEGGGLVA TTTSGSGLSS SRNPITWVPT 1140  
PFYNTLTKGP EMEIHSGSGE EREQPEDKDE SNFVIWTKIR VPGNDAPVES TEMPLAPPLT 1200  
PDLGRESWVP PFSTVMEGLL PSQRPTTSET GTPRVEGMVT EKPANTLLPL GGDHQPPEPSG 1260  
KTANRNHLKL PNNMNQTKSS EPVLTEEDAT SLITEGFLN ASNYKQLTNG HGSAHWIVGN 1320  
WSECSTTCLG GAYWKRVECT TQMSDCAAI QRPDPKRCCH LRPCAGWKVG NWSKCSRNC 1380  
GGFKIREIQ VDSRDRHLR PFHCQFLAGI PPPLSMSCNP EPCAWQVEP WSQCSRSCGG 1440  
GQERGVFPC GGLCDWTKRP TSTMSCNEHL CCHWATGNWD LCSTSCGGGF QKRIVQCVPS 1500  
EGNKTEDQDQ CLCDHKPRPP EPKKCNQQAC KKSADLLCTK DKLSASFQCT LKAMKCSVP 1560  
TVRABCCFSC PQTHITHQQR QRRQLLQKS REL 1593

80 Seq ID NO: C370 Protein Sequence  
Protein Accession #: NP\_001053.1

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MRQSHQLPLV	GLLLFSFIPS	QLCEICEVSE	ENYIRLKLPL	NTMIQSNYNR	GTSAVNVVLS	60
LKLVGIIQIQT	LMQKMIQKQK	YNVKSRLSDV	SSGELALIL	ALGVCRNAEE	NLIYDYHLTD	120
KLENKFQAEI	ENMEAHNGTP	LTNYYQLSLD	VLALCLFNGN	YSTAEVNVHF	TPENKNYYFG	180
SQFSVDTGAM	AVLALTCVKK	SLINGQIKAD	EGSLKNISII	TKSLVEKILS	EKKENGLIGN	240
TFSTGEAMQA	LFVSSDYNE	NDWNCQQTIN	TVLTEISQGA	FSNPNAQAQV	LPALMGKTPL	300
DINKDSSCVS	ASGNFNISAD	EPITVTPPDS	QSYISVNVSV	RINETYFTNV	TVLNGSVPLS	360
VMEKAQXMD	TIFGFTMEER	SWGPIYITCIQ	GLCANNNDRT	YWELSSGGEP	LSQGAGSYVV	420
RNGENLEVRW	SKY					433

Seq ID NO: C371 Protein Sequence  
Protein Accession #: NP\_004582.1

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MCCTKSLLLA	ALMSVLLHL	CGESEASNF	DCCLGYTDRI	LHPKFIVGFT	QLANEGCDI	60
NAIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KKVKNM			96

Seq ID NO: C372 Protein Sequence  
Protein Accession #: NP\_037403.1

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MAGSPLLWGP	RAGGVGLLVL	LLGLFRPPP	ALCARPVKEP	RGLSAASPPL	AETGAPRRFR	60
RSVPRGEAAG	AVQELARALA	HLLEAERQER	ARAEQAQED	QQAARVLAQLL	KVWGAPRNSD	120
PALGLDDDDP	APAAQLARAL	LRARLDPAAL	AAQLVPAPVP	AAALRPPRPV	YDDGPAQDA	180
EEAGDETPDV	DRELLRYLLG	RILAGSADSE	GVAAPRRLRR	AADHDVGSSEL	PPEGVLGALL	240
RVKRLTEPAP	QVPARRLLPP					260

Seq ID NO: C373 Protein Sequence  
Protein Accession #: NP\_002236.1

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MLQSLAGSSC	VRLVERHRS	WCFGFLVLGY	LLYLVFQAVV	FSSVELPYED	LLRQELRKLK	60
RRFLEEHECL	SEQLEQFLG	RVLEASNYGV	SVLSNASGNW	NWFTSALFF	ASTVLSTTGY	120
GHTVPLSDGG	KACFIYSVI	GIPFTLLFLT	AVVQRITVHV	TRRPVLYFHI	RWGFSGQVVA	180
IVHAVLLGTV	TVSCFFFIAP	AVFSVLEDDW	NFLESPIYCF	ISLSTIGLGD	YVPGEGYNQK	240
PRELYKIGIT	CYLLGLLIAM	LVLVLETFCEL	HEKKPKKMP	YVKDKKDEDQ	VHIIHEDQLS	300
FSSITDQAAG	MKEDQKQNEP	FVATQSSACV	DGPANH			336

Seq ID NO: C374 Protein Sequence  
Protein Accession #: NP\_005463.1

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1	11	21	31	41	51	
METTINGTETW	YESLHVLKA	LNATLHSNLL	CRPGFGLGPD	NQTEERRASL	PGRDDNSYMY	60
ILFVMEFLFAV	TVGSLILGYT	RSRKVDKRS	PYHVIKRN	SMI		103

Seq ID NO: C375 Protein Sequence  
Protein Accession #: NP\_005236.1

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1	11	21	31	41	51	
MGRHLALLLL	LLLLFQHFQD	SDGSQRLEQT	PLQFTHLEYN	VTQENSAAK	TYVGHFVKMG	60
VYITHPAWEV	RYKIVSGDSE	NLFKAEEYIL	GDFCFIRIRT	KGNTAILNR	EVKDHVTLIV	120
KALEKNTNVE	ARTKVRVQVL	DTNDRPLFS	PTSYSVSLPE	NTAIRTSIAR	VSATDADIGT	180
NGEFYYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGISSM	240
AKLTVHIEQA	NECAPVITAV	TLSPELDRD	PAYAIIVTDD	CDQGANGDIA	SLSIVAGDLL	300
QQPRTVRSFP	GSKEYVKAI	GDIDWDSHPF	GYNLTQAKD	KGTTPQFSSV	KVIHVTSPQF	360
KAGPVKFEKD	VYRAEISEFA	PPNTPVVMVK	AIPAYSHLRY	VFKRTPGKAK	FSLNYNTGLI	420
SILEFVKRQQ	AAHFELEVTT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AFDENVPIGT	480
TIMSLSAVDP	DEGENGYVTV	SIANLNHVFP	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	540
SDWGLPYRRE	VEVLATITLN	NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	600
LVQYQIEAGN	ELDLFSLNPN	SGVLSLKRSL	MDGLGAKVSF	HSLRITATDG	ENPATPLYIN	660
ITVAASHKLV	NLQCEETGVA	KMLAEKLLQA	NKLNHQGEVE	DIFFDSSHVN	AHIPQFRSTL	720
PTGIQVKENQ	PVGSSVIFMN	STDLDTGFGN	KLVAVSGGN	EDSCFMIDME	TGMLKILSPL	780
DRETTDKYTL	NITVYDLGIP	QKAARLLLEV	VVVDANDNPP	EFLQESYFVE	VSEDKEVHSE	840
IIQVEATDKD	LGPNGHVTVS	ILTDITDTFSI	DSVTGVVNIA	RPLDRELQHE	HSLKIEARDQ	900
AREEPQLFST	VVVVKSLEDV	NDNPPTFIPP	NYRVKVREDL	PEGTVIMWLE	AHDPDLGQSG	960
QVRYSLLDHG	EGNFVDVKLS	GAVRIVQQLD	FEKKQVYNLT	VRAKDKGKPV	SLSSTCYVEV	1020
EVVDVNNENH	PPVFSFVEK	GTVKEDAPVG	SLVMTVSAHD	EDAGRDEGEIR	YSIRDGSGVG	1080
VFKIGETGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS	SFIEIYIEVE	DVNDNAPQTS	1140
EPVYVPEIME	NSPKDVSVVQ	IEAFDPDSSS	NDKLMYKITS	GNPQGFSSIH	PKTGLITTS	1200
RKLDREQQDE	TGSLYTVTDN	GSPPKSTIAR	VIVKILDEND	NKPQFLQKPY	KIRLPEREKP	1260
DRERNARREP	LYRVIAITDK	EGPNAEISYS	IEDGNEHGKF	FIEPKTGVS	SKRPSAAGEY	1320
DILSIKAVDN	GRQKSSITR	LHIEWISKPK	QSLPISFEE	SFFTFTVMES	DPVAHMIGVI	1380
SVEPPGIPLW	PDITGGNYDS	HFDVDKGTGT	IIVAKPLDAE	QKSNYNTLVE	ATDGTITILT	1440
QPKIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VDQDEKNKLI	YTLQSSRDPL	1500
SLKFRFLDPA	TGSLYVTEKL	DHEAVSPAHL	TVMVRDQDVP	VKNRFARIVV	NVSDTNDHAP	1560
WFTASSYKGR	SVSAEAVGSV	VLQVATLADK	KGKNAEVLVS	IESGNIGNIG	NSFMIDPVLG	1620
SIKTAKEKLD	SNQAEYDLMV	KATDKGSPPM	SEITSVRIFV	TIADNASPKF	TSKEYSVELS	1680
ETVSGSFVG	MVTAHSQSSV	VYEIKDGNIG	DAFDINPHSG	TIITQKALDF	ETLPIYTLII	1740
QGTNAGLST	NTTVLVHLQD	ENDNAPVFMQ	AEYTGILISES	ASINSVVLTD	RNVPLVIRAA	1800

	DADKOSNALL	VYHIVEPSVH	TYFAIDSSTG	AIHTVLSLDY	EETSIFHFTV	QVHDMGTPRL	1860
	FAEYANVTV	HVIDINDCP	VFAKPLYEAS	LLLPTYKGVK	VITVNATDAD	SSAFSOLYIS	1920
	ITEGNIGKEF	SMOYKTGALT	VQNTTQLRSR	YELTVRASDG	RFAGLTSVKI	NVKESKESHL	1980
5	KFTQDVYSAV	VKENSTEAE	LAVITAIGSP	INEPLFYHIL	NPDRRFKISR	TSGVLSTTGT	2040
	PFDREQEAF	DVVVEVIEH	KPSAVAHVVV	KVIVEDQNDN	APVFNLPYY	AVVKVDTEVG	2100
	HVIRYVTAVD	RDSGRNGEVH	YYLKEHHEHF	QIGPLGEISL	KKQFELDTLN	KEYLVTVAK	2160
	DGGNPAFSAE	VIVPITVMNK	AMPVFEKPFY	SABIAESIQV	HSPVVHVQAN	SPEGLKVYFS	2220
	ITDGDPPSQF	TINFNTGVIN	VIAPLDFAH	PAYKLSIRAT	DSLTAHAHEV	FVDIIVDDIN	2280
10	DNPPVFAQOS	YAVTLSEASV	IGTSVVQVRA	TDSDSEPNRG	ISYQMFNGHS	KSHDHFHVDS	2340
	STGLISLLRT	LDYEQSRQHT	IFVRAVDGGM	PTLSSDVIVT	VDVTDLNGNP	PLFEQQIYEA	2400
	RISEHAPHGH	FUTCVKAYDA	DSSDIDKLQY	SILSGNDHGH	FVIDSATGII	TLNLRHRHAL	2460
	KPFYSLNLVS	SDGVFRSSTQ	VHVTVIGGNL	HSPAFLQNEY	EVELAENAPL	HTLVMEVKTT	2520
15	DGDSGIYGHV	TYHIVNDFAK	DRFYINERGQ	IFTLEKLDRE	TPAEKVISVR	LMAKDAGGKV	2580
	AFCTVNVILT	DDNDNAPQFR	ATKYEVNIGS	SAAKGTSVVK	SASDADEGSN	ADITYAIED	2640
	SESVKENLEI	LDYEQSRQHT	ESLIGLENEF	FTFFVRAVDN	GSPSKESVVL	VYVKILPEPM	2700
	QLPKFSEPFY	TTTSEDEVVP	GTEIDLIRAE	HSGTVLYSLV	KGMTPESNRD	ESFVIDRQSG	2760
20	RLKLEKSLDH	ETTKWYQFSI	LARCTQDDHE	MVASVDVSIQ	VKDANDNSPV	FESSPYEAFI	2820
	VENLPGGSRV	IQRASDADS	GTNGQVMYSL	DQSQSVEVIE	SFAINMETGW	ITTLKELDHE	2880
	KRDNYQIKVV	ASDHGECIKL	SSTAIVDVTV	TDVNDSPPRF	TAEYIKGTVS	EDDPQGGVIA	2940
	ILSTTDADSE	ENRQVTTYFI	TGGDPLGQFA	VETIQNEWKV	VYKPKLDREK	RDNVLLTITA	3000
	TGDTFSSKAI	VEVKVLDAND	NSPVCEKTLV	SDTIPEDVLP	GKLMQISAT	DADIRSNAEI	3060
	TYTLGSGAE	KFKLNPDGCE	LKTSTPLDRE	EQAVVHLVLR	ATDGGGRFCQ	ASIVVTLEDV	3120
25	NDNAPEFSAD	PYAITVFENT	EPGTLTLRVQ	ATDADAGLNR	KILYSLIDSA	DGQPSINELS	3180
	GIQLEKFLD	RELQAVYTLS	LKAVDQGLPR	RLTATGTIVV	SVLDINDNPP	VFEYREYGAT	3240
	VSEDILVGTG	VLQVYAASRD	IEANAEITYS	IISGNEHGKF	SIDSKTGAVF	IENLDYESS	3300
	HEYYLTVEAT	DGGTSLSDV	ATVNVNVTDI	NDNTPVFSQD	TYTTVISED	VLEQSVITVM	3360
	ADDADGSPNS	HIHYSIIDGN	QSSSFTIDPV	RGEVKVTKLL	DRETISGYTL	TVOASDNGSP	3420
30	PRVNTTNNI	DVSDVNDNAP	VFSRGNYSVI	IQENKPVGFS	VLQLVVTDED	SSHNGPPFPF	3480
	TIVTGNDEKA	FEVNPQGVLL	TSSAIKRKEK	DHYLLQVKA	DNGKPKLSSL	TYIDIRVIEE	3540
	SIYPPAILEL	EIPIYSSGEE	YSGGVIGKIH	ATDQDVYDIL	TYSLDPQMDN	LFSVSSTGGK	3600
	LIAHKKLDIG	QYLLNVSVTD	GKFTTVADIT	VHIRQVTQEM	LNHTIAIRFA	NLTPEEFVGD	3660
	YWRNFQRLAL	NILGVRRNDI	QIVSLQSSEP	HPLDVLLEFV	EKPGSAQIST	KQLLHKINSS	3720
35	VTDIEEIGV	RILNVFKLKC	AGLDCPWKFC	DEKVSVDSEV	MSTHSTARLS	FVTPRHRAA	3780
	VCLCKEGRCP	PVHHCEDDDP	CPEGSECVSD	PWEEKHTCVC	PSGRFGQCPG	SSSMILTGN	3840
	YVKYRLTENE	NKLEMLTMR	LRTYSTHAVV	MYARGTDYSI	LEIHHGRLQY	KFDGSGPGFI	3900
	VSVQSIQVND	QOMHVALEV	NGNYARLVLD	QVHTASGTAP	GLTKTLNLND	VYVFGGHIRQ	3960
	QGTRHGRSPQ	VGNFGRFCMD	SIYLNQQLP	LNSKPRSYAH	IEESVDVSPG	CFLTATEDCA	4020
40	SNPCQNGGVC	NPSAPAGGYC	KCSALYIGTH	CEISVNPCCS	NPCLYGGTCV	VDNNGFVQCQ	4080
	RGLYTGQRQ	LSPYCKDEPC	KNGGTCFDSL	DGAVCQCDG	FRGERQCSDI	DECSGNPLCH	4140
	GALCENTHGS	YHCNCSHEYR	GRCEDAAPN	QYVSTPNWIG	LAEGIGIVVF	VAGIFLLVVV	4200
	FVLCKRMISR	KKKHQAEPKD	KHLGPATAFL	QRPFYDSKLN	KNIYSDIPPQ	VPVRPISTYP	4260
	SIPSDSRNNL	DRNSFECSAI	PEHPEPSTFN	PESVHGHRKA	VAVCSVAPNL	PPPPPSNPS	4320
45	DSDSIQKPSW	DFDYDTKVVD	LDPLCSKKPL	EKPSQPYSA	RESLSEVQSL	SSFQSESCDD	4380
	NGYHWDTSW	MPSVPLFDIQ	EPFNYEVIDE	QTPLYSADPN	AIDTDYYPGG	YDIESDFPPP	4440
	PEDFPADEL	PPLPEFSNQ	FESIHPPRDM	PAAGSLGSSS	RNRQRFNLNQ	YLPNFYPLDM	4500
	SEPQTKGTGE	NSTCREPHAP	YPPGYQRHFE	APAVESMMS	VYASTASCSD	VSACCEVESE	4560
	VMSDYESGD	DGHFEVVTIP	PLDSQQHTEV				4590

Seq ID NO: C376 Protein Sequence  
Protein Accession #: NP\_055035.1

	1	11	21	31	41	51	
55	MCYKGCARCI	GHSVLGLALL	CIAANILLYF	PNGETKYASE	NHLSRFVWFF	SGIVGGGLLM	60
	LLPAFVFIGL	EQDDCCCGCG	HENCGKRCAM	LSSVLAALIG	IAGSGYCVIV	AALGLAEGPL	120
	CIDSLGQWNY	TPASTEGQYL	LDTSWSECT	EPKHIVEWNV	SLFSILLALG	GIEFILCLIQ	180
	VINGVLGGIC	GFCCSHQQQY	DC				202

Seq ID NO: C377 Protein Sequence  
Protein Accession #: NP\_003750.1

	1	11	21	31	41	51	
65	MSTENVEGKP	SNLGERGRAR	SSTFLRVVQP	MFNHSIFTS	VSPAARIRF	ILGEEDDSPA	60
	PPOLFTELDE	LLAVDQEME	WKETARWIKF	EERKEVGGER	WSKPHVATLS	LHSLFELRTC	120
	MEKGSIMLDR	EASSLPOLVE	MIVDHQISTG	LLKPELKDKV	TYTLRLKRHH	QTKKSNLRLS	180
	ADIGKTVSSA	SRMFTNPONG	SPAMTHRNLT	SSSLNDISDK	PEKDQLKNKF	MKKLPRDAEA	240
	SNVLGVEVDF	LDTPPIAFVR	LQQAVALGAL	TEVPVPTREF	FILLGPKGKA	KSYHEIGRAI	300
70	ATLMSDEVFH	DIAYKAKDRH	DLIAGIDEFL	DEVIVLPGE	WDPAIRIEPP	KSLPSSDKRK	360
	NMYSQGENVQ	MNGDTFHDGG	HGGGGHGDCE	ELQRTGRFCG	GLIKDIKRKA	PPFASDFYDA	420
	LNQIALSAIL	FIYLATVINA	ITFGGLLGDA	TDMQGVLES	FLGTAVSGAI	PCLFAGQFLT	480
	ILSSTGPVLV	FERLLNPNFSK	DNNFDYLEFR	LWIGLWSAFL	CLILVATDAS	FLVQYPTFT	540
	EEGFSSLSIF	IFIYDAFKKM	IKLADYYPIN	SNFKVGYNTL	FSCTCVPPDP	ANISISNDTT	600
75	LAFEYLPMTS	SDTMVHNTTF	DWAFLSKKEC	SKYGGNLVGN	NCNFVPDITL	MSFILFLGT	660
	TSSMALKKFK	TSYPFPTTAR	KLISDFAILL	SILIFCVIDA	LGVVDTPKLI	VPSEFKPTSP	720
	NRGWFPVPPG	ENPMWVCLAA	AIPALLVITL	IFMDQQTAV	IVNRKEHKLK	KGAGYHLDLF	780
	WVAILMVICS	LMALPFWYAA	TVISIAHIDS	LKMETETSAP	GEQPKFLGVR	EQRVTGTLVF	840
	ILTGLSVFMA	PILKFIKMPV	LYGVFLYMGV	ASLNGVQFMD	RLKLLMLPLK	HQPDRIYLRH	900
80	VPLRRVHLFT	FLQVCLLALL	WILKSTVAI	IFPVNIALV	AVRKGMDYLF	SOHDLSPFLD	960
	VIPEKDKKKK	EDEKDKKKKK	GSLSDNDSDS	DCPYSEKVP	IKIPMDIMEQ	QPFLSDSKPS	1020
	DRERSPTFLE	RHTSC					1035

Seq ID NO: C378 Protein Sequence  
Protein Accession #: NP\_000949.1

1 11 21 31 41 51  
 5 MSTPGVNSSA SLSPDRLNSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFFYTLVCG 60  
 LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERILA 120  
 INHAYFYSHY VDKRLAGLTL FAVYASNVLF CALPNMGLGS SRLQYPTDWC FIDWITNVTA 180  
 HAAYSYMYAG FSSFLILATV LCNVLVCGAL LRMHRQFMRR TSLGTEQHHH AAAASVASRG 240  
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICSIPLVV RVFVNQLYQP 300  
 10 SLEREVSQNP DLQAIRIASV NPILDPMIYI LLRKTVLSKA IEKIKCLFCR IGSSRRERSG 360  
 QHCSDSQRTS SAMSGHSRSF ISRELKEISS TSQTLPLDLS LPDLSENGLG GRNLLPGVPG 420  
 MGLAQEDTTS LRTLRISETS DSSQGDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480  
 LNLSEKCI 488

Seq ID NO: C379 Protein Sequence  
 Protein Accession #: NP\_002650.1

1 11 21 31 41 51  
 20 MGHPPLLPPL LLLHTCVPAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWEEGEL 60  
 ELVEKSTHS EKTNPITLSYR TGLKITSLTE VVCGLDLCNQ GNSGRAVYTS RSRYLECISC 120  
 GSSDMSCERG RHQSLOCRSP EEQCLDVVTH WIQEGEEGRF KDRHLRGCG YLPGCPGSGN 180  
 FHNNDTFHFL KCCNTTKCNE GPILELENLP QNGRQCYSCK GNSHGCSSSE ETEFLIDCRGP 240  
 MNQCLVATGT HEPKQSYMV RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNHPDLV 300  
 25 QYRSGAAPQP GPAHLSTLIT LMTARLWGG TLLWT 335

Seq ID NO: C380 Protein Sequence  
 Protein Accession #: BAB55406.1

1 11 21 31 41 51  
 30 MDEFSGQVDP LASVILPPNL LENLSPEDSV LVRRRAQTFPF NKTGLFQDVG PORKTLVSYV 60  
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDLN KNKSFGGWNT SGCVAHRDSD 120  
 ASETVCLCNH FTHFGVLMDL PRSASQLDAR NTKVLTFISY IGCGISAFIS AATLLTYVAF 180  
 35 EKLRDYPSPK ILNMLSTALL FLNLLFLLDG WITSFNVNGL CIAVAVLLHF PLLATFTWMG 240  
 LEAIIHYIAL VKVFNITIRR YILKFCIIGW GLPALVVSUV LASRNNNEVY GKESYGKEKG 300  
 DEFCWIDQPV IFYVTCAGYF GVMFFLNIAH FIVVMVQICG RNRGKSNRTL REEVLRNLRS 360  
 VVSLTFLLGM TWGFAPFANG PLNIPFMYLF SIFNSLQGLE IFIFHCAMKE NVQKQWRRHL 420  
 40 CCGRFRLLADN SDWSKTATNI IKKSSDNLGK SLSSSSISGN STYLTSKSKS SSTTYFKRNS 480  
 HTDNVSYEHS FNKSGSLRQC FHGQVLVKTG PC 512

Seq ID NO: C381 Protein Sequence  
 Protein Accession #: NP\_000565.1

1 11 21 31 41 51  
 45 MTVARPSVPA ALPLLGLLPR LLLLVLLCLP AVWGDGCLPP DVPNAQPALE GRTSFPEDTV 60  
 IITYKEESFV KIPGEKDSVI CLKGSQWSDI EPCNRSCEV PTRLNSASLK QPYITQNYFP 120  
 VGTVVVEYCR PGYRREPSSL PKLTCLQNLK WSTAVEPKCK KSCPMPGEIR NGQIDVPGGI 180  
 50 LFGATISFSC NTGYKLFPGST SSFCLISGSS VQWSDPLEPC REIYCPAPPQ IDNGIIQGER 240  
 DHYGYRQSVT YACNKGFMTI GEHSIYCTVN NDEGEWSGPP PEKRGKSLTS KVPPTVQKPT 300  
 TVNVPTTEVS PISQKTTTKT TTPNAQATRS TPVSRTTKHF HETTPNKSGS TTSGTTRLLS 360  
 GHTCFTLTGL LGTLVTMGLL T 381

Seq ID NO: C382 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 60 MDTSLRGVLL SLFVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120  
 LQNNQLRHVP TEALQNLRSL QSLRLDANH I SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVHLHLNN RIHSLGKKCF DGLHSLLETLD 240  
 65 LNYNNLDEFP TAIRTLNLK ELHFYDNPIQ FVGRSAFOHL PELRTLTLNG ASQITEFPDL 300  
 TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSPFSVCQ KLQKIDLRN 360  
 EYIEIKVDTF QQLLSRLSLN LAWNKIAIHH PNAFSTLPFL IKLDLSSNLL SSFPTGLHG 420  
 LTHLKLTLGNH ALQSLISSN FPELKVIEHP YAYQCCAFGV CENAYKISNQ WNKGDNSMD 480  
 DLHKKDAGMF QAQDERDLED FLIDFEEDLK ALHSVQCSPS PGPFKPCFEL LDGWLIRIGV 540  
 70 WTI AVLALTC NALVTSTVPR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAPTFGSF 600  
 ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSKPFET KAPFSSLVKI 660  
 ILLCALLALT MAVPLLGGS KYGASPLCLP LPFGEPSTMG YMVALLILNS LCPLMMTIAY 720  
 TKLYCNLDKG DLENINWDCSM VKHIALLLFT NCILNCPVAF LSFSSILNLT FISPEVIKFI 780  
 LVLVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840  
 75 TQALVTFTSS SIITYDLPPSS VPSPAYPVTE SCHLSSVAFV PCL 883

Seq ID NO: C383 Protein Sequence  
 Protein Accession #: NP\_003658.1

1 11 21 31 41 51  
 80 MDTSLRGVLL SLFVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120  
 LQNNQLRHVP TEALQNLRSL QSLRLDANH I SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVHLHLNN RIHSLGKKCF DGLHSLLETLD 240  
 LNYNNLDEFP TAIRTLNLK ELGFHSNNIR SIPEKAFVGN PSLITIHFYD NPIQFVGRSA 300



5 FOHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360  
 YNLLEDLPSP SVCQKIQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIIHPNAPST 420  
 LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELKV IEMFYAYQCC 480  
 AFGVCENAYK ISNQWNGKDN SSMDDLHKGD AGMFQAQDER DLEDPLLDPE EDLKAHLSVQ 540  
 CSPPSPGPFKP CEHLLDGGLI RIGVWTIAVL ALTGNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 AVNMLTVGSS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLTLAAL 660  
 ERGFSVKYSA KPETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEP 720  
 STMGYMVALI LLNSLCFLMM TIATYKLYCN LDKGDLENIW DCSMVGHIAL LLFTNCILNC 780  
 PVAFLSPSSL INLTIFISPEV IKFILLVVVP LPACLNPLYL ILFNPHFKED LVSLRKQTVV 840  
 10 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900  
 VAFVPCPL 907

Seq ID NO: C384 Protein Sequence  
 Protein Accession #: NP\_003497.1

15 1 11 21 31 41 51  
 MEMFTLLTLC IFPLLRGHGS LFTCEPITVP RCMKAMAYNMT FFPNLMGHYD QSIAAVEMEH 60  
 20 FLEPLANLESC PNIEFTLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRWPEE 120  
 LECDRLOYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPHRLKTSKG QGYKFLGIDQ 180  
 CAPPENMYF KSELEFFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC 240  
 YSIVSLMYFI GFLLDGSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFTMAGTVWW 300  
 VILTTTWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCVFG 360  
 25 LYDLDAARYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKI KKFMRIGVF 420  
 SGLYLVPVLT LLGCYVYEQV NRITWEITWV SDHCROYHIP CPYQAKAKAR PELALPMIKY 480  
 LMTLIVGISA VFVVGSKKTC TEWAGFFKRN RKRDPISER RVLQESCEFF LKHSKVKHK 540  
 KKHYPSSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQBTLEIQ TSPETSMREV 600  
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660  
 30 TGLAQSNILQ VPSSESPSSL KGSTSLLVHF VSGVRKEQGG GCHSDT 706

Seq ID NO: C385 Protein Sequence  
 Protein Accession #: NP\_000573

35 1 11 21 31 41 51  
 MRIAVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQMLLAPQTL 60  
 PSKSNESHDI MDDMDEDDDD DHVDSQDSID SNDSDDVDDT DSHQSDSH HSDESEDLVT 120  
 DFTDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKFP RRPDIQYPA TDEDITSHME 180  
 40 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240  
 NEHSDVIDSQ ELSKVSREFH SHEFHSHEM LVVDFKSKER DKHLKFRISH ELDSASSEVN 300

Seq ID NO: C386 Protein Sequence  
 Protein Accession #: NP\_002812

45 1 11 21 31 41 51  
 MGAARGSPAR PRRLPLLSVL LLPLLGQTQT AIVFIKQPSS QDALQRRAL LRCEVEAPGP 60  
 VHVYNLLDGA PVQDTERRFA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE BARSANASFN 120  
 50 IKWIEAGFVV LKHPASEAEI QPQTQVTLRC HIDGHPRTY QWFRDGTPLS DGQSNHTVSS 180  
 KERNLTLRPA GPEHSGLYSC CAHSAGGQAC SSQNFLLSIA DESFARVVLA PQDVVVARYE 240  
 EAMFHCQFSA QPPPSLQWLF EDETPTNRS RPFHLRRATV FANGSLLLTQ VRPRNAGIYR 300  
 CIGQGQGRGP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG 360  
 VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPDQ 420  
 55 SLEBEGKFGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEYDGTWYR 480  
 CMSSTPAGSI EAQARVQVLE KLKFTPPFPQ QQCEMFDEKA TVPCSATGRE KPTIKNERAD 540  
 GSSLEPWVTD NAGTLHFARV TRDDAGNYTC IASNGPQQOI RAHVQLTVAV FITFKVEPER 600  
 TTVYQGHIAL LQCEAQQDPK PLIQWKGKDR ILDPTKLGR MHIFQNGSLV IHDVAPEDSG 660  
 RYTCTAGNSC NIKHTBAPLY VVDKPVPEES EGPSPPPPYK MIQTIGLSVG AAVAYIIAVL 720  
 60 GLMFYCKKRC KAKRIQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780  
 KRHSTDGMH FPRSSLQPIIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840  
 LDFRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSK 900  
 PLSTKQKVAL CTQVALGMEH LSNRREVHKO LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960  
 YHFRQAWVPL RWMSPEAILE GDFSTKSDWV AFGVLMWEVF THGEMPHGQ ADDEVVLADLQ 1020  
 65 AGKARLPQPE GCPSKLYRLM QRCWALSPKO RPSFSEIASA LGDSTVDSKP 1070

Seq ID NO: C387 Protein Sequence  
 Protein Accession #: NP\_002300.1

70 1 11 21 31 41 51  
 MKVLAAGVVP LLLVLHWKHG AGSPLPITPV NATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60  
 ALPILYTTAQ GEPPFNLDK LCGPNVTFPP PFHANGTEKA KLVELYRIVV YLGTSLGNIT 120  
 RDQKILNPSA LSLHSLKNAT ADILRGLLSN VLCRLCSKYH VGHVDVITYGP DTSGKDVFPK 180  
 75 KKLGCQLGK YKQIIAVLAQ AF 202

Seq ID NO: C388 Protein Sequence  
 Protein Accession #: XP\_097508

80 1 11 21 31 41 51  
 MGRPRLTIVC HVSIIISARD LSMNNLTQL PGLFHHLRFL EELRLSGNHL SHIPGQAFSG 60  
 LYSLKILMLQ NNQLGGIPAE ALWELPSLOS LRLDANLISL VPERSFEGLS SLRHLWLDN 120  
 ALTEIPVRAL NNLPAQAMT LALNRISHIP DYAFQNLTSV VVLHLHNNRI QHLGTHSFEG 180  
 LHNLETLDLN YNKIQEPPVA IRTLGRLEL GFHNNNIKAI PEKAFMGNPL LQTHFYDNP 240

IQFVGRSAFQ YLPKLTLSL NGAMDIQEPF DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300  
 RLRVLELSHN QIEELPSLHR CQKLEIGLQ HNRIWEIGAD TFSQLSSLQA LDLSWNAIRS 360  
 IHPEAFSTLH SLVKLDLTDN QLITLPLAGL GGLMHLKLG NLALSQAFSK DSFFKLRILE 420  
 VPHYACCCPY GMCASFCKAS GQWEAEDLHL DDEESSKRPL GLLARQAENH YDQDLDELQL 480  
 EMEDSKPHPS VQCSPTGPF KPCEYLPESW GIRLAVWAIV LLSVLCNGLV LLTVFAGGPV 540  
 PLPPVKFVVG AIAGANTLTG ISGGLLASVD ALTFGQFSEY GARWETGLGC RATGFLAVLG 600  
 SEASVLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660  
 ASPLCLPYAP PEGQPAALGF TVALVMMSNF CFLVAGAYI KLYCDLPRGD FEAVWDCAMV 720  
 RHVAWLIFAD GLLYCPVAFI SFASMLGLEP VTPEAVKSVL LVVLPPLACL NPLLYLLFNP 780  
 HFRDRLRLR PRAGDSGPLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840  
 TYGFPSVTLI SCQPGAPRL EGSCHVEPEG NHFQNPQPSM DGELLRAEG STPAGGGLSG 900  
 GGGFQPSGLA FASHV 915

Seq ID NO: C389 Protein Sequence  
 Protein Accession #: NP\_570901

1 11 21 31 41 51  
 MASLVSLELG LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLLNT LADRVHCTNG 60  
 PCGKCLSVED ALGLGEPEG GLPPGPVLEA RYVARLSAAA VLYLSNPEG CEDTRAGLWA 120  
 SHADHLALL ESPKALTPGL SWLLQRMQAR AAGQTPKTAC VDIPQLLEE VAGAGPSAG 180  
 GVLAALLDHV RSGSCPHALP SPQYFVDFVF QQHSSEVPMT LAELSALMQR LGVGREASHD 240  
 HSHRHRGASS RDPVPLISSS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP EAWAQLSPAL 300  
 LQQLSGACT SQSRPPVQDQ LSQSERLYG SLATLLICLC AVFGLLLTTC TGRGVVAHYI 360  
 LQTFLSLAVG ALTDGAVLHL TPKVLGLLTH SEEGLSQPPT WRLLAMLALG YAPFLFENLF 420  
 NLLPLRDPED LEDGFCGHSS HSHGGHSHGV SLQAPSELRL QPKPHEGSR ADLVAEESPE 480  
 LLNPEPRRLS PELRLLEPYMI TLGDVHNFA DGLAVGAFA SSWKTGLATS LAVFCHELPH 540  
 ELGDFALALH AGLSVRQALL LNLASALTAF AGLYVALAVG VSESEAWIL AVATGLFLYV 600  
 ALCDMLPAML KVRDPRPWL FLHNVLGLL GWTVLLLSL YEDDITF 648

Seq ID NO: C390 Protein Sequence  
 Protein Accession #: NP\_061844

1 11 21 31 41 51  
 MANASEPGGS GGGEEAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPIYLLLDL 60  
 CLADGLRALA CLPAVMLAAR RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLGVGVT 120  
 YLAIAHRRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL DGGGDEEDAP CALEQRPDGA 180  
 PGALGFLLL AVVVGATHLV YLRLLFFIHD RRMMPARLV PAVSHDWTFF GPGATGQAAA 240  
 NWTAGFGRGP TPVALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LFLLLWGPY 300  
 VVASYLRLV REGAVPQAYL TASVWLTFQA AGINPVVCFI FNRELDCFR AQFPCCQSPR 360  
 TTQATHPCDL KGIGL 375

Seq ID NO: C391 Protein Sequence  
 Protein Accession #: NP\_005622

1 11 21 31 41 51  
 MAAARPARGP ELPLILGLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP 60  
 LSHCGRAAPC EPLRYNVLG SVLPYGATST LLAGDSDSQE EAHGKLVLS GLRNAPRCWA 120  
 VIQPLLCVAV MPKCEMDRVE LPSRTLCOAT RGPCAIVERE RGWPDFLRCT PDRFPPEGCTN 180  
 EVQNIKFNSS GQCEPVLVRT DNPKSWYEDV EGCGIQQNP LFTAEHQDM HSYIAAFGAV 240  
 TGLCTLFILA TVFADWRNSN RYPAVILFYV NACFFVGSIG WLAQFMDGAR REIVCRADGT 300  
 MRLGEPTNE TLSCVIIIFI VYVALLMAGV WVVVLYAWH TSPKALGTYY QPLSGKTSYF 360  
 HLLTNSLFFV LTVALLAVA VDGDVSGIC FVGKKNRYR AGFVLAPIGL VLIIVGGYFLI 420  
 RGVMTLFSIK SNHPGLLEK AASKINETML RLIGFGLFAP GFVLITFSCH FYDFFNQAEW 480  
 ERSFRDYVLC QANVTGLPT KQIPDCEIK NRPSSLVEKI NLFAMGTGI AMSTWVWTKA 540  
 TLLIWRRTWC RLTGQSDDEP KRIKSKMIA KAFSKRHELL QNPQELSPS MHTVSHDGFV 600  
 AGLAPDLNEP SADVSSAWAQ HVTMVARRG AILPQDISVT PVATPVPEE QANLWVVEA 660  
 ISPELQKRLG RKKKRRKRK EVCPLAPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAMG 720  
 AGDSCROGAW TLVSNFFCPE PSPQDPFLP SAPAPVAWAH GRRQGLSPIH SRTNLMDEL 780  
 MDADSDF 788

Seq ID NO: C392 Protein Sequence  
 Protein Accession #: BAC04382

1 11 21 31 41 51  
 MGARSARGA LLLALLLCWD PRLSQAGRKR SGEVLPDSFP SAPAEPLPYF LQEPQDAYIV 60  
 KNKPVELRCR APPATQIYFK CNGENVSOND HVTQEGLEDA TLGARGGLRV REVQIEVSRQ 120  
 QVEELFGLD WQCQCVAMSS AGTTKSRAY VRIAYLRKNF DQEPGLKEVP LDHEVLLQCR 180  
 PPEGVPVAEV EWLKNEVDID PTQDTNFLT IDHNLIRQA RLSDTANYTC VAKNIVAKRR 240  
 STTATVIVIV NGGWSSWAEW SPCSNRCGRG WQKRTTRCTN PAPLNGGAFC EQAPQKTAC 300  
 TTICPVDAW TEWSKWSACS TECAHWSRE CMAPPQNGG RDCSGTLDS KNCTDGLCMQ 360  
 NKKTLSDPNS HLLASGDAA LYAGLVVAIF VVVAIIMAVG VVVYRRNCRD FDTDITDSSA 420  
 ALTGHPHFN FKTARPENPQ LHPSPVPPDL TASAGIYRGP VYALQDSTDK IPMTNSPLLD 480  
 PLPLSKVEVY SSSITGSGPG LADGADLLGV LPPGTYPSPD ARDTHFLHLR SASLGSQQLL 540  
 GLPRDPGSSV SGTGCLGGR LSIPGTGVSL LVPNGAIPQG KPYEMYLLIN KAESTLPLSE 600  
 GTQTVLSPV TCGPTGLLLC RPVILTMFHC AEVSARDWIF QLKTQARQGH WEEVVTLDZ 660  
 TIANPCYQQL EPRACHILLD QLGTIVFTGE SYSRSVAVKRL QLAVFAPALC TSLEYSLRVY 720  
 CLEDTVPALK EVLELERTLG GYLVEEPKPL MFKDSYHNL LSLHDLPHAH WRSKLLAKYQ 780  
 EIPPYHIWSG SQKALHCTFT LERHSLASTE LTCKICVRQV EGEGQIFQLH TTLAETPAGS 840  
 LDTLCSAPGS TVTTQLGPYA FKIPLSIRQK ICNSLDAPNS RGNDRWMLAQ KLSMDRYLNY 900  
 FATRASPTGV ILDLWEALQQ DDGDLNSLAS ALEEMKSEM LVAVATDGDC 950

Seq ID NO: C393 Protein Sequence  
Protein Accession #: NP\_004616

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5      1      11      21      31      41      51
|      |      |      |      |      |
MNRKARRCLG HLFLSLGMVY LRIGGFSSVV ALGASTICNK IPGLAPRQRA ICQSRFDAIL 60
VIGEGSQMGL DECFQFRRNG RWNCSALGER TVFGKELKVG SREAAFTYAI IAAGVAHAIT 120
10    AACTQGNLSD CGCDKEKQGG YHRDEGWKMG GCSADIRYGI GFAGVFVDAR EIKQNARTLM 180
NLHNNAGARK ILEENMKLEC KCHGVSGSCT TKTCWTTLPQ FRELGVVLKD KYNEAVHVEP 240
VRASRNKRPT FLKIKKPLSY RKPMDDLTVY IEKSPNYCEE DPTVGSVGTO GRACNKTAPO 300
ASGCDLMCCG RGYNTHQYAR VWCNCKPFHW CCYVKONTCS ERTEMYTCK 349

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Seq ID NO: C394 Protein Sequence  
Protein Accession #: NP\_003777

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15      1      11      21      31      41      51
|      |      |      |      |      |
MDALCGSGEL GSKFWSNLS VHTENPDLT CPQNSLLAWV PCIYLNVALP CYLLYLRRHC 60
20    RGYIILSHLS KLMVLGVLL WCVSWADLFY SFHGLVHGRA PAPVFFVTPL VVGVTMLLAT 120
LLIQYERLQG VQSSGVLIIIF WFLCVVCAIV PFRSKILLAK ABEISDPFR FTFYIHFAL 180
VLSALILACP REKPPFFSAK NVDPNYPET SAGFLSRLFF WWTKMAIYG YRHPLLEKDL 240
WSLKEEDRSQ MVVQQLLEAW RKQEKQTAH KASAAPGKNA SGEDEVLLGA RPRPRKPSFL 300
25    KALLATFGSS FLISACFKLI QDLLSFINPQ LLSLIRFIS NMAPSWSWG LVAGLMFLCS 360
MMQSLILQHY YHIFVTGVK FRTGIMGVIY RKALVITNSV KRSTVGEIV NLMVSDAQR 420
MDLAPFLNLL WSAPLQIILA IYFLWQNLGP SVLAGVAPMV LLIPNGAVA VKMRAFPQVK 480
MKLKDRIKL MSEILNGIKV LKLYAWEPSP LKQVEGIRQG ELQLLRTAAY LHTTTTFTWM 540
30    CSPFLVTLIT LMVYVVDPN NVLDAEKAFV SVSLFNILRL PLNMLPQLIS NLTQASVSLK 600
RIQQFLSQEE LDPQSVERTK ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV 660
GPVGCCKSSL VSALLGEMEK LEGKVMHMG VAYVPOQAWI QNCTLQENVL FGKALNPKRY 720
QQTLEACALL ADLEMLPGGD QTEIGKEGIN LSGGQRQVRS LARAVYSDAD IPLLDDPLSA 780
VDSHVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTDI IIVLADGQVS EMGPYPALLQ 840
RNGSFANFLC NYAPDEDQGH LEDSWTALEG AEDKEALLIE DTLNHTDLT DNDPVTVVQ 900
35    KQFMRQLSAL SSDGEGQGRP VPRRHLPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW 960
DYAKAVGLCT TLAICLLYVG QSAAAIGANV WLSAWTNDAM ADSRQNTSL RLGVYAALGI 1020
LQGFVLMALM MAMAAGGQIA ARVLHQALLH NKIRSPQSPF DTPSGRILN CFSKDIYVVD 1080
EVLAPVILML LNSFFNAIST LVVIMASTPL FTVVILPLAV LYTLVQRYFA ATSRQLKRL 1140
SVSRSPYISH FSETVTGASV IRAYNRSRDF EIIISDTKVA NQRSCYPYII SNRWLSIGVE 1200
40    FVGNCCVLFV ALFAVIGRSS LNPGLVGLSV SYSLQVTFAL NWMIRMSDL ESNIVAVERV 1260
KEYSKTETEA PWVVEGSRPP EGWPPRGEVE FRNYSVRYRP GLDLVLRDLS LHVHGGEKVG 1320
IVGRTGAGKS SMTLCFLRIL EAKGEIRID GLNVADIGLH DLRSQLTIIIP QDPILFSGTL 1380
RMNLDPFGSY SEEDINWALE LSHLHTFVSS QPAGLDFOCS EGGENLSVGQ RQLVCLARAL 1440
45    LRKSRILVLD EATAAIDLET DNLIQATIRT QFDTCTVLT I AHRLNTIMDY TRVLVLDKGV 1500
VAEFDSPANL IAARGIFYGM ARDAGLA 1527

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Seq ID NO: C395 Protein Sequence  
Protein Accession #: NP\_004617

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50      1      11      21      31      41      51
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MRARPQVCEA LLFALALQTG VCYGIKWLA SKTPSALALN QTOHCKQLEG LVSAQVQLCR 60
SNLELMHTTV HAAREVMKAC RRAFADMRWN CSSIELAPNY LLDLERTRE SAFVYALSAA 120
AISHAIAIARAC TSGDLPGCSC GPVPGEPGP GNRWGGCADN LSYGLMGAK FSDAPMKVKK 180
55    TGSQANKLMR LMSSEVGRQA LRASLEMKCK CHGVSGSCSI RTCWKLQEL QDVAADLKTR 240
YLSATKVVRH PRMTGRKHLV KDLDIRPVKD SELVYLQSSP DFCMKNEKV SHGTQDRQCN 300
KTSNGSDSCD LMCCGRGYNP YTRVVERCH CKYHWCYVT CRRCERTVER YVCK 354

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Seq ID NO: C396 Protein Sequence  
Protein Accession #: NP\_114072

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60      1      11      21      31      41      51
|      |      |      |      |      |
MEWGYLLEVT SLLAALALLQ RSSGAAAASA KELACQBITV PLCKGIGYNY TYMPNQFNHD 60
TQDEAGLEVH QFWPLVEIQ SPDLKFFLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP 120
65    LMRQYGFAMP DRMRCDRLPE QGNFDLCLMD YNRDILTAA PSPPRRLPPP PFGEQPPSGS 180
GHGRPPGARF PHRGGGRGG GGDAAAPPAR GGGGGGKARP PGGAAPCEP GCQCRAPMVS 240
VSSERHPLYN RVKTCQIANC ALPCHNFFPS QDERAFTVFM IGLNSVLCFV STFATVSTFL 300
IDMERFKYPE RPIIFLSACY LFSVGYLVR LVAGHEKVC SGGAPGAGGA GGAGGAAAGA 360
70    GAAGAGAGGP GGRGEYEELG AVEQHVRYET TGPALCTVVF LLVYFFGMAS SIWWVILSLT 420
WFLAAGMKNG NEAIAGYSYQ FHAAWLVPS VKSIAVLALS SVDGDPVAGI CYVGNQSLDN 480
LRGFVLAPLV IYLFIGTMFL LAGFVSLFRI RSVIKQDGP TKTHKLEKLM IRLGLFTVLY 540
TVPAVVVAC LFYEQHNRP WEATHNCPCL RDLQFDQARR PDYAVFMKY FMCLVVGITS 600
75    GVWWSGKTL ESMRSLCTRC CWASKGAAGV GGAGATAAG GGGPGGGGGG GPGGGGGPGG 660
GGGSLYSVDS TGLTWSGTA SSVSYPKQMP LSQV 694

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Seq ID NO: C397 Protein Sequence  
Protein Accession #: XP\_050625

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80      1      11      21      31      41      51
|      |      |      |      |      |
MLQGPGLLL LFLASHCCLG SARGLFLFGQ PDFSYKRENC KPIPANLQLC HGIEYQNMRL 60
PNLLGHETMK EVLEQAGAWI PLVMKQCHPD TKKFLCSLFA PVCLDDDET IQPCHSLCVQ 120
VDRCAPVMS AFGFPWDM L ECDRPPQDND LCIPASSDH LLPATEEAPK VCEACKNKND 180
DDNDIMETLC KNDPALKIKV KEITYINRDT KIILETKSKT IYKLVGVSER DLKKSVLWLK 240

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DSLQCTCEEM NDINAPYLVM GQKQGGLVI TSVKRWQKGQ REFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence  
Protein Accession #: NP\_001297.1

5  
10  
1  
11 21 31 41 51  
MSMGLBITGT ALAVLGNLGT IVCCALPMWR VSAFIGSNII TSONIWEGLW MNCVVQSTGQ 60  
MQCKVYDSSL ALPQDLQAA ALIVVAILLA AFGLLVALVG AQCTNCVQDD TAKAKITIVA 120  
GVFLLAALL TLVPVWSAN TIIRDYPNPV VPEAQKREMG AGLYVGWAAA ALQLLGGALL 180  
CCSCPPEKK YTAIKVYSA PRSTGPGASL GTGYDRKDYV 220

Seq ID NO: C399 Protein Sequence  
Protein Accession #: NP\_036581.1

15  
20  
1  
11 21 31 41 51  
MESRKDITNQ EELWQMKPRR NLEEDDYLHK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60  
LQHTQELFPQ WHLPKIAAI IASLTFLYTL LREVIHPLAT SHQYFYKIP ILVINKVLPM 120  
VSITLLALVY LPPVIAAIVY LHNQTKYKPK PHWLDKMWLT RKQFGLLSFF FAVLHAIYSL 180  
SYPMRSYRY KLLNWAYQQV QNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240  
VSDSLTWREF HYIQSKLGI SLLGLTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV 300  
VLIFKSILPL PCLRKILKI RHGWEDVTKI NKTEICSQL 339

Seq ID NO: C400 Protein Sequence  
Protein Accession #: NP\_001766.1

25  
30  
35  
1  
11 21 31 41 51  
MANCEFPVS GDKPCCLSR RAQLCLGVS LVLILVVVLA VVPRWRQW SGPQTTRFP 60  
ETVLARCVKY TEIHPMRHV DCQSVWDAFK GAFISKHPCN ITEEDYQPLM KLGTQTVPCN 120  
KILLWSRIKD LAHQPTQVR DMFTLEDTL L GYLADDLTWC GEFNTSKINY QSCPDRKDC 180  
SNPNVSVFWK TVSRFPAAEA CDVVHVMLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLA 240  
WVIHGGREDS RDLQCDPTIK ELESIIISRN IQFSCKNYR PDKFLQCVKN PEDSSCTSEI 300

Seq ID NO: C401 Protein Sequence  
Protein Accession #: XP\_120513.2

40  
45  
50  
55  
1  
11 21 31 41 51  
MVSCTFSGPL RETNENVKF YALRAFMRM SSEAAMLGES RTPKPRKHRA TTRAKIFKRF 60  
FSEGESNSR LVEELAVIHT YSDDPAPITS PSSVQPREFG VMQAPRARF GSRTPPAAAE 120  
ASSPHLIGE AACQSGARAA APRAGARRCQ PQRQAAAAA TAQTHLPHA RTRADPAGRR 180  
RRHRSPAPG GEGTCSGPA PRRRMEEMQ PAEEGSPVPK IYKQSPYSV LKTFPSKRPA 240  
LAKRYERPTL VELPHGHLRT PAQPPASPAA ASSSSFAAV VRLGAPPRPP RRGFRARGTI 300  
PLLLPAPGVA GTLLPPPTSS SPPSPRPRPW HAAAPRGTS HTHMWSQST LPSGDTMVS 360  
FGLMAQRWQ HRSLLKQFENG ILGSWGTWPC QDWLEKEGO VAVLLPRSEG NTAPKSRMI 420  
LDAFAQQCSR VLSLLNCGGK LLDNSHSQSM ISCVKQEGSS YNERQEHCHI KGKGVHSQTS 480  
NVDIEMQYM RKQQTSAFLR VFTDSLQNYL LSGSFPTPNP SSASEYGHIA DVPDLSTSPV 540  
HTEINISLDS TASLCKSRHL SREPPVKSDP PNPLQALAG GASRPFSQAQ QSIAYRVNSE 600  
LEDGIRSPVP LSCAELMDL TSLGSKQLLN NYPVYITSQ WDEAVNSKK DGRRLRLYLI 660  
RFVPTDELK YSCGLGKRRK SVQSGETGPE RRLDPVKVT CLRGTASFRS VSPSVISFHR 720  
IGCGSPRTSV QPSVF 735

Seq ID NO: C402 Protein Sequence  
Protein Accession #: BAA92562.1

60  
65  
70  
1  
11 21 31 41 51  
METTVLSGIN FEYKGMTGWE VAGDHIYTA GASDNDFMIL TLVVPGRFP QSVMDTENK 60  
EVARITFVE TLCSVNCELY FMVGVSRTN TPVETWKGSK GKQSYTYIE ENTITSFTWA 120  
FORTTFEAS RKYTNDVAKI YSINVTVNMN GVASYCRPCA LEASDVGSSC TSCPAGYID 180  
RDSGTCHSCP PNTILKAHQ YGVQACVPCG PGTRNKIHS LCYNDCTFSR NTPTRTFNYN 240  
FSALANTVIL AGGFSFTSKG LKYFHHFTLS LGNQGRKMS VCTDNVTDLR IPEGESGFSK 300  
SITAYVCQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESGLI 360  
PDVIFFRSN DVTQSCSSGR STTIRVRCSF QKTVPGSLLL PGTCSDGTCD GCNFHFLWVS 420  
AAACPLCSVA DYHAISSCV AGIQKTTYV REPKLCSGGI SLPEQRVTIC KTIDFWLKV 480  
ISAGTCTAIL LTVLTCTYFW KQKLEYKYS KLVNMATLKD COLPADSCA IMEGEDVEDD 540  
LIFTSKSLF GKIKSFTSKQ PAPVTISLSE DS 572

Seq ID NO: C403 Protein Sequence  
Protein Accession #: NP\_055139.1

75  
80  
1  
11 21 31 41 51  
MALQGISVVE LSGLAPGRXC AMVLADFGAR VVRVDRPGSR YDVSRLGRGK RSLVLDLKQP 60  
REPRAAASQ AVGCAAGALP PRCHGETPAG PRDSAAGKSK AYLQCAEWI PVQESFCRLA 120  
GHDINYLALS GVLSKIGRS ENPYAPLNLV ADPAGGGLMC ALGIIMALFD RTRTDKQVQI 180  
DANMVEGTAY LSSFLWKTQK SSLWEAPRGQ NMLDGGAPFY TTYRTADGEF MAVGAIEPQF 240  
YELLIKGLGL KSDLPNQMS TDDWPEMKKK FADVFARKTK AEWCQIFDGT DACVTPVLTF 300  
EEVVHHDHMK ERGSFITSEE QDVSPRLAPL LLNTPAIPSS KGDPFIGEHT EEILEEFGFS 360  
REEIYQLNSD KIIESNKVKA SL 382

Seq ID NO: C404 Protein Sequence

Protein Accession #: XP\_091332.1

5 1 11 21 31 41 51  
 MQRMTLWAAA FLTLHSAQAF PQTDISISPA LPFLPLPSLC PLFWMFEKGH CYRFFPLANK 60  
 WAEADLYCSE FSVGRKSAKL ASIHSEWENV FVYDLVNSCV PGIPADVWTG LHDHRQEGQP 120  
 EMTDGSYDY SYWDGSPDD GVHADPEED CVQIWYRPTS EQLQAPEPQL PLSISEATDV 180  
 YLPEDFPAEP KLMDQSWVSR KSLKPSKSHL MEPPTPVAKH QKAKTRHRSR RGVWVPSGKA 240  
 GSWKERMNAD YGRRKRSAPR QEGRRLRCRER RLRAASGGQR PEGQRKQRQQ ERQERGWEEL 300  
 10 GGVSPMRGAQ NQHQHGLGAGS QRGAAPECGE NHQAPELGST WRGQRLOPQT AALCHFALRK 360  
 LPGAHLGLAA AFVQPALQVQ EEKNNRTRFS GAYFTMSDPT CDQDSKEQSL RRRGREAEKD 420  
 GPYRLVKKKR GPVACPSFFE LQSGGEVCLD FPVELRAGTW IAREPP 466

Seq ID NO: C405 Protein Sequence  
 Protein Accession #: XP\_054869.2

20 1 11 21 31 41 51  
 MHTCCPPVTL EQDLHRKMHS WMLQTLAFV TSLVLSCAET IDYYGEICDN ACPCEEKDIGI 60  
 LTVSCENRGI ISLSISIPPR FPIYHLLLSG NLLNRLYPNE FVNYTGASIL HLGSNVIQDI 120  
 ETGAFPHGLRG LRRLHLNNNK LELLRDDTFL GLENLEYLQV DYNYSVIEP NAFGKLHLHQ 180  
 VLILADNLLS SLFNNLFRFV PLTHLDLRGN RLKLLPYVGL LQHMCKVVEL QLEENPWNC 240  
 CELISLKDML DSISYSALVG DVVCETPPRL HGRDLDEVSK QELCPRLIS DYEMRPQTPL 300  
 STTGYLHTTP ASVNSVATSS SAVYKPLKP PKGTRQPNKP RVRPTSRQPS KDLGYSNYGP 360  
 25 SIAYQTKSPV PLECPATCSC NLQISDLGLN VNCQERKIES IAELOPKPYN PKMYLTENY 420  
 IAVVRTDFL EATGDLHLH GNNRISMIQD RAFGDLTNLR RLVLNGNRIE RLSPELFYGL 480  
 QSLQYLFQY NLRRIQSGT FDPVFNQLL FLNNLLQAM PSGVFSGLTL LRLNLRNHF 540  
 TSLPVSGVLD QLSLIQIDL HDNPWDCTCD IVGMKLWVEQ LKVGVLVDEV ICKAPKKPAE 600  
 TDMRSIKSEL LCPDYSVVV STPTSSSIQV PARTSAVTPA VRLNSTGAPA SLGAGGGGAG 660  
 30 VPLSVLILSL LNVFMSVFEV AAGLFVLVMK RRKNQSDHT STNNSDVSSF NMQYSVYGGG 720  
 GGTGHPHAAH VHRGPALEPK VKTPAGHYVE YIPHLGHMC KNPIYRSREG NSVEDYKDLH 780  
 ELKVYSSNH HQQQQQPPP PQQPQQQPP POLQLQPGEE ERRESHLRS PAYSVSTIEP 840  
 REDLLSPQD ADRFYRGILE PDKHCSTTPA GNSLPEYKPK PCSPAAYTFS PNYDLRRPHQ 900  
 35 YLHPGAGDSR LRPVLVYSP SAVFVEPNRN EYLELKAKLN VEPDYLEVLE KQTTFSQF 958

Seq ID NO: C406 Protein Sequence  
 Protein Accession #: NP\_000784.2

40 1 11 21 31 41 51  
 MGILSVLLI TLQILPVFFS NCLFLALYDS VILLKHVVLL LSRSKSTRGE WRRMLTSEGL 60  
 RCVMKSFLLD AYKQVLGED APNSSVVHVS STEGGDNNGN GTQEKIAGA TCHLLDFASP 120  
 ERPLVVNFGS ATUPPFTSQL PAFKRLVEEF SSVADFLVY IDEAHPSDGM AIPGDSSLSF 180  
 45 EVKHKQNGED RCAAQQLLE RPSLPQCRV VADRMNNAN IAYGVAFERV CIVQRQKIAY 240  
 LGKGGFPSYN LQEVHRWLEK NFSKRUKKTR LAG 273

Seq ID NO: C407 Protein Sequence  
 Protein Accession #: NP\_006540.2

50 1 11 21 31 41 51  
 MSSCVSSQPS SNRAAPQDEL GGRGSSSSSES QKPCEALRGL SLSIHLGME SPIVVTECEP 60  
 GCAVDLGLAR DRPLEADGQE VPLDSSGSQA RPHLSGRKLS LQERSQGLA AGGSLDMNGR 120  
 55 CIPCPLPYSP VSSQSSPRL PRRPTVESHV VSIITGMQDCV QLNQYTLKDE IGKGSYGVVK 180  
 LAYNENDNTY YAMKVLKSKK LIRQAGFPFR PPRGTRPAP GGCIQPRGPI EQVYQEIALL 240  
 KKLDPNVVK LVEVLDDPNE DHLVMVPELV NQGVMEVPT LKPLESDQAR FYFQDLIKGI 300  
 EYLEYQKIIH RDIKPSNLLV GEDGHKIID FGVSNFPGKS DALLSNTVGT PAFMAPESLS 360  
 ETRKIFSGKA LDVWAMGVTL YCFVFGQCPF MDERIMCLHS KIKSQALEFP DQPDIAEDLK 420  
 60 DLITRMLDKN PESRIVVPBI KLHPVWTRHG AEPLPSEDEN CTLVEVTEEE VENSVKHIPS 480  
 LATVILVKTM IRKRSFGNPF EGSRREERSL SAPGNLLTKK PTRECBLSLE LKEARQRRQP 540  
 PGRPAFRGG GGSALVRGSP CVESWAPAP GSPARMHPLR PEEAMEPE 588

Seq ID NO: C408 Protein Sequence  
 Protein Accession #: NP\_061116.2

65 1 11 21 31 41 51  
 MGLSLPKEKG LILCLWSKFC RWFQRRESWA QSRDEQNLLQ QKRIWESPLL LAAKNDVQA 60  
 LNKLLKYEDC KVPQRGAMGE TALHIAALYD NLEAAMVME AAPLVFEPM TSELYEGQTA 120  
 70 LHIAVNVQNM NLVRALLARR ASVSARATGT AFRRSFCNLI YFGEHPLSFA ACVNSEIIVR 180  
 LLIEHGDNTY AQDSLGNLTVL HILILQPNKT FACQMYNLLL SYDRHGDHLQ PLDLVPHNQG 240  
 LTPFKLAGVE GATVMPQHLM QKRKHTQWTY GPLTSTLYDL TEIDSSGDEQ SLLELIITTK 300  
 KREARQILDQ TPVKELVSLK WKRYGRPYFC MLGAILLYI ICFTMCCIYR PLKPRTNNT 360  
 75 SPRDNTLLQ KLLQEAAYTP KDDIRLVGEL VTVIGAILL LVEVPDIFRM GVTRFFGQTI 420  
 LGGPFHVLIY TYAFMVLVTM VMRLISASGE VVPMSPALVL GWCNVMYFAR GFQMLGPFTI 480  
 MIQKMIPODL MRFCMLMAVV ILGFASAFYI IFQTEDPEEL GHFYDYPMAL FSTFELFTI 540  
 IDGPANYVDV LPFMYISITYA AFATITATLLM LNLIAMMGD THWRVAHERD ELNRAQIVAT 600  
 TVMLERKLPR CLWPRSGICG REYGLGDRWF LRVEDRQDLN RQRIQRYAQA FHTRGSEDL 660  
 80 KDSVEKLELG CFFSPHLSLP MPFSVSRSTSR SSANWERLRQ GTLRRLDRGI INRGLEDGES 720  
 WEYQI 725

Seq ID NO: C409 Protein Sequence  
 Protein Accession #: NP\_068710.1

1 11 21 31 41 51  
 | | | | |  
 MQKVTILGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60  
 RSSSEQAGRG WGSPPPLTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence  
 Protein Accession #: NP\_005962.1

10 1 11 21 31 41 51  
 | | | | |  
 MQKVTILGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60  
 CKCKFGQKSG HHPGETPPLI TPGSAQS 87

Seq ID NO: C411 Protein Sequence  
 Protein Accession #: NP\_004952.1

15 1 11 21 31 41 51  
 | | | | |  
 20 MLSKVLPLVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60  
 TGSRVGKLPE ASRILNTILS NYDHKLRFGI GEKPTVVTV E IAVNSLGPLS ILDMYETIDI 120  
 IPSQTWYDER LCYNDTFESL VLNQNVVSQ L WIPDTFFRNS KRTHHEITM PNQMVRIYKD 180  
 GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIIKWENF KLEINEKNSW 240  
 KLFQDFDTGV SNKTEIITTP VGDFMVTIF FNVSRRFYGV AFQNYVPSSV TTMLSWVSFW 300  
 25 IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIACFPV CFCALLEFAV 360  
 LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TTEGSDGEER 420  
 PSCSAQQPPS PGSPGPRSL CSKLACCWCW KRFFKYFCMV PDCBSTWQQ GRLCIHVYRL 480  
 DNYSRVVPV TFFFNVLVY LVCLNL 506

Seq ID NO: C412 Protein Sequence  
 Protein Accession #: NP\_068819.1

30 1 11 21 31 41 51  
 | | | | |  
 35 MEYTIIDIFS QTWYDERLCY NDTFESLVN GNVVSQWIP DTFFRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTI RMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNSWKL F QDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTIM 180  
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240  
 ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARHQE AFVCQIVTTE 300  
 40 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCWCKRF KKYFCMVPC EGSTWQQARL 360  
 CHVYRLDNY SRVVPVTF FNVLYWLV LNL 393

Seq ID NO: C413 Protein Sequence  
 Protein Accession #: NP\_068822.1

45 1 11 21 31 41 51  
 | | | | |  
 MEYTIIDIFS QTWNSKRTH HEITMPNQMV RIYKDGKVLV YTI RMTIDAGC SLHMLRFPMD 60  
 SHSCPLSPSS FSYPENEMII KWENFKLEIN EKNSWKLQF DFTGVSNKTE IITTPVGDPM 120  
 50 VMTIFFNVSR RFGYVAFQNY VPSSVTIMLS WVSFWIKTES APARTSLGIT SVLTMITLGT 180  
 FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTAKAHSP KLRHPRINSR 240  
 AHARTRARSR ACARQHQEAF VCQIVTTEGS DGEERPSCSA QPPSPGSPF GPRSLCSKLA 300  
 CCEWCKRFKK YFCMVPCBG STWQQGRLCI HVYRLDNYSR VVPVTFVFFF NVLYWLVCLN 360  
 L 361

Seq ID NO: C414 Protein Sequence  
 Protein Accession #: NP\_068830.1

55 1 11 21 31 41 51  
 | | | | |  
 60 MEYTIIDIFS QTWYDERLCY NDTFESLVN GNVVSQWIP DTFFRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTI RMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNSWKL F QDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTIM 180  
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240  
 65 ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARHQE AFVCQIVTTE 300  
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCWCKRF KKYFCMVPC EGSTWQQGR L 360  
 CIEVYRLDNY SRVVPVTF FNVLYWLV LNL 393

Seq ID NO: C415 Protein Sequence  
 Protein Accession #: NP\_068591.1

70 1 11 21 31 41 51  
 | | | | |  
 MPAVSGPGPL FCLLLLLLD HSPETGCPPL RRFYKLSFK GPRLALPGAG IPFWSHHGDA 60  
 ILGLEEVRLT PSMNRNSGAV WSRASVPFSA WEVEVQMRVT GLGRRGAGM AVVYTRGRGH 120  
 75 VGSVLGGLAS WDGIGIFFDS PAEDTQDSPA IRVLASDGH I PSEQPGDGAS QGLGSCWDF 180  
 RNRHPPFRAR IYWGQRLRM SLNSGLTSPD PGEFCVDVGP LLLVPGGFFG VSAATGTLD 240  
 DHDVLSPLTF SLSEPSPEVP PQPFLEMQLL RLARQLEGLW ARLGLGTRED VTPKSDSEAQ 300  
 GEGERLFDLE ETLGRHRRIL QALRGLSKQL AQAERQWKQ LGPPGQARPD GGWALDASCQ 360  
 80 IPSTPGRGGH LSMNLKDSA KVGALLHGQW TLLQALQEMR DAAVRMAEA QVSYLEVFGIE 420  
 HHFLELDHIL GLLQELRGP AKAAAKAPRP PQQPPRASSC LQPGIFLFYL LIQTGVGFGY 480  
 VHFRELKNS LQECSTGSL PLGPAPHTPR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence  
 Protein Accession #: XP\_117036.1

1 11 21 31 41 51  
 5 MERRTRGALG SRRPPPPPLPA LRHLCTGLQA AGMAWPGTLW RHTCQGRAXA AEGPWGLFRP 60  
 HRCPREAGQA PVGSPETQG VAHVCSRARV SVDEREPGGG AYAMRVTPRW KGCHRHSGRT 120  
 VRGSVSWKRP EQAAPETGGR PAVARGSGDG NECCGWG 156

Seq ID NO: C417 Protein Sequence  
 Protein Accession #: XP\_167803.2

10 1 11 21 31 41 51  
 15 MPKGKQKRTA TNKPGGLPGA PGVVGIGGHCL YVLECKCFIK NKTKTHHHKK KNFAAKRNEE 60  
 KLKKKKQKEK KNHTKFFHHT YPLSQQDFLF AKSYFCGNGP CFLWQGLF 108

Seq ID NO: C418 Protein Sequence  
 Protein Accession #: NP\_079056.1

20 1 11 21 31 41 51  
 25 MFRIVERIEM PRHEVYVLLI RNIFLKISII GILCYIWLNT VALSGEECWE TLIGQDIYRL 60  
 LLMDVFSIVL NSFGEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL VWIGIFFCPL 120  
 LPFIQIMIMLF IMFYSKNISL MNMFQPPSKA WRASQMMTFP IFLFFPSFT GVLCITLAI 180  
 WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNIGSVH FFFILTILVL 240  
 IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP SSLVLERREV 300  
 EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 330

Seq ID NO: C419 Protein Sequence  
 Protein Accession #: Eos sequence

30 1 11 21 31 41 51  
 35 MLDSDHVEI IIQVENVSSG VQSHPSNQI FOEKVLLDSS INMVLISIDI DVIDSQTISK 60  
 RNDQKGNQVL RFSTSLNESM SQTLSLECM GIDTPGSSHE TVQQKLIAS LIPMTSRDRI 120  
 KAIRNQPRM EKRNLRRIV DKEKSKQTHR ILQINCCIQC LNSISRAYRR SKNSLSEILN 180  
 SISLWQKTLK IIGKFGTSV LSYFNFLRWL LKFNIFSFIL NFSFIIIPQF TVAKKNTLQF 240  
 TGLEFFTGVG YFRDTVMYIG FYTNSTIQHG NSGASYNMQL AYIFTIGACL TTCFFSLLFS 300  
 MAKYFRNNFI NPHIYSGGIT KLIFCWDFTV THEKAVKLKQ KNLSTEIREN LSELQENSK 360  
 LTFNQLLTRF SAYMVAVVVS TGVAIACCAA VYLAENYLE FLKTHSNPGA VLLLPFVVC 420  
 40 INLAIVCIYS MFRIVERIEM PRHEVYVLLI RNIFLKISII GILCYIWLNT VALSGEECWE 480  
 TLIGQDIYRL LLMDVFSIVL NSFGEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL 540  
 VWIGIFFCPL LPFIQIMIMLF IMFYSKNISL MNMFQPPSKA WRASQMMTFP IFLFFPSFT 600  
 GVLCITLAI WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNIGSVH 660  
 45 FFFILTILVL IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP 720  
 SSLVLERREV EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 760

Seq ID NO: C420 Protein Sequence  
 Protein Accession #: NP\_002241.1

50 1 11 21 31 41 51  
 55 MGGDLVLGLG ALRRRKRLE QEKSLAGWAL VLAGTGIGLM VLHAEMWFG GCSWALYLF 60  
 VKCTISISTF LLLCLIVAFH AKEVQLFMTD NGLRDWRVAL TGRQAAQIVL ELVVCGLHPA 120  
 PVRGPFCQD LGAPLTSQP WPGFLGQGEA LLSLAMLRL YLVPRAVLLR SGVLLNASYR 180  
 SIGALNQVRF RHWFAKLYM NTHPGRLLLG LTLGLMLTTA WVLSVAERQA VNATGHLSDT 240  
 LWLIPITFLT IGYGDVVPQT MWGKIVCLCT GVMGVCCTAL LVAVVARKLE FNKAEKVHN 300  
 FMMDIQYTK MESAAARVQ EAMMFYKTR RKESHAARRH QRKLLAANA FRQVRLGHRK 360  
 60 LREQVNSMVD ISKMHMILVD LQQNLSSSHR ALEKQIDTLA GKLDALTELL STALGPRQLP 420  
 BPSQSK 427

Seq ID NO: C421 Protein Sequence  
 Protein Accession #: NP\_079533.1

65 1 11 21 31 41 51  
 70 MGGKQRDEDD EAYGKPVKYD PSFRGPIKNR SCTDVICCVL FLLFILGYIV VGIWAWLYGD 60  
 PRQVLYPRNS TGAYCGMGEN KDKPYLLLYFN IPSCILSNI ISVAENGLQC PTPQVCVSSC 120  
 PEDPWTVGKN EFSQTVGEVF YTKNRNFCLE GVPWNMTVIT SLQQLCPSE LLPAPALGR 180  
 CFPWTNITPP ALPGITNDIT IQQGISGLID SLNARDISVK IFEDFAQSWY WILVALGVAL 240  
 VLSLLPILLL RLIVAGPLVLV LILGVLGVLA YGIYCNWEEY RVLRDKGASI SOLGETINLS 300  
 AYQSVQETWL AALIVLAVLE AILLVLIFL RQRIRIAIAL LKEASKAVGQ MMSTMFYPLV 360  
 TVFLLICIA YWAMTALYPL PTQPATLGYV LWASNISSPG CEKVPINTSC NPTAHLVNS 420  
 75 CPGLMVFQGS YSSKGLIORS VFNLIQYGV LGLFWTLNWL ALGQCVLAGA PASFYWAFHK 480  
 PQDIPFPPLI SAFIRTLRYH TGSIAFGALI LTLVQIARVI LEYIDHKLRG VQNPVARCIM 540  
 CCPCCLWCL EKFIFLNRN AYIMIAIYK NFCVSAKNAP MLMNRNIVRV VVLDKVTDL 600  
 LFFGKLLVVG GVGVLSPFFP SGRIPGLGKD FKSPLNYYW LPIMTSILGA YVIASGPFV 660  
 80 LFMCVDTLFL CFLEDLERNN GSLDRPYMS KSLKILGKK NEAPPDNKKR KK 712

Seq ID NO: C422 Protein Sequence  
 Protein Accession #: NP\_057264.1

1 11 21 31 41 51  
 MGSNSGQAGR HIYKSLADDG PFDSVEPPKR PTERLIMHSM AMFGREFCYA VEAAYVTPVL 60

LSVGLPSSLY SIVWFLSPIL GFLLQPVVGS ASDHCRSRWG RRRPYILTLG VMMLVGMALY 120  
 LMGATVVAAL IANPRRKLWV AISVTMIGVV LFDFAADFID GPIKAYLFDV CSHQDKEKGL 180  
 HYHALFTGGF GALGYLLGAI DWAHLELGRLL LGTEFQVMPF FSALVLTLCF TVHLCSISEA 240  
 PLTEVAKGIP PQQTPQDPPL SSDGMVEYGS IEKVNGYVNV PELAMQGAKN KNHAEQTRRA 300  
 MTLKSLLRAL VNMPPHYRYL CISHLIGWTA FLNMLFFTD FMGQIVYRGD PYSAHNSTEF 360  
 LIYERGVVEG CWGFCINSVF SSLYSYFQKV LVSYIGLKGL YFTGYLLFGL GTGFIGLFPN 420  
 VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEEKERQQA PGGDPDNSVR KGKMDCATLT 480  
 CMVQLAQILV GGGGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

Seq ID NO: C423 Protein Sequence  
 Protein Accession #: NP\_003264.1

1 11 21 31 41 51  
 | | | | |  
 15 MEGEGGVGGR GTRGFAAKGV WRGRAEERGVP LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60  
 PGKGTGRQRG AWGPRADGCV RRRITLGMPRG SRRDVAPCG PAGSWGARGG RRRDGPSRRR 120  
 RGSATAAARH HVPPAPGGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180  
 AGAGGAGPAR GRSCEGESEWA RRGKGRPGFY QSLGPAVAE GQELKDKSRL RYPINGFOAL 240  
 VLTALLVGLG MSAGLPLGAL PEMLLPLAFV ATLTAFIPSL FLYMKAQVAP VSALAPGNGS 300  
 20 GNPIYDFPLG RELNPRICFF DFKYFCELRP GLIGWVLINL ALLMKEAELR GSPSLAMWL 360  
 NGFQLLYVGD ALWHEEAVLT TMDITHDGFQ FMLAFGDMAN VPFTYSLAQ FLHHPQPLG 420  
 LPMASVICLI NATGYIIFRG ANSQKNTFRK NPSDPRVAGL ETISTATGRK LLVSGWNGMV 480  
 RHPNYLGLDI MALAWSLFCG VSHLLPYFYL LYFTALLVHR EARDERSACR STAWPGRSTA 540  
 25 GVCLTASCPT STEAAPPPQV GHVPTHPPAH PGPAGSTHLG LKGLHPTQP 589

Seq ID NO: C424 Protein Sequence  
 Protein Accession #: NP\_056535.1

1 11 21 31 41 51  
 | | | | |  
 30 MGRLLRAARL PELLSPLLLL LVGGAFLGAC VAGSDEPGPE GLTSTSLDL LLPTGLEPLD 60  
 SEEPSETMGL GAGLGAPGSG FPSEENEESR ILQPPQYFWE EEEELNDSSL DLGPTADYVF 120  
 PDLTEKAGSI ETSQAQELP NLPSPLEPMN LVEPPNHHMP REEEEEEEEE EEREKEEVEK 180  
 35 QEEEEEEELL PVNGSQEAK PQVRDFSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG 240  
 PSLLLPSTVP TTVTPGDQDS TSQEAETVL PAAGLGVEFE APQEAEEAT AGAAGLSGQH 300  
 EEVPALPFPF QTTPAPSGAEH PDDEDPLGRT SASSPLAPGD MELTPSSATL QGEDLNQQLL 360  
 EQAAAEAGSR IPWDSIQVIC KDWSNLAKGN YIILNMTENI DCEVFRQHRG PQLLALVEEV 420  
 LPRHSGSHHG AWHISLSKPS EKEQHLLMTL VGEQGVVPTQ DVLSMLGDIR RSLEEIGION 480  
 40 YSTTSSCQAR ASQVRSDYGT LFVVLVVIGA ICIIIALGL LYNCWQRRLP KLKHVSHGEE 540  
 LRFVENGCHD NPTLDVASDS QSEMKEGHPN LNGGALNGP GSWGALMGK RDPEDSDVFE 600  
 EDTHL 605

Seq ID NO: C425 Protein Sequence  
 Protein Accession #: NP\_001188.1

1 11 21 31 41 51  
 | | | | |  
 45 MSEVRPLSRD ILMETLLYEQ LLEPFTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR 60  
 LACIGDEMVD SLRAPRLAQL SEVAMHSIGL AFIYDQTEDI RDVLRSPMDG FTTLKENIMR 120  
 50 FWRSPNPGSW VSCQVLLAL LLLALLLPL LSGLHLLLK 160

Seq ID NO: C426 Protein Sequence  
 Protein Accession #: AAF76225.1

1 11 21 31 41 51  
 | | | | |  
 55 MATPLPPSP RHLRLRLRL SGLVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPPGA 60  
 HACGFCLOPF QEDQGLCVP RMRPPGGGR PQPRLEDEID FLAQELARKE SGQSTPPLFK 120  
 60 DRQRLPEPAT LGFSARGQL ELGLPSTPGT PTPHTHTSLG SPVSSDPVHM SPLEPRGGQG 180  
 DGLALVLILA FCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ 240  
 RLQAQSAEMH YQHQRQOMLC LERHKEPPEK LDTASSDEEN EDGDFTVYEC PGLAPTGEHE 300  
 VRNPLFDHAA LSAPLPAPSS PPALP 325

Seq ID NO: C427 Protein Sequence  
 Protein Accession #: NP\_004436.1

1 11 21 31 41 51  
 | | | | |  
 70 MVCSLWVLL VSSVLALIEV LLDTTGETSE IGWLTYPFGG WDEVSVLDDQ RRLTRTFEAC 60  
 HVAGAPPGTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTCT ETFTLYYRQA 120  
 EEPDSDPSVS SWHLKRWTKV DTIAADESFP SSSSSSSSSS SAANAVGPHG AGQRAGLQLN 180  
 VKERSFGPLT QRGFVAFQD TGACIALVAV RLFSYTCPAV LRSFASFPET QASGAGGASL 240  
 75 VAAVGTCAVA AEPEEDGVGG QAGGSFPRHL CNBEGKMWVA VGGCRCPQGY QPARGDKACQ 300  
 ACPRGLYKSS AGNAPCSPCP ARSHAPNPAA PFCPCLEGFY RASSDPPEAP CTGPSPAPQE 360  
 LWFEVQGSAL MLHWRLPREL GGRGDLLENV VCCECEGRQE PASGGGGTCH RCRDEVHFD 420  
 RQRGLTESRV LVGGRLRAHV YILEVQAVNG VSELSPPDPQ AAANVSTSH EVPSAVPVVH 480  
 QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSETNTA TVTQLSPGHI 540  
 YGFQVRARTA AGHGPYGGKV YFQTLQOGL SSQPLERLSL VIGSILGALA FLLLAITVL 600  
 80 AVVFQRKRRG TGYTEQLQY SSPGLGVKYY IDPSTYEDPC QAIRELAREV DPAYIKIEEV 660  
 IGTGSPGEVR QGRLLQPRGR EQTVAIQALW AGGAESLQMT FLGRAAVLQG FOHPNILRL 720  
 GVVTKSRFLM VLTEFPELGP LDSFLRQREG QFSSILQIVM QRGVAAAMQY LSSFAFVHR 780  
 LSAHSVLVNS HLCVKVARLG HSPQGPSCLL RWAAPVIAH GKHTTSSDVN SFGILMWEVM 840  
 SYGERPYNDM SEQEVINAIE QEFRLPPPG CPGHLHLLML DTWQKDRAR PHFDQLVAAF 900  
 DKMIRKPDTL QAGGDPGERP SQALLTPVAL DFPCLDSPQA WLSAIGLECY QDNFSKFGLC 960



TFSDVAQLSL EDLPALGITL AGHQKLLHH IQLLQHLRQ QGSVEV

1006

Seq ID NO: C428 Protein Sequence  
Protein Accession #: XP\_043340.2

1 11 21 31 41 51  
 MPFDFRRFDI YRKVPKDLTQ PTYTGAIIIS CCCLFILFLF LSELTGFITT EVVNELYVDD 60  
 PDKDSGGKID VSLNISLPLN HCELVLGLDIQ DEMGRHEVGH IDNSMKIPLN NGAGCRFEGQ 120  
 FSINKVPGNF HVSTHSATAQ PQNPDMTHVI HKLSFGDTLQ VQNIHGAPNA LGGADRLTSN 180  
 PLASHDYILK IVPITYEDKS GKQRYSYQYT VANKEYVAYS HTGRIIPAIN FRYDLSPITV 240  
 KYTERRQPLY RPITITICAI GGTFTVAGIL DSCIFTASEA WKIKQLGKMH 290

Seq ID NO: C429 Protein Sequence  
Protein Accession #: NP\_002142.1

1 11 21 31 41 51  
 MAQKEGGRTV PCCSRPKVAA LTAGTLLLLT AIGAASWAIV AVLLRSQDEP LYPVQVSSAD 60  
 ARLMVFDKTE GTWRLLCSSR SNARVAGLSC EEMGFRLALT HSELDVRTAG ANGTSGFFCV 120  
 DEGRLPHTQR LLEVISVDCD PRGRFLAaic QDCGRRLFPV DRIVGGRTS LGRNFWQVSL 180  
 RYDGAHLCCG SLLSGDWLVT AAHCFPERNR VLSRWRFVAG AVAQASPHGL QLGVAQVYH 240  
 GGYLPFRDPN SEENSNDIAL VHLSSPLPLT EYIQPVCLPA AGQALVDGKI CTVTGWGMTQ 300  
 YYGQAGVLQ EARVPIISND VCGADFYGN QIKPKMFCAG YPEGGIDACQ GDSGGPFVCE 360  
 DSISRTPPWR LCGIVSWGTV CALAQKPGVY TKVSDFREWI FQAIKTHSEA SGMVTQL 417

Seq ID NO: C430 Protein Sequence  
Protein Accession #: BAA92562.1

1 11 21 31 41 51  
 METTVLSGIN FEYKGMTGWE VAGDHIYTAA GASDNDFMIL TLVVPGRFP P QSMVADTENK 60  
 EVARITFVFE TLCSVNCELY PMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTTSFTWA 120  
 FQRTTFHEAS RKYTNDVAKI YSINVNVNM GVASYCRPCA LEASDVGSSC TSCPAGYIID 180  
 RDSGTCHSCP PNTILKAHQF YGVQACVPCG PGTKNNKIHS LCYNDCITFSR NTPTRTFNIN 240  
 FSALANTVTL AGGSPSTSKG LKYFHHFTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK 300  
 SITAYYCAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESIGI 360  
 PDVIFYRNSN DVTQSCSSGR STTIRVRCSP QKTVPGLSLP PGTCSDGTCD GCNHFHLES 420  
 AAACPLCSVA DYHAISSCV AGIQKTTYVW REPKLCSGGI SLPEQRVTIC KTIDFWLKV 480  
 ISAGTCTAIL LTVLTCTYFK KQKLEYKYS KLVNMATLKD CDLPAADESCA IMEGEDVEDD 540  
 LIFTSKSLF GKIKSFTSQ PAPVTISLSE DS 572

Seq ID NO: C431 Protein Sequence  
Protein Accession #: NP\_004855.1

1 11 21 31 41 51  
 MPQGELETVN GSQMLLVLLV LSWLPHGGAL SLAEASRAS PGPSELHSED SRFRELKRY 60  
 EDLLTLRLAN QSWEDSNIDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLEASRL 120  
 HRALFRLSPT ASRSWVTPRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSARPQL 180  
 ELHLRQQAAR GRRRARARNG DDCPLGPGRC CRLHTVRA SL EDLGWADWVL SPREVQVIMC 240  
 IGACPSQFRA ANMHAQIKTS LHLKPDTEP APCCVPASYN PMVLIQKITT GVSQTYDDL 300  
 LAKDCHCI 308

Seq ID NO: C433 Protein Sequence  
Protein Accession #: NP\_443090.1

1 11 21 31 41 51  
 MEDPSGAREP RARPRERDPG RRPHPDQGR HTDRPRDRPG PRRKRSSDGN RRRDGD RDPK 60  
 RDQERDGNRD RNRDRERERE RERDPDRGFR RDTHRDAGRP AGEHGVWEKP RQSRTRDGR 120  
 GLTWDAAPP GPAPWEAPEP PQPQKGDGPG RRRPESEPPS ERYLPSTPRP GREVEEYQS 180  
 EAEGLECHK CYLCTGRAC CQMLEVLLNL LILACSSVS SSGGYTGIT SLGGIYYQF 240  
 GGAYSGFDGA DGEKAQQLDV QFYQLKLPV TVAMACSGAL TALCCLFVAM GVLRVPWCEP 300  
 LLLVTEGLLD MLIAGGYIPA LYFYHYLSA AYGSFVCKER QALYQSKGYS GFGCSFHGAD 360  
 IGAGIFAALG IUVFALGAVL AIKGYRKVRK LKEKPAEMFE F 401

Seq ID NO: C435 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPNWPGH DQDHVHIGQ 60  
 GKTLTLLTSSA TVYSIHISEG GKLVIKDHE PIVLRTRHIL IDNGGELHAG SALCPFGNF 120  
 TIILYGRADE GIQDPFYGL KYIGVGKGA LELHGQKLS WTLNKLTHP GGMAEGGYFF 180  
 ERSWGHGRVI VHVDPKSGT VIHSDRFDY RSKKESERLV QYLNVPDGR ILSVAVNDEG 240  
 SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVMGNPSS SVEDHIEYHG HRGSAARVF 300  
 KLPQTEHGEY FNVSLSEENV QDVWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360  
 IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYVR FLGKFPVRPK LTVTIDTNVN 420  
 STILNLEDNV QSNKPGDTLV IASTDYSMY AEEFQVLPGR SCAPNQVKVA GKPMYLHIGE 480  
 EIDGVDMRAE VGLLSRNIIV MGEMEDKCYP YRNHCNFFD FDTFGGHIKF ALGFKAAHLE 540  
 GTELKMGQQ LVGQYPIHF LAGDVDERGG YDPTIYIDL SIHHTFSRCV TVHGSNGLLI 600  
 KDVVGVNSIG RCFETEDGPE ERNTFDHCLG LLVKSGLTLP SDRDSKMKCM ITEDSYPGYI 660  
 FKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWPIFH HVPTGPSVGM YSPGYSEHIP 720

LGKFYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGGD	VWLDSCFRG	EAQEGFLLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLLK	LVTGSPFAH	VSLAHS				866

5

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein  
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1           1.       A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%  
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,  
4 thereby determining the presence or absence of said pathological cell.
- 1           2.       The method of Claim 1, wherein:  
2           a) said pathology is described in Table 1, including a cancer; and/or  
3           b) said biological sample comprises isolated nucleic acids.
- 1           3.       The method of Claim 1, wherein said biological sample is tissue from an organ  
2 which is affected by said pathology of Table 1, including a cancer.
- 1           4.       The method of Claim 2, wherein said nucleic acids are mRNA
- 1           5.       The method of Claim 2:  
2           a) further comprising a step of amplifying nucleic acids before said step of detecting  
3           said nucleic acid; or  
4           b) where said detecting is of a protein encoded by said nucleic acid.
- 1           6.       The method of Claim 1, wherein said nucleic acid comprises a sequence as  
2 described in Tables 2A-80.
- 1           7.       The method of Claim 2, wherein:  
2           a) said detecting step is carried out by:  
3           i) using a labeled nucleic acid probe;  
4           ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence  
5           as described in Tables 2A-80; or  
6           iii) detecting a polypeptide encoded by said nucleic acid; or  
7           b) said patient is:  
8           i) undergoing a therapeutic regimen to treat said pathology of Table 1; or  
9           ii) is suspected of having said pathology or cancer.
- 1           8.       An isolated nucleic acid molecule comprising a sequence as described in  
2 Tables 2A-80.

- 1           9.     The nucleic acid molecule of Claim 8, which is labeled.
- 1           10.    An expression vector comprising the nucleic acid of Claim 8.
- 1           11.    A host cell comprising the expression vector of Claim 10.
- 1           12.    An isolated polypeptide which is encoded by a nucleic acid molecule  
2 comprising a sequence as described in Tables 2A-80.
- 1           13.    An antibody that specifically binds a polypeptide of Claim 12.
- 1           14.    The antibody of Claim 13:  
2 a) conjugated to an effector component;  
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a  
4 cytotoxic chemical;  
5 c) which is an antibody fragment; or  
6 d) which is a humanized antibody.
- 1           15.    A method for specifically targeting a compound to a pathological cell in a  
2 patient, said method comprising administering to said patient an antibody of Claim 13,  
3 thereby providing said targetting.
- 1           16.    A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1           17.    The method of Claim 16, wherein:  
2 a) said antibody is conjugated to:  
3 i) an effector component; or  
4 ii) a fluorescent label; or  
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1           18.    A method for identifying a compound that modulates a pathology-associated  
2 polypeptide, said method comprising the steps of:

- 3 a) contacting said compound with a pathology-associated polypeptide, said  
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence  
5 at least 80% identical to a sequence as described in Tables 2A-80; and  
6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a  
3 cell isolated therefrom; and  
4 b) comparing the level of gene expression of a polynucleotide that selectively  
5 hybridizes to a sequence at least 80% identical to a sequence as described in  
6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said  
7 polynucleotide in a control cell or mammal, wherein a test compound that  
8 modulates said level of expression of the polynucleotide is a candidate for the  
9 treatment of said pathology.  
10

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International Bureau



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60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
60/355,250	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.

WO 2003/042661 A3

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : C12Q 1/68; C07H 21/02, 21/04

US CL : 435/6; 536/23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
WEST, PubMed**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SATO, H. et al., Cloning and Expression of a Plasma Membrane Cystine/Glutamate Exchange Transporter Composed of Two Distinct Proteins, J. Biol. Chem. 23 April 1999, Vol. 247, No. 17, pp. 11455-11458.	1-7
A	KIM, J. Y. et al., Human cystine/glutamate transporter: cDNA cloning and upregulation by oxidative stress in glioma cells, B.B. Acta. June 2001, Vol. 1512, pp. 335-344.	1-7

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

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# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO: 19

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

PCT/US02/36810

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, drawn to a special technical feature of a method for determining presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

Group II, claim(s) 8-11, drawn to a special technical feature of an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, expression vector comprising the nucleic acid and a host cell comprising the expression vector.

Group III, claim(s) 12, drawn to a special technical feature of an isolated polypeptide which is encoded by an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

Group IV, claim(s) 13, 14, drawn to a special technical feature of an antibody which specifically binds to polypeptide of claim 12.

Group V, claim(s) 15, drawn to a special technical feature of a method for specifically targeting a compound to a pathological cell in a patient, comprising administering to a patient an antibody of claim 13.

Group VI, claim(s) 16, 17, drawn to a special technical feature of a method for determining the presence or absence of a pathological cell in a patient, comprising contacting a biological sample with an antibody of claim 13.

Group VII, claim(s) 18, drawn to a special technical feature of a method for identifying a compound that modulates a pathology-associated polypeptide by contacting the compound with a pathology-associated polypeptide encoded by a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 and determining the functional effect of the compound on the polypeptide.

Group VIII, claim(s) 19, drawn to a special technical feature of a drug screening assay comprising the steps of: administering a test compound to a mammal having pathology of Table 1 or a cell isolated therefrom; comparing the level of gene expression of a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal.

The inventions listed as Groups I-VIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: claim 8 is anticipated by a sequence with accession No. BE440042 (Table 2A, first entry) (July 25, 2000), therefore there is no contribution of claim 8 over prior art.

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**Richard** [US/US]; 22643 Woodridge Court, Cupertino, CA 95014 (US). **WATSON, Susan, R.** [GB/US]; 805 Balra Drive, El Cerrito, CA 94530 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

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60/397,775	22 July 2002 (22.07.2002)	US
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



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